

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
19 July 2001 (19.07.2001)

PCT

(10) International Publication Number
WO 01/51633 A2

(51) International Patent Classification⁷: C12N 15/12,
C07K 14/47, C12N 5/10, 5/08, 1/21, C07K 16/18, G01N
33/68, C07K 19/00, C12N 15/11, A61K 38/17, C12Q 1/68

(21) International Application Number: PCT/US01/01574

(22) International Filing Date: 16 January 2001 (16.01.2001)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
09/483,672 14 January 2000 (14.01.2000) US

(71) Applicant (for all designated States except US): **CORIXA CORPORATION** [US/US]; 1124 Columbia Street, Suite 200, Seattle, WA 98104 (US).

(72) Inventors; and

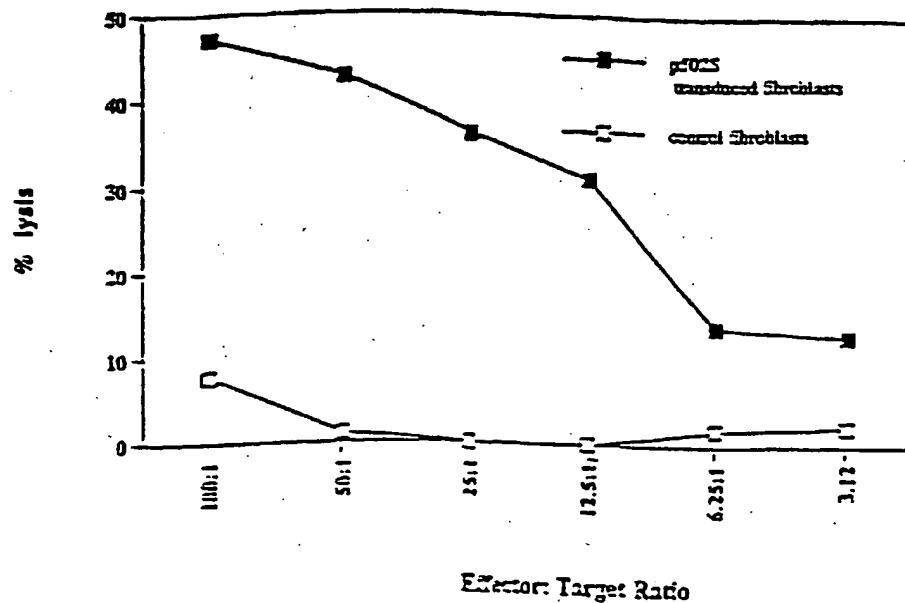
(75) Inventors/Applicants (for US only): **XU, Jiangchun** [US/US]; 15805 S.E. 43rd Place, Bellevue, WA 98006 (US). **DILLON, Davin, C.** [US/US]; 18112 N.W. Montreux Drive, Issaquah, WA 98027 (US). **MITCHAM,**

Jennifer, L. [US/US]; 16677 N.E. 88th Street, Redmond, WA 98052 (US). **HARLOCKER, Susan, L.** [US/US]; 7522 13th Avenue W., Seattle, WA 98117 (US). **JIANG, Yuqiu** [CN/US]; 5001 South 232nd Street, Kent, WA 98032 (US). **REED, Steven, G.** [US/US]; 2843 122nd Place N.E., Bellevue, WA 98005 (US). **KALOS, Michael, D.** [US/US]; 8116 Dayton Ave. N., Seattle, WA 98103 (US). **FANGER, Gary, Richard** [US/US]; 15906 29th Drive S.E., Mill Creek, WA 98012 (US). **DAY, Craig, H.** [US/US]; 11501 Stone Ave. N., C122, Seattle, WA 98133 (US). **REITER, Marc, W.** [US/US]; 33402 N.E. 43rd Place, Carnation, WA 98104 (US). **STOLK, John, A.** [US/US]; 7436 Northeast 144th Place, Bothell, WA 98011 (US). **SKEIKY, Yasir, A.W.** [LB/US]; 15106 S.E. 47th Place, Bellevue, WA 98006 (US). **WANG, Aijun** [CN/US]; 3106 213th Place S.E., Issaquah, WA 98029 (US). **MEAGHER, Madeleine, Joy** [US/US]; 507 N.E. 71st, #1, Seattle, WA 98115 (US).

(74) Agents: **POTTER, Jane, E.R.**; Seed Intellectual Property Law Group PLLC, Suite 6300, 701 Fifth Avenue, Seattle, WA 98104-7092 et al. (US).

[Continued on next page]

(54) Title: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF PROSTATE CANCER



(57) Abstract: Compositions and methods for the therapy and diagnosis of cancer, particularly prostate cancer, are disclosed. Illustrative compositions comprise one or more prostate-specific polypeptides, immunogenic portions thereof, polynucleotides that encode such polypeptides, antigen presenting cell that expresses such polypeptides, and T cells that are specific for cells expressing such polypeptides. The disclosed compositions are useful, for example, in the diagnosis, prevention and/or treatment of diseases, particularly prostate cancer.

WO 01/51633 A2



(81) **Designated States (national):** AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published:

— without international search report and to be republished upon receipt of that report

(84) **Designated States (regional):** ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF PROSTATE CANCER

5 TECHNICAL FIELD OF THE INVENTION

The present invention relates generally to therapy and diagnosis of cancer, such as prostate cancer. The invention is more specifically related to polypeptides, comprising at least a portion of a prostate-specific protein, and to polynucleotides encoding such polypeptides. Such polypeptides and polynucleotides
10 are useful in pharmaceutical compositions, *e.g.*, vaccines, and other compositions for the diagnosis and treatment of prostate cancer.

BACKGROUND OF THE INVENTION

Cancer is a significant health problem throughout the world. Although
Cancer is a significant health problem throughout the world. Although advances have
15 been made in detection and therapy of cancer, no vaccine or other universally successful method for prevention or treatment is currently available. Current therapies, which are generally based on a combination of chemotherapy or surgery and radiation, continue to prove inadequate in many patients.

Prostate cancer is the most common form of cancer among males, with
20 an estimated incidence of 30% in men over the age of 50. Overwhelming clinical evidence shows that human prostate cancer has the propensity to metastasize to bone, and the disease appears to progress inevitably from androgen dependent to androgen refractory status, leading to increased patient mortality. This prevalent disease is currently the second leading cause of cancer death among men in the U.S.

25 In spite of considerable research into therapies for the disease, prostate cancer remains difficult to treat. Commonly, treatment is based on surgery and/or radiation therapy, but these methods are ineffective in a significant percentage of cases. Two previously identified prostate specific proteins - prostate specific antigen (PSA)

and prostatic acid phosphatase (PAP) - have limited therapeutic and diagnostic potential. For example, PSA levels do not always correlate well with the presence of prostate cancer, being positive in a percentage of non-prostate cancer cases, including benign prostatic hyperplasia (BPH). Furthermore, PSA measurements correlate with
5 prostate volume, and do not indicate the level of metastasis.

In spite of considerable research into therapies for these and other cancers, prostate cancer remains difficult to diagnose and treat effectively. Accordingly, there is a need in the art for improved methods for detecting and treating such cancers. The present invention fulfills these needs and further provides other related advantages.

10 SUMMARY OF THE INVENTION

In one aspect, the present invention provides polynucleotide compositions comprising a sequence selected from the group consisting of:

(a) sequences provided in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524,
15 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-626, 630, 631, 634, 636, 639-655, 674, 680, 681, 711, 713, 716, 720-722, 735, 737-739, 751, 753, 764, 765, 773-776 and 786-788;

(b) complements of the sequences provided in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382
20 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-626, 630, 631, 634, 636, 639-655, 674, 680, 681, 711, 713, 716, 720-722, 735, 737-739, 751, 753, 764, 765, 773-776 and 786-788;

(c) sequences consisting of at least 20 contiguous residues of a sequence provided in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315,
25 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-626, 630, 631, 634, 636, 639-655, 674, 680, 681, 711, 713, 716, 720-722, 735, 737-739, 751, 753, 764, 765, 773-776 and 786-788;

(d) sequences that hybridize to a sequence provided in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375,

381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-626, 630, 631, 634, 636, 639-655, 674, 680, 681, 711, 713, 716, 720-722, 735, 737-739, 751, 753, 764, 765, 773-776 and 786-788, under moderately stringent conditions;

5 (e) sequences having at least 75% identity to a sequence of SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-626, 630, 631, 634, 636, 639-655, 674, 680, 681, 711, 713, 716, 720-722, 735, 737-739, 751, 753, 764, 765, 773-776 and 786-788;

10 (f) sequences having at least 90% identity to a sequence of SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-626, 630, 631, 634, 636, 639-655, 674, 680, 681, 711, 713, 716, 720-722, 735, 737-739, 751, 753, 764, 765, 773-776 and 786-788; and

15 (g) degenerate variants of a sequence provided in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-626, 630, 631, 634, 636, 639-655, 674, 680, 681, 711, 713, 716, 720-722, 735, 737-739, 751, 753, 764, 765, 773-776 and 786-788.

20 In one preferred embodiment, the polynucleotide compositions of the invention are expressed in at least about 20%, more preferably in at least about 30%, and most preferably in at least about 50% of prostate tissue samples tested, at a level that is at least about 2-fold, preferably at least about 5-fold, and most preferably at least about 10-fold higher than that for other normal tissues.

25 The present invention, in another aspect, provides polypeptide compositions comprising an amino acid sequence that is encoded by a polynucleotide sequence described above.

The present invention further provides polypeptide compositions comprising an amino acid sequence selected from the group consisting of sequences
30 recited in SEQ ID NO: 112-114, 172, 176, 178, 327, 329, 331, 336, 339, 376-380, 383,

477-483, 496, 504, 505, 519, 520, 522, 525, 527, 532, 534, 537-551, 553-568, 573-586, 588-590, 592, 627-629, 632, 633, 635, 637, 638, 656-671, 675, 683, 684, 710, 712, 714, 715, 717-719, 723-734, 736, 740-750, 752, 754, 755, 766-772, 777-785 and 789-791.

In certain preferred embodiments, the polypeptides and/or
5 polynucleotides of the present invention are immunogenic, *i.e.*, they are capable of eliciting an immune response, particularly a humoral and/or cellular immune response, as further described herein.

The present invention further provides fragments, variants and/or derivatives of the disclosed polypeptide and/or polynucleotide sequences, wherein the
10 fragments, variants and/or derivatives preferably have a level of immunogenic activity of at least about 50%, preferably at least about 70% and more preferably at least about 90% of the level of immunogenic activity of a polypeptide sequence set forth in SEQ ID NO: 112-114, 172, 176, 178, 327, 329, 331, 336, 339, 376-380, 383, 477-483, 496, 504, 505, 519, 520, 522, 525, 527, 532, 534, 537-551, 553-568, 573-586, 588-590, 592, 627-
15 629, 632, 633, 635, 637, 638, 656-671, 675, 683, 684, 710, 712, 714, 715, 717-719, 723-734, 736, 740-750, 752, 754, 755, 766-772, 777-785 or 789-791, or a polypeptide sequence encoded by a polynucleotide sequence set forth in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-626,
20 630, 631, 634, 636, 639-655, 674, 680, 681, 711, 713, 716, 720-722, 735, 737-739, 751, 753, 764, 765, 773-776 and 786-788.

The present invention further provides polynucleotides that encode a polypeptide described above, expression vectors comprising such polynucleotides and host cells transformed or transfected with such expression vectors.

25 Within other aspects, the present invention provides pharmaceutical compositions comprising a polypeptide or polynucleotide as described above and a physiologically acceptable carrier.

Within a related aspect of the present invention, pharmaceutical compositions, *e.g.*, vaccine compositions, are provided for prophylactic or therapeutic
30 applications. Such compositions generally comprise an immunogenic polypeptide or

polynucleotide of the invention and an immunostimulant, such as an adjuvant, together with a physiologically acceptable carrier.

The present invention further provides pharmaceutical compositions that comprise: (a) an antibody or antigen-binding fragment thereof that specifically binds to
5 a polypeptide of the present invention, or a fragment thereof; and (b) a physiologically acceptable carrier.

Within further aspects, the present invention provides pharmaceutical compositions comprising: (a) an antigen presenting cell that expresses a polypeptide as described above and (b) a pharmaceutically acceptable carrier or excipient. Illustrative
10 antigen presenting cells include dendritic cells, macrophages, monocytes, fibroblasts and B cells.

Within related aspects, pharmaceutical compositions are provided that comprise: (a) an antigen presenting cell that expresses a polypeptide as described above and (b) an immunostimulant.

15 The present invention further provides, in other aspects, fusion proteins that comprise at least one polypeptide as described above, as well as polynucleotides encoding such fusion proteins, typically in the form of pharmaceutical compositions, *e.g.*, vaccine compositions, comprising a physiologically acceptable carrier and/or an immunostimulant. The fusions proteins may comprise multiple immunogenic
20 polypeptides or portions/variants thereof, as described herein, and may further comprise one or more polypeptide segments for facilitating and/or enhancing the expression, purification and/or immunogenicity of the polypeptide(s).

Within further aspects, the present invention provides methods for stimulating an immune response in a patient, preferably a T cell response in a human
25 patient, comprising administering a pharmaceutical composition described herein. The patient may be afflicted with prostate cancer, in which case the methods provide treatment for the disease, or a patient considered to be at risk for such a disease may be treated prophylactically.

Within further aspects, the present invention provides methods for
30 inhibiting the development of a cancer in a patient, comprising administering to a

patient a pharmaceutical composition as recited above. The patient may be afflicted with prostate cancer, in which case the methods provide treatment for the disease, or a patient considered to be at risk for such a disease may be treated prophylactically.

The present invention further provides, within other aspects, methods for
5 removing tumor cells from a biological sample, comprising contacting a biological sample with T cells that specifically react with a polypeptide of the present invention, wherein the step of contacting is performed under conditions and for a time sufficient to permit the removal of cells expressing the polypeptide from the sample.

Within related aspects, methods are provided for inhibiting the
10 development of a cancer in a patient, comprising administering to a patient a biological sample treated as described above.

Methods are further provided, within other aspects, for stimulating and/or expanding T cells specific for a polypeptide of the present invention, comprising contacting T cells with one or more of: (i) a polypeptide as described above; (ii) a
15 polynucleotide encoding such a polypeptide; and (iii) an antigen presenting cell that expresses such a polypeptide; under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells. Isolated T cell populations comprising T cells prepared as described above are also provided.

Within further aspects, the present invention provides methods for
20 inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a T cell population as described above.

The present invention further provides methods for inhibiting the development of a cancer in a patient, comprising the steps of: (a) incubating CD4⁺ and/or CD8⁺ T cells isolated from a patient with one or more of: (i) a polypeptide
25 comprising at least an immunogenic portion of polypeptide disclosed herein; (ii) a polynucleotide encoding such a polypeptide; and (iii) an antigen-presenting cell that expressed such a polypeptide; and (b) administering to the patient an effective amount of the proliferated T cells, thereby inhibiting the development of a cancer in the patient. Proliferated cells may, but need not, be cloned prior to administration to the patient.

Within further aspects, the present invention provides methods for determining the presence or absence of a cancer, preferably a prostate cancer, in a patient comprising: (a) contacting a biological sample obtained from a patient with a binding agent that binds to a polypeptide as recited above; (b) detecting in the sample an amount of polypeptide that binds to the binding agent; and (c) comparing the amount of polypeptide with a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient. Within preferred embodiments, the binding agent is an antibody, more preferably a monoclonal antibody.

The present invention also provides, within other aspects, methods for monitoring the progression of a cancer in a patient. Such methods comprise the steps of: (a) contacting a biological sample obtained from a patient at a first point in time with a binding agent that binds to a polypeptide as recited above; (b) detecting in the sample an amount of polypeptide that binds to the binding agent; (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and (d) comparing the amount of polypeptide detected in step (c) with the amount detected in step (b), and therefrom monitoring the progression of the cancer in the patient.

The present invention further provides, within other aspects, methods for determining the presence or absence of a cancer in a patient, comprising the steps of: (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide of the present invention; (b) detecting in the sample a level of a polynucleotide, preferably mRNA, that hybridizes to the oligonucleotide; and (c) comparing the level of polynucleotide that hybridizes to the oligonucleotide with a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient. Within certain embodiments, the amount of mRNA is detected via polymerase chain reaction using, for example, at least one oligonucleotide primer that hybridizes to a polynucleotide of the present invention, or a complement of such a polynucleotide. Within other embodiments, the amount of mRNA is detected using a hybridization technique, employing an oligonucleotide probe that hybridizes to an inventive polynucleotide, or a complement of such a polynucleotide.

In related aspects, methods are provided for monitoring the progression of a cancer in a patient, comprising the steps of: (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide of the present invention; (b) detecting in the sample an amount of a polynucleotide that
5 hybridizes to the oligonucleotide; (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and (d) comparing the amount of polynucleotide detected in step (c) with the amount detected in step (b), and therefrom monitoring the progression of the cancer in the patient.

Within further aspects, the present invention provides antibodies, such as
10 monoclonal antibodies, that bind to a polypeptide as described above, as well as diagnostic kits comprising such antibodies. Diagnostic kits comprising one or more oligonucleotide probes or primers as described above are also provided.

These and other aspects of the present invention will become apparent upon reference to the following detailed description and attached drawings. All
15 references disclosed herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

BRIEF DESCRIPTION OF THE DRAWINGS AND SEQUENCE IDENTIFIERS

Figure 1 illustrates the ability of T cells to kill fibroblasts expressing the representative prostate-specific polypeptide P502S, as compared to control fibroblasts.
20 The percentage lysis is shown as a series of effector:target ratios, as indicated.

Figures 2A and 2B illustrate the ability of T cells to recognize cells expressing the representative prostate-specific polypeptide P502S. In each case, the number of γ -interferon spots is shown for different numbers of responders. In Figure 2A, data is presented for fibroblasts pulsed with the P2S-12 peptide, as compared to
25 fibroblasts pulsed with a control E75 peptide. In Figure 2B, data is presented for fibroblasts expressing P502S, as compared to fibroblasts expressing HER-2/*neu*.

Figure 3 represents a peptide competition binding assay showing that the P1S#10 peptide, derived from P501S, binds HLA-A2. Peptide P1S#10 inhibits HLA-A2 restricted presentation of fluM58 peptide to CTL clone D150M58 in TNF release

bioassay. D150M58 CTL is specific for the HLA-A2 binding influenza matrix peptide fluM58.

Figure 4 illustrates the ability of T cell lines generated from P1S#10 immunized mice to specifically lyse P1S#10-pulsed Jurkat A2Kb targets and P501S-
5 transduced Jurkat A2Kb targets, as compared to EGFP-transduced Jurkat A2Kb. The percent lysis is shown as a series of effector to target ratios, as indicated.

Figure 5 illustrates the ability of a T cell clone to recognize and specifically lyse Jurkat A2Kb cells expressing the representative prostate-specific polypeptide P501S, thereby demonstrating that the P1S#10 peptide may be a naturally
10 processed epitope of the P501S polypeptide.

Figures 6A and 6B are graphs illustrating the specificity of a CD8⁺ cell line (3A-1) for a representative prostate-specific antigen (P501S). Figure 6A shows the results of a ⁵¹Cr release assay. The percent specific lysis is shown as a series of effector:target ratios, as indicated. Figure 6B shows the production of interferon-
15 gamma by 3A-1 cells stimulated with autologous B-LCL transduced with P501S, at varying effector:target ratios as indicated.

Figure 7 is a Western blot showing the expression of P501S in baculovirus.

Figure 8 illustrates the results of epitope mapping studies on P501S.

20 Figure 9 is a schematic representation of the P501S protein showing the location of transmembrane domains and predicted intracellular and extracellular domains.

Figure 10 is a genomic map showing the location of the prostate genes P775P, P704P, B305D, P712P and P774P within the Cat Eye Syndrome region of
25 chromosome 22q11.2

Figure 11 shows the results of an ELISA assay to determine the specificity of rabbit polyclonal antisera raised against P501S.

SEQ ID NO: 1 is the determined cDNA sequence for F1-13

SEQ ID NO: 2 is the determined 3' cDNA sequence for F1-12

30 SEQ ID NO: 3 is the determined 5' cDNA sequence for F1-12

SEQ ID NO: 4 is the determined 3' cDNA sequence for F1-16
SEQ ID NO: 5 is the determined 3' cDNA sequence for H1-1
SEQ ID NO: 6 is the determined 3' cDNA sequence for H1-9
SEQ ID NO: 7 is the determined 3' cDNA sequence for H1-4
5 SEQ ID NO: 8 is the determined 3' cDNA sequence for J1-17
SEQ ID NO: 9 is the determined 5' cDNA sequence for J1-17
SEQ ID NO: 10 is the determined 3' cDNA sequence for L1-12
SEQ ID NO: 11 is the determined 5' cDNA sequence for L1-12
SEQ ID NO: 12 is the determined 3' cDNA sequence for N1-1862
10 SEQ ID NO: 13 is the determined 5' cDNA sequence for N1-1862
SEQ ID NO: 14 is the determined 3' cDNA sequence for J1-13
SEQ ID NO: 15 is the determined 5' cDNA sequence for J1-13
SEQ ID NO: 16 is the determined 3' cDNA sequence for J1-19
SEQ ID NO: 17 is the determined 5' cDNA sequence for J1-19
15 SEQ ID NO: 18 is the determined 3' cDNA sequence for J1-25
SEQ ID NO: 19 is the determined 5' cDNA sequence for J1-25
SEQ ID NO: 20 is the determined 5' cDNA sequence for J1-24
SEQ ID NO: 21 is the determined 3' cDNA sequence for J1-24
SEQ ID NO: 22 is the determined 5' cDNA sequence for K1-58
20 SEQ ID NO: 23 is the determined 3' cDNA sequence for K1-58
SEQ ID NO: 24 is the determined 5' cDNA sequence for K1-63
SEQ ID NO: 25 is the determined 3' cDNA sequence for K1-63
SEQ ID NO: 26 is the determined 5' cDNA sequence for L1-4
SEQ ID NO: 27 is the determined 3' cDNA sequence for L1-4
25 SEQ ID NO: 28 is the determined 5' cDNA sequence for L1-14
SEQ ID NO: 29 is the determined 3' cDNA sequence for L1-14
SEQ ID NO: 30 is the determined 3' cDNA sequence for J1-12
SEQ ID NO: 31 is the determined 3' cDNA sequence for J1-16
SEQ ID NO: 32 is the determined 3' cDNA sequence for J1-21
30 SEQ ID NO: 33 is the determined 3' cDNA sequence for K1-48

SEQ ID NO: 34 is the determined 3' cDNA sequence for K1-55
SEQ ID NO: 35 is the determined 3' cDNA sequence for L1-2
SEQ ID NO: 36 is the determined 3' cDNA sequence for L1-6
SEQ ID NO: 37 is the determined 3' cDNA sequence for N1-1858
5 SEQ ID NO: 38 is the determined 3' cDNA sequence for N1-1860
SEQ ID NO: 39 is the determined 3' cDNA sequence for N1-1861
SEQ ID NO: 40 is the determined 3' cDNA sequence for N1-1864
SEQ ID NO: 41 is the determined cDNA sequence for P5
SEQ ID NO: 42 is the determined cDNA sequence for P8
10 SEQ ID NO: 43 is the determined cDNA sequence for P9
SEQ ID NO: 44 is the determined cDNA sequence for P18
SEQ ID NO: 45 is the determined cDNA sequence for P20
SEQ ID NO: 46 is the determined cDNA sequence for P29
SEQ ID NO: 47 is the determined cDNA sequence for P30
15 SEQ ID NO: 48 is the determined cDNA sequence for P34
SEQ ID NO: 49 is the determined cDNA sequence for P36
SEQ ID NO: 50 is the determined cDNA sequence for P38
SEQ ID NO: 51 is the determined cDNA sequence for P39
SEQ ID NO: 52 is the determined cDNA sequence for P42
20 SEQ ID NO: 53 is the determined cDNA sequence for P47
SEQ ID NO: 54 is the determined cDNA sequence for P49
SEQ ID NO: 55 is the determined cDNA sequence for P50
SEQ ID NO: 56 is the determined cDNA sequence for P53
SEQ ID NO: 57 is the determined cDNA sequence for P55
25 SEQ ID NO: 58 is the determined cDNA sequence for P60
SEQ ID NO: 59 is the determined cDNA sequence for P64
SEQ ID NO: 60 is the determined cDNA sequence for P65
SEQ ID NO: 61 is the determined cDNA sequence for P73
SEQ ID NO: 62 is the determined cDNA sequence for P75
30 SEQ ID NO: 63 is the determined cDNA sequence for P76

SEQ ID NO: 64 is the determined cDNA sequence for P79
SEQ ID NO: 65 is the determined cDNA sequence for P84
SEQ ID NO: 66 is the determined cDNA sequence for P68
SEQ ID NO: 67 is the determined cDNA sequence for P80 (also referred

5 to as P704P)

SEQ ID NO: 68 is the determined cDNA sequence for P82
SEQ ID NO: 69 is the determined cDNA sequence for U1-3064
SEQ ID NO: 70 is the determined cDNA sequence for U1-3065
SEQ ID NO: 71 is the determined cDNA sequence for V1-3692
10 SEQ ID NO: 72 is the determined cDNA sequence for 1A-3905
SEQ ID NO: 73 is the determined cDNA sequence for V1-3686
SEQ ID NO: 74 is the determined cDNA sequence for R1-2330
SEQ ID NO: 75 is the determined cDNA sequence for 1B-3976
SEQ ID NO: 76 is the determined cDNA sequence for V1-3679
15 SEQ ID NO: 77 is the determined cDNA sequence for 1G-4736
SEQ ID NO: 78 is the determined cDNA sequence for 1G-4738
SEQ ID NO: 79 is the determined cDNA sequence for 1G-4741
SEQ ID NO: 80 is the determined cDNA sequence for 1G-4744
SEQ ID NO: 81 is the determined cDNA sequence for 1G-4734
20 SEQ ID NO: 82 is the determined cDNA sequence for 1H-4774
SEQ ID NO: 83 is the determined cDNA sequence for 1H-4781
SEQ ID NO: 84 is the determined cDNA sequence for 1H-4785
SEQ ID NO: 85 is the determined cDNA sequence for 1H-4787
SEQ ID NO: 86 is the determined cDNA sequence for 1H-4796
25 SEQ ID NO: 87 is the determined cDNA sequence for 1I-4807
SEQ ID NO: 88 is the determined cDNA sequence for 1I-4810
SEQ ID NO: 89 is the determined cDNA sequence for 1I-4811
SEQ ID NO: 90 is the determined cDNA sequence for 1J-4876
SEQ ID NO: 91 is the determined cDNA sequence for 1K-4884
30 SEQ ID NO: 92 is the determined cDNA sequence for 1K-4896

- SEQ ID NO: 93 is the determined cDNA sequence for 1G-4761
SEQ ID NO: 94 is the determined cDNA sequence for 1G-4762
SEQ ID NO: 95 is the determined cDNA sequence for 1H-4766
SEQ ID NO: 96 is the determined cDNA sequence for 1H-4770
5 SEQ ID NO: 97 is the determined cDNA sequence for 1H-4771
SEQ ID NO: 98 is the determined cDNA sequence for 1H-4772
SEQ ID NO: 99 is the determined cDNA sequence for 1D-4297
SEQ ID NO: 100 is the determined cDNA sequence for 1D-4309
SEQ ID NO: 101 is the determined cDNA sequence for 1D.1-4278
10 SEQ ID NO: 102 is the determined cDNA sequence for 1D-4288
SEQ ID NO: 103 is the determined cDNA sequence for 1D-4283
SEQ ID NO: 104 is the determined cDNA sequence for 1D-4304
SEQ ID NO: 105 is the determined cDNA sequence for 1D-4296
SEQ ID NO: 106 is the determined cDNA sequence for 1D-4280
15 SEQ ID NO: 107 is the determined full length cDNA sequence for F1-12
(also referred to as P504S)
SEQ ID NO: 108 is the predicted amino acid sequence for F1-12
SEQ ID NO: 109 is the determined full length cDNA sequence for J1-17
SEQ ID NO: 110 is the determined full length cDNA sequence for L1-12
20 (also referred to as P501S)
SEQ ID NO: 111 is the determined full length cDNA sequence for N1-
1862 (also referred to as P503S)
SEQ ID NO: 112 is the predicted amino acid sequence for J1-17
SEQ ID NO: 113 is the predicted amino acid sequence for L1-12 (also
25 referred to as P501S)
SEQ ID NO: 114 is the predicted amino acid sequence for N1-1862 (also
referred to as P503S)
SEQ ID NO: 115 is the determined cDNA sequence for P89
SEQ ID NO: 116 is the determined cDNA sequence for P90
30 SEQ ID NO: 117 is the determined cDNA sequence for P92

SEQ ID NO: 118 is the determined cDNA sequence for P95
SEQ ID NO: 119 is the determined cDNA sequence for P98
SEQ ID NO: 120 is the determined cDNA sequence for P102
SEQ ID NO: 121 is the determined cDNA sequence for P110
5 SEQ ID NO: 122 is the determined cDNA sequence for P111
SEQ ID NO: 123 is the determined cDNA sequence for P114
SEQ ID NO: 124 is the determined cDNA sequence for P115
SEQ ID NO: 125 is the determined cDNA sequence for P116
SEQ ID NO: 126 is the determined cDNA sequence for P124
10 SEQ ID NO: 127 is the determined cDNA sequence for P126
SEQ ID NO: 128 is the determined cDNA sequence for P130
SEQ ID NO: 129 is the determined cDNA sequence for P133
SEQ ID NO: 130 is the determined cDNA sequence for P138
SEQ ID NO: 131 is the determined cDNA sequence for P143
15 SEQ ID NO: 132 is the determined cDNA sequence for P151
SEQ ID NO: 133 is the determined cDNA sequence for P156
SEQ ID NO: 134 is the determined cDNA sequence for P157
SEQ ID NO: 135 is the determined cDNA sequence for P166
SEQ ID NO: 136 is the determined cDNA sequence for P176
20 SEQ ID NO: 137 is the determined cDNA sequence for P178
SEQ ID NO: 138 is the determined cDNA sequence for P179
SEQ ID NO: 139 is the determined cDNA sequence for P185
SEQ ID NO: 140 is the determined cDNA sequence for P192
SEQ ID NO: 141 is the determined cDNA sequence for P201
25 SEQ ID NO: 142 is the determined cDNA sequence for P204
SEQ ID NO: 143 is the determined cDNA sequence for P208
SEQ ID NO: 144 is the determined cDNA sequence for P211
SEQ ID NO: 145 is the determined cDNA sequence for P213
SEQ ID NO: 146 is the determined cDNA sequence for P219
30 SEQ ID NO: 147 is the determined cDNA sequence for P237

SEQ ID NO: 148 is the determined cDNA sequence for P239
SEQ ID NO: 149 is the determined cDNA sequence for P248
SEQ ID NO: 150 is the determined cDNA sequence for P251
SEQ ID NO: 151 is the determined cDNA sequence for P255
5 SEQ ID NO: 152 is the determined cDNA sequence for P256
SEQ ID NO: 153 is the determined cDNA sequence for P259
SEQ ID NO: 154 is the determined cDNA sequence for P260
SEQ ID NO: 155 is the determined cDNA sequence for P263
SEQ ID NO: 156 is the determined cDNA sequence for P264
10 SEQ ID NO: 157 is the determined cDNA sequence for P266
SEQ ID NO: 158 is the determined cDNA sequence for P270
SEQ ID NO: 159 is the determined cDNA sequence for P272
SEQ ID NO: 160 is the determined cDNA sequence for P278
SEQ ID NO: 161 is the determined cDNA sequence for P105
15 SEQ ID NO: 162 is the determined cDNA sequence for P107
SEQ ID NO: 163 is the determined cDNA sequence for P137
SEQ ID NO: 164 is the determined cDNA sequence for P194
SEQ ID NO: 165 is the determined cDNA sequence for P195
SEQ ID NO: 166 is the determined cDNA sequence for P196
20 SEQ ID NO: 167 is the determined cDNA sequence for P220
SEQ ID NO: 168 is the determined cDNA sequence for P234
SEQ ID NO: 169 is the determined cDNA sequence for P235
SEQ ID NO: 170 is the determined cDNA sequence for P243
SEQ ID NO: 171 is the determined cDNA sequence for P703P-DE1
25 SEQ ID NO: 172 is the predicted amino acid sequence for P703P-DE1
SEQ ID NO: 173 is the determined cDNA sequence for P703P-DE2
SEQ ID NO: 174 is the determined cDNA sequence for P703P-DE6
SEQ ID NO: 175 is the determined cDNA sequence for P703P-DE13
SEQ ID NO: 176 is the predicted amino acid sequence for P703P-DE13
30 SEQ ID NO: 177 is the determined cDNA sequence for P703P-DE14

SEQ ID NO: 178 is the predicted amino acid sequence for P703P-DE14

SEQ ID NO: 179 is the determined extended cDNA sequence for 1G-

4736

SEQ ID NO: 180 is the determined extended cDNA sequence for 1G-

5 4738

SEQ ID NO: 181 is the determined extended cDNA sequence for 1G-

4741

SEQ ID NO: 182 is the determined extended cDNA sequence for 1G-

4744

10

SEQ ID NO: 183 is the determined extended cDNA sequence for 1H-

4774

SEQ ID NO: 184 is the determined extended cDNA sequence for 1H-

4781

SEQ ID NO: 185 is the determined extended cDNA sequence for 1H-

15 4785

SEQ ID NO: 186 is the determined extended cDNA sequence for 1H-

4787

SEQ ID NO: 187 is the determined extended cDNA sequence for 1H-

4796

20

SEQ ID NO: 188 is the determined extended cDNA sequence for 1I-

4807

SEQ ID NO: 189 is the determined 3' cDNA sequence for 1I-4810

SEQ ID NO: 190 is the determined 3' cDNA sequence for 1I-4811

SEQ ID NO: 191 is the determined extended cDNA sequence for 1J-

25 4876

SEQ ID NO: 192 is the determined extended cDNA sequence for 1K-

4884

SEQ ID NO: 193 is the determined extended cDNA sequence for 1K-

4896

SEQ ID NO: 194 is the determined extended cDNA sequence for 1G-
4761

SEQ ID NO: 195 is the determined extended cDNA sequence for 1G-
4762

5 SEQ ID NO: 196 is the determined extended cDNA sequence for 1H-
4766

SEQ ID NO: 197 is the determined 3' cDNA sequence for 1H-4770
SEQ ID NO: 198 is the determined 3' cDNA sequence for 1H-4771
SEQ ID NO: 199 is the determined extended cDNA sequence for 1H-
10 4772

SEQ ID NO: 200 is the determined extended cDNA sequence for 1D-
4309

SEQ ID NO: 201 is the determined extended cDNA sequence for 1D.1-
4278

15 SEQ ID NO: 202 is the determined extended cDNA sequence for 1D-
4288

SEQ ID NO: 203 is the determined extended cDNA sequence for 1D-
4283

SEQ ID NO: 204 is the determined extended cDNA sequence for 1D-
20 4304

SEQ ID NO: 205 is the determined extended cDNA sequence for 1D-
4296

SEQ ID NO: 206 is the determined extended cDNA sequence for 1D-
4280

25 SEQ ID NO: 207 is the determined cDNA sequence for 10-d8fwd
SEQ ID NO: 208 is the determined cDNA sequence for 10-H10con
SEQ ID NO: 209 is the determined cDNA sequence for 11-C8rev
SEQ ID NO: 210 is the determined cDNA sequence for 7.g6fwd
SEQ ID NO: 211 is the determined cDNA sequence for 7.g6rev
30 SEQ ID NO: 212 is the determined cDNA sequence for 8-b5fwd

SEQ ID NO: 213 is the determined cDNA sequence for 8-b5rev
SEQ ID NO: 214 is the determined cDNA sequence for 8-b6fwd
SEQ ID NO: 215 is the determined cDNA sequence for 8-b6 rev
SEQ ID NO: 216 is the determined cDNA sequence for 8-d4fwd
5 SEQ ID NO: 217 is the determined cDNA sequence for 8-d9rev
SEQ ID NO: 218 is the determined cDNA sequence for 8-g3fwd
SEQ ID NO: 219 is the determined cDNA sequence for 8-g3rev
SEQ ID NO: 220 is the determined cDNA sequence for 8-h11rev
SEQ ID NO: 221 is the determined cDNA sequence for g-f12fwd
10 SEQ ID NO: 222 is the determined cDNA sequence for g-f3rev
SEQ ID NO: 223 is the determined cDNA sequence for P509S
SEQ ID NO: 224 is the determined cDNA sequence for P510S
SEQ ID NO: 225 is the determined cDNA sequence for P703DE5
SEQ ID NO: 226 is the determined cDNA sequence for 9-A11
15 SEQ ID NO: 227 is the determined cDNA sequence for 8-C6
SEQ ID NO: 228 is the determined cDNA sequence for 8-H7
SEQ ID NO: 229 is the determined cDNA sequence for JPTPN13
SEQ ID NO: 230 is the determined cDNA sequence for JPTPN14
SEQ ID NO: 231 is the determined cDNA sequence for JPTPN23
20 SEQ ID NO: 232 is the determined cDNA sequence for JPTPN24
SEQ ID NO: 233 is the determined cDNA sequence for JPTPN25
SEQ ID NO: 234 is the determined cDNA sequence for JPTPN30
SEQ ID NO: 235 is the determined cDNA sequence for JPTPN34
SEQ ID NO: 236 is the determined cDNA sequence for PTPN35
25 SEQ ID NO: 237 is the determined cDNA sequence for JPTPN36
SEQ ID NO: 238 is the determined cDNA sequence for JPTPN38
SEQ ID NO: 239 is the determined cDNA sequence for JPTPN39
SEQ ID NO: 240 is the determined cDNA sequence for JPTPN40
SEQ ID NO: 241 is the determined cDNA sequence for JPTPN41
30 SEQ ID NO: 242 is the determined cDNA sequence for JPTPN42

SEQ ID NO: 243 is the determined cDNA sequence for JPTPN45
SEQ ID NO: 244 is the determined cDNA sequence for JPTPN46
SEQ ID NO: 245 is the determined cDNA sequence for JPTPN51
SEQ ID NO: 246 is the determined cDNA sequence for JPTPN56
5 SEQ ID NO: 247 is the determined cDNA sequence for PTPN64
SEQ ID NO: 248 is the determined cDNA sequence for JPTPN65
SEQ ID NO: 249 is the determined cDNA sequence for JPTPN67
SEQ ID NO: 250 is the determined cDNA sequence for JPTPN76
SEQ ID NO: 251 is the determined cDNA sequence for JPTPN84
10 SEQ ID NO: 252 is the determined cDNA sequence for JPTPN85
SEQ ID NO: 253 is the determined cDNA sequence for JPTPN86
SEQ ID NO: 254 is the determined cDNA sequence for JPTPN87
SEQ ID NO: 255 is the determined cDNA sequence for JPTPN88
SEQ ID NO: 256 is the determined cDNA sequence for JP1F1
15 SEQ ID NO: 257 is the determined cDNA sequence for JP1F2
SEQ ID NO: 258 is the determined cDNA sequence for JP1C2
SEQ ID NO: 259 is the determined cDNA sequence for JP1B1
SEQ ID NO: 260 is the determined cDNA sequence for JP1B2
SEQ ID NO: 261 is the determined cDNA sequence for JP1D3
20 SEQ ID NO: 262 is the determined cDNA sequence for JP1A4
SEQ ID NO: 263 is the determined cDNA sequence for JP1F5
SEQ ID NO: 264 is the determined cDNA sequence for JP1E6
SEQ ID NO: 265 is the determined cDNA sequence for JP1D6
SEQ ID NO: 266 is the determined cDNA sequence for JP1B5
25 SEQ ID NO: 267 is the determined cDNA sequence for JP1A6
SEQ ID NO: 268 is the determined cDNA sequence for JP1E8
SEQ ID NO: 269 is the determined cDNA sequence for JP1D7
SEQ ID NO: 270 is the determined cDNA sequence for JP1D9
SEQ ID NO: 271 is the determined cDNA sequence for JP1C10
30 SEQ ID NO: 272 is the determined cDNA sequence for JP1A9

SEQ ID NO: 273 is the determined cDNA sequence for JP1F12
SEQ ID NO: 274 is the determined cDNA sequence for JP1E12
SEQ ID NO: 275 is the determined cDNA sequence for JP1D11
SEQ ID NO: 276 is the determined cDNA sequence for JP1C11
5 SEQ ID NO: 277 is the determined cDNA sequence for JP1C12
SEQ ID NO: 278 is the determined cDNA sequence for JP1B12
SEQ ID NO: 279 is the determined cDNA sequence for JP1A12
SEQ ID NO: 280 is the determined cDNA sequence for JP8G2
SEQ ID NO: 281 is the determined cDNA sequence for JP8H1
10 SEQ ID NO: 282 is the determined cDNA sequence for JP8H2
SEQ ID NO: 283 is the determined cDNA sequence for JP8A3
SEQ ID NO: 284 is the determined cDNA sequence for JP8A4
SEQ ID NO: 285 is the determined cDNA sequence for JP8C3
SEQ ID NO: 286 is the determined cDNA sequence for JP8G4
15 SEQ ID NO: 287 is the determined cDNA sequence for JP8B6
SEQ ID NO: 288 is the determined cDNA sequence for JP8D6
SEQ ID NO: 289 is the determined cDNA sequence for JP8F5
SEQ ID NO: 290 is the determined cDNA sequence for JP8A8
SEQ ID NO: 291 is the determined cDNA sequence for JP8C7
20 SEQ ID NO: 292 is the determined cDNA sequence for JP8D7
SEQ ID NO: 293 is the determined cDNA sequence for P8D8
SEQ ID NO: 294 is the determined cDNA sequence for JP8E7
SEQ ID NO: 295 is the determined cDNA sequence for JP8F8
SEQ ID NO: 296 is the determined cDNA sequence for JP8G8
25 SEQ ID NO: 297 is the determined cDNA sequence for JP8B10
SEQ ID NO: 298 is the determined cDNA sequence for JP8C10
SEQ ID NO: 299 is the determined cDNA sequence for JP8E9
SEQ ID NO: 300 is the determined cDNA sequence for JP8E10
SEQ ID NO: 301 is the determined cDNA sequence for JP8F9
30 SEQ ID NO: 302 is the determined cDNA sequence for JP8H9

- SEQ ID NO: 303 is the determined cDNA sequence for JP8C12
SEQ ID NO: 304 is the determined cDNA sequence for JP8E11
SEQ ID NO: 305 is the determined cDNA sequence for JP8E12
SEQ ID NO: 306 is the amino acid sequence for the peptide PS2#12
5 SEQ ID NO: 307 is the determined cDNA sequence for P711P
SEQ ID NO: 308 is the determined cDNA sequence for P712P
SEQ ID NO: 309 is the determined cDNA sequence for CLONE23
SEQ ID NO: 310 is the determined cDNA sequence for P774P
SEQ ID NO: 311 is the determined cDNA sequence for P775P
10 SEQ ID NO: 312 is the determined cDNA sequence for P715P
SEQ ID NO: 313 is the determined cDNA sequence for P710P
SEQ ID NO: 314 is the determined cDNA sequence for P767P
SEQ ID NO: 315 is the determined cDNA sequence for P768P
SEQ ID NO: 316-325 are the determined cDNA sequences of previously
15 isolated genes
SEQ ID NO: 326 is the determined cDNA sequence for P703PDE5
SEQ ID NO: 327 is the predicted amino acid sequence for P703PDE5
SEQ ID NO: 328 is the determined cDNA sequence for P703P6.26
SEQ ID NO: 329 is the predicted amino acid sequence for P703P6.26
20 SEQ ID NO: 330 is the determined cDNA sequence for P703PX-23
SEQ ID NO: 331 is the predicted amino acid sequence for P703PX-23
SEQ ID NO: 332 is the determined full length cDNA sequence for
P509S
SEQ ID NO: 333 is the determined extended cDNA sequence for P707P
25 (also referred to as 11-C9)
SEQ ID NO: 334 is the determined cDNA sequence for P714P
SEQ ID NO: 335 is the determined cDNA sequence for P705P (also
referred to as 9-F3)
SEQ ID NO: 336 is the predicted amino acid sequence for P705P
30 SEQ ID NO: 337 is the amino acid sequence of the peptide P1S#10

- SEQ ID NO: 338 is the amino acid sequence of the peptide p5
SEQ ID NO: 339 is the predicted amino acid sequence of P509S
SEQ ID NO: 340 is the determined cDNA sequence for P778P
SEQ ID NO: 341 is the determined cDNA sequence for P786P
5 SEQ ID NO: 342 is the determined cDNA sequence for P789P
SEQ ID NO: 343 is the determined cDNA sequence for a clone showing
homology to Homo sapiens MM46 mRNA
SEQ ID NO: 344 is the determined cDNA sequence for a clone showing
homology to Homo sapiens TNF-alpha stimulated ABC protein (ABC50) mRNA
10 SEQ ID NO: 345 is the determined cDNA sequence for a clone showing
homology to Homo sapiens mRNA for E-cadherin
SEQ ID NO: 346 is the determined cDNA sequence for a clone showing
homology to Human nuclear-encoded mitochondrial serine hydroxymethyltransferase
(SHMT)
15 SEQ ID NO: 347 is the determined cDNA sequence for a clone showing
homology to Homo sapiens natural resistance-associated macrophage protein2
(NRAMP2)
SEQ ID NO: 348 is the determined cDNA sequence for a clone showing
homology to Homo sapiens phosphoglucomutase-related protein (PGMRP)
20 SEQ ID NO: 349 is the determined cDNA sequence for a clone showing
homology to Human mRNA for proteosome subunit p40
SEQ ID NO: 350 is the determined cDNA sequence for P777P
SEQ ID NO: 351 is the determined cDNA sequence for P779P
SEQ ID NO: 352 is the determined cDNA sequence for P790P
25 SEQ ID NO: 353 is the determined cDNA sequence for P784P
SEQ ID NO: 354 is the determined cDNA sequence for P776P
SEQ ID NO: 355 is the determined cDNA sequence for P780P
SEQ ID NO: 356 is the determined cDNA sequence for P544S
SEQ ID NO: 357 is the determined cDNA sequence for P745S
30 SEQ ID NO: 358 is the determined cDNA sequence for P782P

- SEQ ID NO: 359 is the determined cDNA sequence for P783P
- SEQ ID NO: 360 is the determined cDNA sequence for unknown 17984
- SEQ ID NO: 361 is the determined cDNA sequence for P787P
- SEQ ID NO: 362 is the determined cDNA sequence for P788P
- 5 SEQ ID NO: 363 is the determined cDNA sequence for unknown 17994
- SEQ ID NO: 364 is the determined cDNA sequence for P781P
- SEQ ID NO: 365 is the determined cDNA sequence for P785P
- SEQ ID NO: 366-375 are the determined cDNA sequences for splice variants of B305D.
- 10 SEQ ID NO: 376 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 366.
- SEQ ID NO: 377 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 372.
- SEQ ID NO: 378 is the predicted amino acid sequence encoded by the
- 15 sequence of SEQ ID NO: 373.
- SEQ ID NO: 379 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 374.
- SEQ ID NO: 380 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 375.
- 20 SEQ ID NO: 381 is the determined cDNA sequence for B716P.
- SEQ ID NO: 382 is the determined full-length cDNA sequence for P711P.
- SEQ ID NO: 383 is the predicted amino acid sequence for P711P.
- SEQ ID NO: 384 is the cDNA sequence for P1000C.
- 25 SEQ ID NO: 385 is the cDNA sequence for CGI-82.
- SEQ ID NO: 386 is the cDNA sequence for 23320.
- SEQ ID NO: 387 is the cDNA sequence for CGI-69.
- SEQ ID NO: 388 is the cDNA sequence for L-iditol-2-dehydrogenase.
- SEQ ID NO: 389 is the cDNA sequence for 23379.
- 30 SEQ ID NO: 390 is the cDNA sequence for 23381.

SEQ ID NO:391 is the cDNA sequence for KIAA0122.

SEQ ID NO:392 is the cDNA sequence for 23399.

SEQ ID NO:393 is the cDNA sequence for a previously identified gene.

SEQ ID NO:394 is the cDNA sequence for HCLBP.

5 SEQ ID NO:395 is the cDNA sequence for transglutaminase.

SEQ ID NO:396 is the cDNA sequence for a previously identified gene.

SEQ ID NO:397 is the cDNA sequence for PAP.

SEQ ID NO:398 is the cDNA sequence for Ets transcription factor

PDEF.

10 SEQ ID NO:399 is the cDNA sequence for hTGR.

SEQ ID NO:400 is the cDNA sequence for KIAA0295.

SEQ ID NO:401 is the cDNA sequence for 22545.

SEQ ID NO:402 is the cDNA sequence for 22547.

SEQ ID NO:403 is the cDNA sequence for 22548.

15 SEQ ID NO:404 is the cDNA sequence for 22550.

SEQ ID NO:405 is the cDNA sequence for 22551.

SEQ ID NO:406 is the cDNA sequence for 22552.

SEQ ID NO:407 is the cDNA sequence for 22553 (also known as

P1020C).

20 SEQ ID NO:408 is the cDNA sequence for 22558.

SEQ ID NO:409 is the cDNA sequence for 22562.

SEQ ID NO:410 is the cDNA sequence for 22565.

SEQ ID NO:411 is the cDNA sequence for 22567.

SEQ ID NO:412 is the cDNA sequence for 22568.

25 SEQ ID NO:413 is the cDNA sequence for 22570.

SEQ ID NO:414 is the cDNA sequence for 22571.

SEQ ID NO:415 is the cDNA sequence for 22572.

SEQ ID NO:416 is the cDNA sequence for 22573.

SEQ ID NO:417 is the cDNA sequence for 22573.

30 SEQ ID NO:418 is the cDNA sequence for 22575.

SEQ ID NO:419 is the cDNA sequence for 22580.
SEQ ID NO:420 is the cDNA sequence for 22581.
SEQ ID NO:421 is the cDNA sequence for 22582.
SEQ ID NO:422 is the cDNA sequence for 22583.
5 SEQ ID NO:423 is the cDNA sequence for 22584.
SEQ ID NO:424 is the cDNA sequence for 22585.
SEQ ID NO:425 is the cDNA sequence for 22586.
SEQ ID NO:426 is the cDNA sequence for 22587.
SEQ ID NO:427 is the cDNA sequence for 22588.
10 SEQ ID NO:428 is the cDNA sequence for 22589.
SEQ ID NO:429 is the cDNA sequence for 22590.
SEQ ID NO:430 is the cDNA sequence for 22591.
SEQ ID NO:431 is the cDNA sequence for 22592.
SEQ ID NO:432 is the cDNA sequence for 22593.
15 SEQ ID NO:433 is the cDNA sequence for 22594.
SEQ ID NO:434 is the cDNA sequence for 22595.
SEQ ID NO:435 is the cDNA sequence for 22596.
SEQ ID NO:436 is the cDNA sequence for 22847.
SEQ ID NO:437 is the cDNA sequence for 22848.
20 SEQ ID NO:438 is the cDNA sequence for 22849.
SEQ ID NO:439 is the cDNA sequence for 22851.
SEQ ID NO:440 is the cDNA sequence for 22852.
SEQ ID NO:441 is the cDNA sequence for 22853.
SEQ ID NO:442 is the cDNA sequence for 22854.
25 SEQ ID NO:443 is the cDNA sequence for 22855.
SEQ ID NO:444 is the cDNA sequence for 22856.
SEQ ID NO:445 is the cDNA sequence for 22857.
SEQ ID NO:446 is the cDNA sequence for 23601.
SEQ ID NO:447 is the cDNA sequence for 23602.
30 SEQ ID NO:448 is the cDNA sequence for 23605.

- SEQ ID NO:449 is the cDNA sequence for 23606.
- SEQ ID NO:450 is the cDNA sequence for 23612.
- SEQ ID NO:451 is the cDNA sequence for 23614.
- SEQ ID NO:452 is the cDNA sequence for 23618.
- 5 SEQ ID NO:453 is the cDNA sequence for 23622.
- SEQ ID NO:454 is the cDNA sequence for folate hydrolase.
- SEQ ID NO:455 is the cDNA sequence for LIM protein.
- SEQ ID NO:456 is the cDNA sequence for a known gene.
- SEQ ID NO:457 is the cDNA sequence for a known gene.
- 10 SEQ ID NO:458 is the cDNA sequence for a previously identified gene.
- SEQ ID NO:459 is the cDNA sequence for 23045.
- SEQ ID NO:460 is the cDNA sequence for 23032.
- SEQ ID NO:461 is the cDNA sequence for clone 23054.
- SEQ ID NO:462-467 are cDNA sequences for known genes.
- 15 SEQ ID NO:468-471 are cDNA sequences for P710P.
- SEQ ID NO:472 is a cDNA sequence for P1001C.
- SEQ ID NO: 473 is the determined cDNA sequence for a first splice variant of P775P (referred to as 27505).
- SEQ ID NO: 474 is the determined cDNA sequence for a second splice
- 20 variant of P775P (referred to as 19947).
- SEQ ID NO: 475 is the determined cDNA sequence for a third splice variant of P775P (referred to as 19941).
- SEQ ID NO: 476 is the determined cDNA sequence for a fourth splice variant of P775P (referred to as 19937).
- 25 SEQ ID NO: 477 is a first predicted amino acid sequence encoded by the sequence of SEQ ID NO: 474.
- SEQ ID NO: 478 is a second predicted amino acid sequence encoded by the sequence of SEQ ID NO: 474.
- SEQ ID NO: 479 is the predicted amino acid sequence encoded by the
- 30 sequence of SEQ ID NO: 475.

SEQ ID NO: 480 is a first predicted amino acid sequence encoded by the sequence of SEQ ID NO: 473.

SEQ ID NO: 481 is a second predicted amino acid sequence encoded by the sequence of SEQ ID NO: 473.

5 SEQ ID NO: 482 is a third predicted amino acid sequence encoded by the sequence of SEQ ID NO: 473.

SEQ ID NO: 483 is a fourth predicted amino acid sequence encoded by the sequence of SEQ ID NO: 473.

10 SEQ ID NO: 484 is the first 30 amino acids of the *M. tuberculosis* antigen Ra12.

SEQ ID NO: 485 is the PCR primer AW025.

SEQ ID NO: 486 is the PCR primer AW003.

SEQ ID NO: 487 is the PCR primer AW027.

SEQ ID NO: 488 is the PCR primer AW026.

15 SEQ ID NO: 489-501 are peptides employed in epitope mapping studies.

SEQ ID NO: 502 is the determined cDNA sequence of the complementarity determining region for the anti-P503S monoclonal antibody 20D4.

SEQ ID NO: 503 is the determined cDNA sequence of the complementarity determining region for the anti-P503S monoclonal antibody JA1.

20 SEQ ID NO: 504 & 505 are peptides employed in epitope mapping studies.

SEQ ID NO: 506 is the determined cDNA sequence of the complementarity determining region for the anti-P703P monoclonal antibody 8H2.

25 SEQ ID NO: 507 is the determined cDNA sequence of the complementarity determining region for the anti-P703P monoclonal antibody 7H8.

SEQ ID NO: 508 is the determined cDNA sequence of the complementarity determining region for the anti-P703P monoclonal antibody 2D4.

SEQ ID NO: 509-522 are peptides employed in epitope mapping studies.

30 SEQ ID NO: 523 is a mature form of P703P used to raise antibodies against P703P.

SEQ ID NO: 524 is the putative full-length cDNA sequence of P703P.

SEQ ID NO: 525 is the predicted amino acid sequence encoded by SEQ
ID NO: 524.

SEQ ID NO: 526 is the full-length cDNA sequence for P790P.

5 SEQ ID NO: 527 is the predicted amino acid sequence for P790P.

SEQ ID NO: 528 & 529 are PCR primers.

SEQ ID NO: 530 is the cDNA sequence of a splice variant of SEQ ID
NO: 366.

10 SEQ ID NO: 531 is the cDNA sequence of the open reading frame of
SEQ ID NO: 530.

SEQ ID NO: 532 is the predicted amino acid encoded by the sequence of
SEQ ID NO: 531.

SEQ ID NO: 533 is the DNA sequence of a putative ORF of P775P.

15 SEQ ID NO: 534 is the predicted amino acid sequence encoded by SEQ
ID NO: 533.

SEQ ID NO: 535 is a first full-length cDNA sequence for P510S.

SEQ ID NO: 536 is a second full-length cDNA sequence for P510S.

SEQ ID NO: 537 is the predicted amino acid sequence encoded by SEQ
ID NO: 535.

20 SEQ ID NO: 538 is the predicted amino acid sequence encoded by SEQ
ID NO: 536.

SEQ ID NO: 539 is the peptide P501S-370.

SEQ ID NO: 540 is the peptide P501S-376.

SEQ ID NO: 541-551 are epitopes of P501S.

25 SEQ ID NO: 552 is an extended cDNA sequence for P712P.

SEQ ID NO: 553-568 are the amino acid sequences encoded by
predicted open reading frames within SEQ ID NO: 552.

SEQ ID NO: 569 is an extended cDNA sequence for P776P.

30 SEQ ID NO: 570 is the determined cDNA sequence for a splice variant
of P776P referred to as contig 6.

SEQ ID NO: 571 is the determined cDNA sequence for a splice variant of P776P referred to as contig 7.

SEQ ID NO: 572 is the determined cDNA sequence for a splice variant of P776P referred to as contig 14.

5 SEQ ID NO: 573 is the amino acid sequence encoded by a first predicted ORF of SEQ ID NO: 570.

SEQ ID NO: 574 is the amino acid sequence encoded by a second predicted ORF of SEQ ID NO: 570.

10 SEQ ID NO: 575 is the amino acid sequence encoded by a predicted ORF of SEQ ID NO: 571.

SEQ ID NO: 576-586 are amino acid sequences encoded by predicted ORFs of SEQ ID NO: 569.

SEQ ID NO: 587 is a DNA consensus sequence of the sequences of P767P and P777P.

15 SEQ ID NO: 588-590 are amino acid sequences encoded by predicted ORFs of SEQ ID NO: 587.

SEQ ID NO: 591 is an extended cDNA sequence for P1020C.

SEQ ID NO: 592 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: P1020C.

20 SEQ ID NO: 593 is a splice variant of P775P referred to as 50748.

SEQ ID NO: 594 is a splice variant of P775P referred to as 50717.

SEQ ID NO: 595 is a splice variant of P775P referred to as 45985.

SEQ ID NO: 596 is a splice variant of P775P referred to as 38769.

SEQ ID NO: 597 is a splice variant of P775P referred to as 37922.

25 SEQ ID NO: 598 is a splice variant of P510S referred to as 49274.

SEQ ID NO: 599 is a splice variant of P510S referred to as 39487.

SEQ ID NO: 600 is a splice variant of P504S referred to as 5167.16.

SEQ ID NO: 601 is a splice variant of P504S referred to as 5167.1.

SEQ ID NO: 602 is a splice variant of P504S referred to as 5163.46.

30 SEQ ID NO: 603 is a splice variant of P504S referred to as 5163.42.

SEQ ID NO: 604 is a splice variant of P504S referred to as 5163.34.

SEQ ID NO: 605 is a splice variant of P504S referred to as 5163.17.

SEQ ID NO: 606 is a splice variant of P501S referred to as 10640.

SEQ ID NO: 607-615 are the sequences of PCR primers.

5 SEQ ID NO: 616 is the determined cDNA sequence of a fusion of P703P
and PSA.

SEQ ID NO: 617 is the amino acid sequence of the fusion of P703P and
PSA.

SEQ ID NO: 618 is the cDNA sequence of the gene DD3.

10 SEQ ID NO: 619 is an extended cDNA sequence for P714P.

SEQ ID NO: 620-622 are the cDNA sequences for splice variants of
P704P.

SEQ ID NO: 623 is the cDNA sequence of a splice variant of P553S
referred to as P553S-14.

15 SEQ ID NO: 624 is the cDNA sequence of a splice variant of P553S
referred to as P553S-12.

SEQ ID NO: 625 is the cDNA sequence of a splice variant of P553S
referred to as P553S-10.

20 SEQ ID NO: 626 is the cDNA sequence of a splice variant of P553S
referred to as P553S-6.

SEQ ID NO: 627 is the amino acid sequence encoded by SEQ ID NO:
626.

SEQ ID NO: 628 is a first amino acid sequence encoded by SEQ ID NO:
623.

25 SEQ ID NO: 629 is a second amino acid sequence encoded by SEQ ID
NO: 623.

SEQ ID NO: 630 is a first full-length cDNA sequence for prostate-
specific transglutaminase gene (also referred to herein as P558S).

30 SEQ ID NO: 631 is a second full-length cDNA sequence for prostate-
specific transglutaminase gene.

SEQ ID NO: 632 is the amino acid sequence encoded by the sequence of
SEQ ID NO: 630.

SEQ ID NO: 633 is the amino acid sequence encoded by the sequence of
SEQ ID NO: 631.

5 SEQ ID NO: 634 is the full-length cDNA sequence for P788P.

SEQ ID NO: 635 is the amino acid sequence encoded by SEQ ID NO:
634.

SEQ ID NO: 636 is the determined cDNA sequence for a polymorphic
variant of P788P.

10 SEQ ID NO: 637 is the amino acid sequence encoded by SEQ ID NO:
636.

SEQ ID NO: 638 is the amino acid sequence of peptide 4 from P703P.

SEQ ID NO: 639 is the cDNA sequence that encodes peptide 4 from
P703P.

15 SEQ ID NO: 640-655 are cDNA sequences encoding epitopes of P703P.

SEQ ID NO: 656-671 are the amino acid sequences of epitopes of
P703P.

SEQ ID NO: 672 and 673 are PCR primers.

20 SEQ ID NO: 674 is the cDNA sequence encoding an N-terminal portion
of P788P expressed in *E. coli*.

SEQ ID NO: 675 is the amino acid sequence of the N-terminal portion of
P788P expressed in *E. coli*.

SEQ ID NO: 676 is the amino acid sequence of the *M. tuberculosis*
antigen Ra12.

25 SEQ ID NO: 677 and 678 are PCR primers.

SEQ ID NO: 679 is the cDNA sequence for the Ra12-P510S-C
construct.

SEQ ID NO: 680 is the cDNA sequence for the P510S-C construct.

SEQ ID NO: 681 is the cDNA sequence for the P510S-E3 construct.

SEQ ID NO: 682 is the amino acid sequence for the Ra12-P510S-C construct.

SEQ ID NO: 683 is the amino acid sequence for the P510S-C construct.

SEQ ID NO: 684 is the amino acid sequence for the P510S-E3 construct.

5 SEQ ID NO: 685-690 are PCR primers.

SEQ ID NO: 691 is the cDNA sequence of the construct Ra12-P775P-ORF3.

SEQ ID NO: 692 is the amino acid sequence of the construct Ra12-P775P-ORF3.

10 SEQ ID NO: 693 and 694 are PCR primers.

SEQ ID NO: 695 is the determined amino acid sequence for a P703P His tag fusion protein.

SEQ ID NO: 696 is the determined cDNA sequence for a P703P His tag fusion protein.

15 SEQ ID NO: 697 and 698 are PCR primers.

SEQ ID NO: 699 is the determined amino acid sequence for a P705P His tag fusion protein.

SEQ ID NO: 700 is the determined cDNA sequence for a P705P His tag fusion protein.

20 SEQ ID NO: 701 and 702 are PCR primers.

SEQ ID NO: 703 is the determined amino acid sequence for a P711P His tag fusion protein.

SEQ ID NO: 704 is the determined cDNA sequence for a P711P His tag fusion protein.

25 SEQ ID NO: 705 is the amino acid sequence of the *M. tuberculosis* antigen Ra12.

SEQ ID NO: 706 and 707 are PCR primers.

SEQ ID NO: 708 is the determined cDNA sequence for the construct Ra12-P501S-E2.

SEQ ID NO: 709 is the determined amino acid sequence for the construct Ra12-P501S-E2.

SEQ ID NO: 710 is the amino acid sequence for an epitope of P501S.

SEQ ID NO: 711 is the DNA sequence encoding SEQ ID NO: 710.

5 SEQ ID NO: 712 is the amino acid sequence for an epitope of P501S.

SEQ ID NO: 713 is the DNA sequence encoding SEQ ID NO: 712.

SEQ ID NO: 714 is a peptide employed in epitope mapping studies.

SEQ ID NO: 715 is the amino acid sequence for an epitope of P501S.

SEQ ID NO: 716 is the DNA sequence encoding SEQ ID NO: 715.

10 SEQ ID NO: 717-719 are the amino acid sequences for CD4 epitopes of P501S.

SEQ ID NO: 720-722 are the DNA sequences encoding the sequences of SEQ ID NO: 717-719.

15 SEQ ID NO: 723-734 are the amino acid sequences for putative CTL epitopes of P703P.

SEQ ID NO: 735 is the full-length cDNA sequence for P789P.

SEQ ID NO: 736 is the amino acid sequence encoded by SEQ ID NO: 735.

20 SEQ ID NO: 737 is the determined full-length cDNA sequence for the splice variant of P776P referred to as contig 6.

SEQ ID NO: 738-739 are determined full-length cDNA sequences for the splice variant of P776P referred to as contig 7.

SEQ ID NO: 740-744 are amino acid sequences encoded by SEQ ID NO: 737.

25 SEQ ID NO: 745-750 are amino acid sequences encoded by the splice variant of P776P referred to as contig 7.

SEQ ID NO: 751 is the full-length cDNA sequence for human transmembrane protease serine 2.

30 SEQ ID NO: 752 is the amino acid sequence encoded by SEQ ID NO: 751.

SEQ ID NO: 753 is the cDNA sequence encoding the first 209 amino acids of human transmembrane protease serine 2.

SEQ ID NO: 754 is the first 209 amino acids of human transmembrane protease serine 2.

5 SEQ ID NO: 755 is the amino acid sequence of peptide 296-322 of P501S.

SEQ ID NO: 756-759 are PCR primers.

SEQ ID NO: 760 is the determined cDNA sequence of the Vb chain of a T cell receptor for the P501S-specific T cell clone 4E5.

10 SEQ ID NO: 761 is the determined cDNA sequence of the Va chain of a T cell receptor for the P501S-specific T cell clone 4E5.

SEQ ID NO: 762 is the amino acid sequence encoded by SEQ ID NO 760.

15 SEQ ID NO: 763 is the amino acid sequence encoded by SEQ ID NO 761.

SEQ ID NO: 764 is the full-length open reading frame for P768P including stop codon.

SEQ ID NO: 765 is the full-length open reading frame for P768P without stop codon.

20 SEQ ID NO: 766 is the amino acid sequence encoded by SEQ ID NO: 765.

SEQ ID NO: 767-772 are the amino acid sequences for predicted domains of P768P.

SEQ ID NO: 773 is the full-length cDNA sequence of P835P.

25 SEQ ID NO: 774 is the cDNA sequence of the previously identified clone FLJ13581.

SEQ ID NO: 775 is the cDNA sequence of the open reading frame for P835P with stop codon.

30 SEQ ID NO: 776 is the cDNA sequence of the open reading frame for P835P without stop codon.

SEQ ID NO: 777 is the full-length amino acid sequence for P835P.

SEQ ID NO: 778-785 are the amino acid sequences of extracellular and intracellular domains of P835P.

SEQ ID NO: 786 is the full-length cDNA sequence for P1000C.

5 SEQ ID NO: 787 is the cDNA sequence of the open reading frame for P1000C, including stop codon.

SEQ ID NO: 788 is the cDNA sequence of the open reading frame for P1000C, without stop codon.

SEQ ID NO: 789 is the full-length amino acid sequence for P1000C.

10 SEQ ID NO: 790 is amino acids 1-100 of SEQ ID NO: 789.

SEQ ID NO: 791 is amino acids 100-492 of SEQ ID NO: 789.

SEQ ID NO: 792 is the amino acid sequence of an α prepro-P501S recombinant protein.

15 DETAILED DESCRIPTION OF THE INVENTION

The present invention is directed generally to compositions and their use in the therapy and diagnosis of cancer, particularly prostate cancer. As described further below, illustrative compositions of the present invention include, but are not restricted to, polypeptides, particularly immunogenic polypeptides, polynucleotides encoding such polypeptides, antibodies and other binding agents, antigen presenting cells (APCs) and immune system cells (*e.g.*, T cells).

The practice of the present invention will employ, unless indicated specifically to the contrary, conventional methods of virology, immunology, microbiology, molecular biology and recombinant DNA techniques within the skill of the art, many of which are described below for the purpose of illustration. Such techniques are explained fully in the literature. See, *e.g.*, Sambrook, et al. *Molecular Cloning: A Laboratory Manual* (2nd Edition, 1989); Maniatis et al. *Molecular Cloning: A Laboratory Manual* (1982); DNA Cloning: A Practical Approach, vol. I & II (D. Glover, ed.); Oligonucleotide Synthesis (N. Gait, ed., 1984); Nucleic Acid

Hybridization (B. Hames & S. Higgins, eds., 1985); Transcription and Translation (B. Hames & S. Higgins, eds., 1984); Animal Cell Culture (R. Freshney, ed., 1986); Perbal, A Practical Guide to Molecular Cloning (1984).

All publications, patents and patent applications cited herein, whether
5 supra or infra, are hereby incorporated by reference in their entirety.

As used in this specification and the appended claims, the singular forms "a," "an" and "the" include plural references unless the content clearly dictates otherwise.

Polypeptide Compositions

10 As used herein, the term "polypeptide" " is used in its conventional meaning, *i.e.*, as a sequence of amino acids. The polypeptides are not limited to a specific length of the product; thus, peptides, oligopeptides, and proteins are included within the definition of polypeptide, and such terms may be used interchangeably herein unless specifically indicated otherwise. This term also does not refer to or exclude post-
15 expression modifications of the polypeptide, for example, glycosylations, acetylations, phosphorylations and the like, as well as other modifications known in the art, both naturally occurring and non-naturally occurring. A polypeptide may be an entire protein, or a subsequence thereof. Particular polypeptides of interest in the context of this invention are amino acid subsequences comprising epitopes, *i.e.*, antigenic
20 determinants substantially responsible for the immunogenic properties of a polypeptide and being capable of evoking an immune response.

Particularly illustrative polypeptides of the present invention comprise those encoded by a polynucleotide sequence set forth in any one of SEQ ID NOs: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382
25 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-626, 630, 631, 634, 636, 639-655, 674, 680, 681, 711, 713, 716, 720-722, 735, 737-739, 751, 753, 764, 765, 773-776 and 786-788, or a sequence that hybridizes under moderately stringent conditions, or, alternatively, under highly stringent conditions, to a polynucleotide sequence set forth in any one of SEQ ID NOs: 1-111, 115-171, 173-175,

177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-626, 630, 631, 634, 636, 639-655, 674, 680, 681, 711, 713, 716, 720-722, 735, 737-739, 751, 753, 764, 765, 773-776 and 786-788. In specific embodiments, the polypeptides of the invention
5 comprise amino acid sequences as set forth in any one of SEQ ID NO: 112-114, 172, 176, 178, 327, 329, 331, 336, 339, 376-380, 383, 477-483, 496, 504, 505, 519, 520, 522, 525, 527, 532, 534, 537-551, 553-568, 573-586, 588-590, 592, 627-629, 632, 633, 635, 637, 638, 656-671, 675, 683, 684, 710, 712, 714, 715, 717-719, 723-734, 736, 740-750, 752, 754, 755, 766-772, 777-785 and 789-791.

10 The polypeptides of the present invention are sometimes herein referred to as prostate-specific proteins or prostate-specific polypeptides, as an indication that their identification has been based at least in part upon their increased levels of expression in prostate tissue samples. Thus, a "prostate-specific polypeptide" or "prostate-specific protein," refers generally to a polypeptide sequence of the present
15 invention, or a polynucleotide sequence encoding such a polypeptide, that is expressed in a substantial proportion of prostate tissue samples, for example preferably greater than about 20%, more preferably greater than about 30%, and most preferably greater than about 50% or more of prostate tissue samples tested, at a level that is at least two fold, and preferably at least five fold, greater than the level of expression in other
20 normal tissues, as determined using a representative assay provided herein. A prostate-specific polypeptide sequence of the invention, based upon its increased level of expression in tumor cells, has particular utility both as a diagnostic marker as well as a therapeutic target, as further described below.

 In certain preferred embodiments, the polypeptides of the invention are
25 immunogenic, i.e., they react detectably within an immunoassay (such as an ELISA or T-cell stimulation assay) with antisera and/or T-cells from a patient with prostate cancer. Screening for immunogenic activity can be performed using techniques well known to the skilled artisan. For example, such screens can be performed using methods such as those described in Harlow and Lane, *Antibodies: A Laboratory*
30 *Manual*, Cold Spring Harbor Laboratory, 1988. In one illustrative example, a

polypeptide may be immobilized on a solid support and contacted with patient sera to allow binding of antibodies within the sera to the immobilized polypeptide. Unbound sera may then be removed and bound antibodies detected using, for example, ¹²⁵I-labeled Protein A.

- 5 As would be recognized by the skilled artisan, immunogenic portions of the polypeptides disclosed herein are also encompassed by the present invention. An "immunogenic portion," as used herein, is a fragment of an immunogenic polypeptide of the invention that itself is immunologically reactive (*i.e.*, specifically binds) with the B-cells and/or T-cell surface antigen receptors that recognize the polypeptide.
- 10 Immunogenic portions may generally be identified using well known techniques, such as those summarized in Paul, *Fundamental Immunology*, 3rd ed., 243-247 (Raven Press, 1993) and references cited therein. Such techniques include screening polypeptides for the ability to react with antigen-specific antibodies, antisera and/or T-cell lines or clones. As used herein, antisera and antibodies are "antigen-specific" if they
- 15 specifically bind to an antigen (*i.e.*, they react with the protein in an ELISA or other immunoassay, and do not react detectably with unrelated proteins). Such antisera and antibodies may be prepared as described herein, and using well-known techniques.

- In one preferred embodiment, an immunogenic portion of a polypeptide of the present invention is a portion that reacts with antisera and/or T-cells at a level that
- 20 is not substantially less than the reactivity of the full-length polypeptide (*e.g.*, in an ELISA and/or T-cell reactivity assay). Preferably, the level of immunogenic activity of the immunogenic portion is at least about 50%, preferably at least about 70% and most preferably greater than about 90% of the immunogenicity for the full-length polypeptide. In some instances, preferred immunogenic portions will be identified that
- 25 have a level of immunogenic activity greater than that of the corresponding full-length polypeptide, *e.g.*, having greater than about 100% or 150% or more immunogenic activity.

- In certain other embodiments, illustrative immunogenic portions may include peptides in which an N-terminal leader sequence and/or transmembrane domain
- 30 has been deleted. Other illustrative immunogenic portions will contain a small N-

and/or C-terminal deletion (*e.g.*, 1-30 amino acids, preferably 5-15 amino acids), relative to the mature protein.

In another embodiment, a polypeptide composition of the invention may also comprise one or more polypeptides that are immunologically reactive with T cells
5 and/or antibodies generated against a polypeptide of the invention, particularly a polypeptide having an amino acid sequence disclosed herein, or to an immunogenic fragment or variant thereof.

In another embodiment of the invention, polypeptides are provided that comprise one or more polypeptides that are capable of eliciting T cells and/or antibodies
10 that are immunologically reactive with one or more polypeptides described herein, or one or more polypeptides encoded by contiguous nucleic acid sequences contained in the polynucleotide sequences disclosed herein, or immunogenic fragments or variants thereof, or to one or more nucleic acid sequences which hybridize to one or more of these sequences under conditions of moderate to high stringency.

The present invention, in another aspect, provides polypeptide fragments
15 comprising at least about 5, 10, 15, 20, 25, 50, or 100 contiguous amino acids, or more, including all intermediate lengths, of a polypeptide composition set forth herein, such as those set forth in SEQ ID NO: 112-114, 172, 176, 178, 327, 329, 331, 336, 339, 376-380, 383, 477-483, 496, 504, 505, 519, 520, 522, 525, 527, 532, 534, 537-551, 553-568,
20 573-586, 588-590, 592, 627-629, 632, 633, 635, 637, 638, 656-671, 675, 683, 684, 710, 712, 714, 715, 717-719, 723-734, 736, 740-750, 752, 754, 755, 766-772, 777-785 and 789-791, or those encoded by a polynucleotide sequence set forth in a sequence of SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591,
25 593-606, 618-626, 630, 631, 634, 636, 639-655, 674, 680, 681, 711, 713, 716, 720-722, 735, 737-739, 751, 753, 764, 765, 773-776 and 786-788.

In another aspect, the present invention provides variants of the polypeptide compositions described herein. Polypeptide variants generally encompassed by the present invention will typically exhibit at least about 70%, 75%,
30 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or more identity

(determined as described below), along its length, to a polypeptide sequence set forth herein.

In one preferred embodiment, the polypeptide fragments and variants provided by the present invention are immunologically reactive with an antibody and/or
5 T-cell that reacts with a full-length polypeptide specifically set forth herein.

In another preferred embodiment, the polypeptide fragments and variants provided by the present invention exhibit a level of immunogenic activity of at least about 50%, preferably at least about 70%, and most preferably at least about 90% or more of that exhibited by a full-length polypeptide sequence specifically set forth
10 herein.

A polypeptide "variant," as the term is used herein, is a polypeptide that typically differs from a polypeptide specifically disclosed herein in one or more substitutions, deletions, additions and/or insertions. Such variants may be naturally occurring or may be synthetically generated, for example, by modifying one or more of
15 the above polypeptide sequences of the invention and evaluating their immunogenic activity as described herein using any of a number of techniques well known in the art.

For example, certain illustrative variants of the polypeptides of the invention include those in which one or more portions, such as an N-terminal leader sequence or transmembrane domain, have been removed. Other illustrative variants
20 include variants in which a small portion (*e.g.*, 1-30 amino acids, preferably 5-15 amino acids) has been removed from the N- and/or C-terminal of the mature protein.

In many instances, a variant will contain conservative substitutions. A "conservative substitution" is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide
25 chemistry would expect the secondary structure and hydropathic nature of the polypeptide to be substantially unchanged. As described above, modifications may be made in the structure of the polynucleotides and polypeptides of the present invention and still obtain a functional molecule that encodes a variant or derivative polypeptide with desirable characteristics, *e.g.*, with immunogenic characteristics. When it is
30 desired to alter the amino acid sequence of a polypeptide to create an equivalent, or

even an improved, immunogenic variant or portion of a polypeptide of the invention, one skilled in the art will typically change one or more of the codons of the encoding DNA sequence according to Table 1.

For example, certain amino acids may be substituted for other amino acids in a protein structure without appreciable loss of interactive binding capacity with structures such as, for example, antigen-binding regions of antibodies or binding sites on substrate molecules. Since it is the interactive capacity and nature of a protein that defines that protein's biological functional activity, certain amino acid sequence substitutions can be made in a protein sequence, and, of course, its underlying DNA coding sequence, and nevertheless obtain a protein with like properties. It is thus contemplated that various changes may be made in the peptide sequences of the disclosed compositions, or corresponding DNA sequences which encode said peptides without appreciable loss of their biological utility or activity.

TABLE 1

Amino Acids			Codons						
Alanine	Ala	A	GCA	GCC	GCG	GCU			
Cysteine	Cys	C	UGC	UGU					
Aspartic acid	Asp	D	GAC	GAU					
Glutamic acid	Glu	E	GAA	GAG					
Phenylalanine	Phe	F	UUC	UUU					
Glycine	Gly	G	GGA	GGC	GGG	GGU			
Histidine	His	H	CAC	CAU					
Isoleucine	Ile	I	AUA	AUC	AUU				
Lysine	Lys	K	AAA	AAG					
Leucine	Leu	L	UUA	UUG	CUA	CUC	CUG	CUU	
Methionine	Met	M	AUG						
Asparagine	Asn	N	AAC	AAU					
Proline	Pro	P	CCA	CCC	CCG	CCU			
Glutamine	Gln	Q	CAA	CAG					
Arginine	Arg	R	AGA	AGG	CGA	CGC	CGG	CGU	
Serine	Ser	S	AGC	AGU	UCA	UCC	UCG	UCU	
Threonine	Thr	T	ACA	ACC	ACG	ACU			
Valine	Val	V	GUA	GUC	GUG	GUU			
Tryptophan	Trp	W	UGG						
Tyrosine	Tyr	Y	UAC	UAU					

In making such changes, the hydropathic index of amino acids may be considered. The importance of the hydropathic amino acid index in conferring interactive biologic function on a protein is generally understood in the art (Kyte and Doolittle, 1982, incorporated herein by reference). It is accepted that the relative hydropathic character of the amino acid contributes to the secondary structure of the resultant protein, which in turn defines the interaction of the protein with other molecules, for example, enzymes, substrates, receptors, DNA, antibodies, antigens, and the like. Each amino acid has been assigned a hydropathic index on the basis of its

hydrophobicity and charge characteristics (Kyte and Doolittle, 1982). These values are: isoleucine (+4.5); valine (+4.2); leucine (+3.8); phenylalanine (+2.8); cysteine/cystine (+2.5); methionine (+1.9); alanine (+1.8); glycine (−0.4); threonine (−0.7); serine (−0.8); tryptophan (−0.9); tyrosine (−1.3); proline (−1.6); histidine (−3.2); glutamate (−3.5);
5 glutamine (−3.5); aspartate (−3.5); asparagine (−3.5); lysine (−3.9); and arginine (−4.5).

It is known in the art that certain amino acids may be substituted by other amino acids having a similar hydropathic index or score and still result in a protein with similar biological activity, *i.e.* still obtain a biological functionally equivalent protein. In making such changes, the substitution of amino acids whose hydropathic indices are
10 within ± 2 is preferred, those within ± 1 are particularly preferred, and those within ± 0.5 are even more particularly preferred. It is also understood in the art that the substitution of like amino acids can be made effectively on the basis of hydrophilicity. U. S. Patent 4,554,101 (specifically incorporated herein by reference in its entirety), states that the greatest local average hydrophilicity of a protein, as governed by the hydrophilicity of
15 its adjacent amino acids, correlates with a biological property of the protein.

As detailed in U. S. Patent 4,554,101, the following hydrophilicity values have been assigned to amino acid residues: arginine (+3.0); lysine (+3.0); aspartate (+3.0 \pm 1); glutamate (+3.0 \pm 1); serine (+0.3); asparagine (+0.2); glutamine (+0.2); glycine (0); threonine (−0.4); proline (−0.5 \pm 1); alanine (−0.5); histidine (−0.5); cysteine
20 (−1.0); methionine (−1.3); valine (−1.5); leucine (−1.8); isoleucine (−1.8); tyrosine (−2.3); phenylalanine (−2.5); tryptophan (−3.4). It is understood that an amino acid can be substituted for another having a similar hydrophilicity value and still obtain a biologically equivalent, and in particular, an immunologically equivalent protein. In such changes, the substitution of amino acids whose hydrophilicity values are within ± 2
25 is preferred, those within ± 1 are particularly preferred, and those within ± 0.5 are even more particularly preferred.

As outlined above, amino acid substitutions are generally therefore based on the relative similarity of the amino acid side-chain substituents, for example, their hydrophobicity, hydrophilicity, charge, size, and the like. Exemplary substitutions that
30 take various of the foregoing characteristics into consideration are well known to those

of skill in the art and include: arginine and lysine; glutamate and aspartate; serine and threonine; glutamine and asparagine; and valine, leucine and isoleucine.

In addition, any polynucleotide may be further modified to increase stability *in vivo*. Possible modifications include, but are not limited to, the addition of
5 flanking sequences at the 5' and/or 3' ends; the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages in the backbone; and/or the inclusion of nontraditional bases such as inosine, queosine and wybutosine, as well as acetyl-methyl-, thio- and other modified forms of adenine, cytidine, guanine, thymine and uridine.

10 Amino acid substitutions may further be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity and/or the amphipathic nature of the residues. For example, negatively charged amino acids include aspartic acid and glutamic acid; positively charged amino acids include lysine and arginine; and amino acids with uncharged polar head groups having similar hydrophilicity values
15 include leucine, isoleucine and valine; glycine and alanine; asparagine and glutamine; and serine, threonine, phenylalanine and tyrosine. Other groups of amino acids that may represent conservative changes include: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his. A variant may also, or alternatively, contain nonconservative changes. In a
20 preferred embodiment, variant polypeptides differ from a native sequence by substitution, deletion or addition of five amino acids or fewer. Variants may also (or alternatively) be modified by, for example, the deletion or addition of amino acids that have minimal influence on the immunogenicity, secondary structure and hydrophobic nature of the polypeptide.

25 As noted above, polypeptides may comprise a signal (or leader) sequence at the N-terminal end of the protein, which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (e.g., poly-His), or to enhance binding of the polypeptide to a solid support. For
30 example, a polypeptide may be conjugated to an immunoglobulin Fc region.

When comparing polypeptide sequences, two sequences are said to be "identical" if the sequence of amino acids in the two sequences is the same when aligned for maximum correspondence, as described below. Comparisons between two sequences are typically performed by comparing the sequences over a comparison window to identify and compare local regions of sequence similarity. A "comparison window" as used herein, refers to a segment of at least about 20 contiguous positions, usually 30 to about 75, 40 to about 50, in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned.

- Optimal alignment of sequences for comparison may be conducted using the Megalign program in the Lasergene suite of bioinformatics software (DNASTAR, Inc., Madison, WI), using default parameters. This program embodies several alignment schemes described in the following references: Dayhoff, M.O. (1978) A model of evolutionary change in proteins – Matrices for detecting distant relationships. In Dayhoff, M.O. (ed.) *Atlas of Protein Sequence and Structure*, National Biomedical Research Foundation, Washington DC Vol. 5, Suppl. 3, pp. 345-358; Hein J. (1990) Unified Approach to Alignment and Phylogenies pp. 626-645 *Methods in Enzymology* vol. 183, Academic Press, Inc., San Diego, CA; Higgins, D.G. and Sharp, P.M. (1989) *CABIOS* 5:151-153; Myers, E.W. and Muller W. (1988) *CABIOS* 4:11-17; Robinson, E.D. (1971) *Comb. Theor* 11:105; Santou, N. Nes, M. (1987) *Mol. Biol. Evol.* 4:406-425; Sneath, P.H.A. and Sokal, R.R. (1973) *Numerical Taxonomy – the Principles and Practice of Numerical Taxonomy*, Freeman Press, San Francisco, CA; Wilbur, W.J. and Lipman, D.J. (1983) *Proc. Natl. Acad. Sci. USA* 80:726-730.

Alternatively, optimal alignment of sequences for comparison may be conducted by the local identity algorithm of Smith and Waterman (1981) *Add. APL. Math* 2:482, by the identity alignment algorithm of Needleman and Wunsch (1970) *J. Mol. Biol.* 48:443, by the search for similarity methods of Pearson and Lipman (1988) *Proc. Natl. Acad. Sci. USA* 85: 2444, by computerized implementations of these algorithms (GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics

Software Package, Genetics Computer Group (GCG), 575 Science Dr., Madison, WI), or by inspection.

One preferred example of algorithms that are suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul et al. (1977) *Nucl. Acids Res.* 25:3389-3402 and Altschul et al. (1990) *J. Mol. Biol.* 215:403-410, respectively. BLAST and BLAST 2.0 can be used, for example with the parameters described herein, to determine percent sequence identity for the polynucleotides and polypeptides of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information. For amino acid sequences, a scoring matrix can be used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T and X determine the sensitivity and speed of the alignment.

In one preferred approach, the "percentage of sequence identity" is determined by comparing two optimally aligned sequences over a window of comparison of at least 20 positions, wherein the portion of the polypeptide sequence in the comparison window may comprise additions or deletions (*i.e.*, gaps) of 20 percent or less, usually 5 to 15 percent, or 10 to 12 percent, as compared to the reference sequences (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the reference sequence (*i.e.*, the window size) and multiplying the results by 100 to yield the percentage of sequence identity.

Within other illustrative embodiments, a polypeptide may be a fusion polypeptide that comprises multiple polypeptides as described herein, or that comprises at least one polypeptide as described herein and an unrelated sequence, such as a known

tumor protein. A fusion partner may, for example, assist in providing T helper epitopes (an immunological fusion partner), preferably T helper epitopes recognized by humans, or may assist in expressing the protein (an expression enhancer) at higher yields than the native recombinant protein. Certain preferred fusion partners are both immunological and expression enhancing fusion partners. Other fusion partners may be selected so as to increase the solubility of the polypeptide or to enable the polypeptide to be targeted to desired intracellular compartments. Still further fusion partners include affinity tags, which facilitate purification of the polypeptide.

Fusion polypeptides may generally be prepared using standard techniques, including chemical conjugation. Preferably, a fusion polypeptide is expressed as a recombinant polypeptide, allowing the production of increased levels, relative to a non-fused polypeptide, in an expression system. Briefly, DNA sequences encoding the polypeptide components may be assembled separately, and ligated into an appropriate expression vector. The 3' end of the DNA sequence encoding one polypeptide component is ligated, with or without a peptide linker, to the 5' end of a DNA sequence encoding the second polypeptide component so that the reading frames of the sequences are in phase. This permits translation into a single fusion polypeptide that retains the biological activity of both component polypeptides.

A peptide linker sequence may be employed to separate the first and second polypeptide components by a distance sufficient to ensure that each polypeptide folds into its secondary and tertiary structures. Such a peptide linker sequence is incorporated into the fusion polypeptide using standard techniques well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a secondary structure that could interact with functional epitopes on the first and second polypeptides; and (3) the lack of hydrophobic or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as linkers include those disclosed in Maratea et al., *Gene* 40:39-46, 1985; Murphy et al.,

Proc. Natl. Acad. Sci. USA 83:8258-8262, 1986; U.S. Patent No. 4,935,233 and U.S. Patent No. 4,751,180. The linker sequence may generally be from 1 to about 50 amino acids in length. Linker sequences are not required when the first and second polypeptides have non-essential N-terminal amino acid regions that can be used to
5 separate the functional domains and prevent steric interference.

The ligated DNA sequences are operably linked to suitable transcriptional or translational regulatory elements. The regulatory elements responsible for expression of DNA are located only 5' to the DNA sequence encoding the first polypeptides. Similarly, stop codons required to end translation and
10 transcription termination signals are only present 3' to the DNA sequence encoding the second polypeptide.

The fusion polypeptide can comprise a polypeptide as described herein together with an unrelated immunogenic protein, such as an immunogenic protein capable of eliciting a recall response. Examples of such proteins include tetanus,
15 tuberculosis and hepatitis proteins (*see, for example, Stoute et al. New Engl. J. Med.*, 336:86-91, 1997).

In one preferred embodiment, the immunological fusion partner is derived from a *Mycobacterium* sp., such as a *Mycobacterium tuberculosis*-derived Ra12 fragment. Ra12 compositions and methods for their use in enhancing the expression
20 and/or immunogenicity of heterologous polynucleotide/polypeptide sequences is described in U.S. Patent Application 60/158,585, the disclosure of which is incorporated herein by reference in its entirety. Briefly, Ra12 refers to a polynucleotide region that is a subsequence of a *Mycobacterium tuberculosis* MTB32A nucleic acid. MTB32A is a serine protease of 32 KD molecular weight encoded by a gene in virulent
25 and avirulent strains of *M. tuberculosis*. The nucleotide sequence and amino acid sequence of MTB32A have been described (for example, U.S. Patent Application 60/158,585; *see also, Skeiky et al., Infection and Immun.* (1999) 67:3998-4007, incorporated herein by reference). C-terminal fragments of the MTB32A coding sequence express at high levels and remain as a soluble polypeptides throughout the
30 purification process. Moreover, Ra12 may enhance the immunogenicity of heterologous

immunogenic polypeptides with which it is fused. One preferred Ra12 fusion polypeptide comprises a 14 KD C-terminal fragment corresponding to amino acid residues 192 to 323 of MTB32A. Other preferred Ra12 polynucleotides generally comprise at least about 15 consecutive nucleotides, at least about 30 nucleotides, at least about 60 nucleotides, at least about 100 nucleotides, at least about 200 nucleotides, or at least about 300 nucleotides that encode a portion of a Ra12 polypeptide. Ra12 polynucleotides may comprise a native sequence (*i.e.*, an endogenous sequence that encodes a Ra12 polypeptide or a portion thereof) or may comprise a variant of such a sequence. Ra12 polynucleotide variants may contain one or more substitutions, additions, deletions and/or insertions such that the biological activity of the encoded fusion polypeptide is not substantially diminished, relative to a fusion polypeptide comprising a native Ra12 polypeptide. Variants preferably exhibit at least about 70% identity, more preferably at least about 80% identity and most preferably at least about 90% identity to a polynucleotide sequence that encodes a native Ra12 polypeptide or a portion thereof.

Within other preferred embodiments, an immunological fusion partner is derived from protein D, a surface protein of the gram-negative bacterium *Haemophilus influenza B* (WO 91/18926). Preferably, a protein D derivative comprises approximately the first third of the protein (*e.g.*, the first N-terminal 100-110 amino acids), and a protein D derivative may be lipidated. Within certain preferred embodiments, the first 109 residues of a Lipoprotein D fusion partner is included on the N-terminus to provide the polypeptide with additional exogenous T-cell epitopes and to increase the expression level in *E. coli* (thus functioning as an expression enhancer). The lipid tail ensures optimal presentation of the antigen to antigen presenting cells. Other fusion partners include the non-structural protein from influenzae virus, NS1 (hemagglutinin). Typically, the N-terminal 81 amino acids are used, although different fragments that include T-helper epitopes may be used.

In another embodiment, the immunological fusion partner is the protein known as LYTA, or a portion thereof (preferably a C-terminal portion). LYTA is derived from *Streptococcus pneumoniae*, which synthesizes an N-acetyl-L-alanine

amidase known as amidase LYTA (encoded by the *LytA* gene; *Gene* 43:265-292, 1986). LYTA is an autolysin that specifically degrades certain bonds in the peptidoglycan backbone. The C-terminal domain of the LYTA protein is responsible for the affinity to the choline or to some choline analogues such as DEAE. This property has been exploited for the development of *E. coli* C-LYTA expressing plasmids useful for expression of fusion proteins. Purification of hybrid proteins containing the C-LYTA fragment at the amino terminus has been described (see *Biotechnology* 10:795-798, 1992). Within a preferred embodiment, a repeat portion of LYTA may be incorporated into a fusion polypeptide. A repeat portion is found in the C-terminal region starting at residue 178. A particularly preferred repeat portion incorporates residues 188-305.

Yet another illustrative embodiment involves fusion polypeptides, and the polynucleotides encoding them, wherein the fusion partner comprises a targeting signal capable of directing a polypeptide to the endosomal/lysosomal compartment, as described in U.S. Patent No. 5,633,234. An immunogenic polypeptide of the invention, when fused with this targeting signal, will associate more efficiently with MHC class II molecules and thereby provide enhanced in vivo stimulation of CD4⁺ T-cells specific for the polypeptide.

Polypeptides of the invention are prepared using any of a variety of well known synthetic and/or recombinant techniques, the latter of which are further described below. Polypeptides, portions and other variants generally less than about 150 amino acids can be generated by synthetic means, using techniques well known to those of ordinary skill in the art. In one illustrative example, such polypeptides are synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain. See Merrifield, *J. Am. Chem. Soc.* 85:2149-2146, 1963. Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin Elmer/Applied BioSystems Division (Foster City, CA), and may be operated according to the manufacturer's instructions.

In general, polypeptide compositions (including fusion polypeptides) of the invention are isolated. An "isolated" polypeptide is one that is removed from its

original environment. For example, a naturally-occurring protein or polypeptide is isolated if it is separated from some or all of the coexisting materials in the natural system. Preferably, such polypeptides are also purified, *e.g.*, are at least about 90% pure, more preferably at least about 95% pure and most preferably at least about 99%
5 pure.

Polynucleotide Compositions

The present invention, in other aspects, provides polynucleotide compositions. The terms "DNA" and "polynucleotide" are used essentially interchangeably herein to refer to a DNA molecule that has been isolated free of total
10 genomic DNA of a particular species. "Isolated," as used herein, means that a polynucleotide is substantially away from other coding sequences, and that the DNA molecule does not contain large portions of unrelated coding DNA, such as large chromosomal fragments or other functional genes or polypeptide coding regions. Of course, this refers to the DNA molecule as originally isolated, and does not exclude
15 genes or coding regions later added to the segment by the hand of man.

As will be understood by those skilled in the art, the polynucleotide compositions of this invention can include genomic sequences, extra-genomic and plasmid-encoded sequences and smaller engineered gene segments that express, or may be adapted to express, proteins, polypeptides, peptides and the like. Such segments may
20 be naturally isolated, or modified synthetically by the hand of man.

As will be also recognized by the skilled artisan, polynucleotides of the invention may be single-stranded (coding or antisense) or double-stranded, and may be DNA (genomic, cDNA or synthetic) or RNA molecules. RNA molecules may include HnRNA molecules, which contain introns and correspond to a DNA molecule in a one-
25 to-one manner, and mRNA molecules, which do not contain introns. Additional coding or non-coding sequences may, but need not, be present within a polynucleotide of the present invention, and a polynucleotide may, but need not, be linked to other molecules and/or support materials.

Polynucleotides may comprise a native sequence (*i.e.*, an endogenous sequence that encodes a polypeptide/protein of the invention or a portion thereof) or may comprise a sequence that encodes a variant or derivative, preferably an immunogenic variant or derivative, of such a sequence.

5 Therefore, according to another aspect of the present invention, polynucleotide compositions are provided that comprise some or all of a polynucleotide sequence set forth in any one of SEQ ID NOs: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-626, 630, 631, 634, 636, 639-655, 10 674, 680, 681, 711, 713, 716, 720-722, 735, 737-739, 751, 753, 764, 765, 773-776 and 786-788, complements of a polynucleotide sequence set forth in any one of SEQ ID NOs: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-626, 630, 631, 634, 636, 639-655, 674, 680, 681, 711, 713, 716, 720-722, 15 735, 737-739, 751, 753, 764, 765, 773-776 and 786-788, and degenerate variants of a polynucleotide sequence set forth in any one of SEQ ID NOs: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-626, 630, 631, 634, 636, 639-655, 674, 680, 681, 711, 713, 716, 720-722, 735, 737-739, 751, 753, 764, 765, 20 773-776 and 786-788. In certain preferred embodiments, the polynucleotide sequences set forth herein encode immunogenic polypeptides, as described above.

 In other related embodiments, the present invention provides polynucleotide variants having substantial identity to the sequences disclosed herein in SEQ ID NOs: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332- 25 335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-626, 630, 631, 634, 636, 639-655, 674, 680, 681, 711, 713, 716, 720-722, 735, 737-739, 751, 753, 764, 765, 773-776 and 786-788, for example those comprising at least 70% sequence identity, preferably at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% or higher, sequence identity compared to a 30 polynucleotide sequence of this invention using the methods described herein, (*e.g.*,

BLAST analysis using standard parameters, as described below). One skilled in this art will recognize that these values can be appropriately adjusted to determine corresponding identity of proteins encoded by two nucleotide sequences by taking into account codon degeneracy, amino acid similarity, reading frame positioning and the
5 like.

Typically, polynucleotide variants will contain one or more substitutions, additions, deletions and/or insertions, preferably such that the immunogenicity of the polypeptide encoded by the variant polynucleotide is not substantially diminished relative to a polypeptide encoded by a polynucleotide sequence specifically set forth
10 herein). The term "variants" should also be understood to encompass homologous genes of xenogenic origin.

In additional embodiments, the present invention provides polynucleotide fragments comprising various lengths of contiguous stretches of sequence identical to, or complementary to, one or more of the sequences disclosed
15 herein. For example, polynucleotides are provided by this invention that comprise at least about 10, 15, 20, 30, 40, 50, 75, 100, 150, 200, 300, 400, 500 or 1000 or more contiguous nucleotides of one or more of the sequences disclosed herein as well as all intermediate lengths there between. It will be readily understood that "intermediate lengths", in this context, means any length between the quoted values, such as 16, 17,
20 18, 19, *etc.*; 21, 22, 23, *etc.*; 30, 31, 32, *etc.*; 50, 51, 52, 53, *etc.*; 100, 101, 102, 103, *etc.*; 150, 151, 152, 153, *etc.*; including all integers through 200-500; 500-1,000, and the like.

In another embodiment of the invention, polynucleotide compositions are provided that are capable of hybridizing under moderate to high stringency conditions to
25 a polynucleotide sequence provided herein, or a fragment thereof, or a complementary sequence thereof. Hybridization techniques are well known in the art of molecular biology. For purposes of illustration, suitable moderately stringent conditions for testing the hybridization of a polynucleotide of this invention with other polynucleotides include prewashing in a solution of 5 X SSC, 0.5% SDS, 1.0 mM EDTA (pH 8.0);
30 hybridizing at 50°C-60°C, 5 X SSC, overnight; followed by washing twice at 65°C for

20 minutes with each of 2X, 0.5X and 0.2X SSC containing 0.1% SDS. One skilled in the art will understand that the stringency of hybridization can be readily manipulated, such as by altering the salt content of the hybridization solution and/or the temperature at which the hybridization is performed. For example, in another embodiment, suitable
5 highly stringent hybridization conditions include those described above, with the exception that the temperature of hybridization is increased, *e.g.*, to 60-65°C or 65-70°C.

In certain preferred embodiments, the polynucleotides described above, *e.g.*, polynucleotide variants, fragments and hybridizing sequences, encode polypeptides
10 that are immunologically cross-reactive with a polypeptide sequence specifically set forth herein. In other preferred embodiments, such polynucleotides encode polypeptides that have a level of immunogenic activity of at least about 50%, preferably at least about 70%, and more preferably at least about 90% of that for a polypeptide sequence specifically set forth herein.

15 The polynucleotides of the present invention, or fragments thereof, regardless of the length of the coding sequence itself, may be combined with other DNA sequences, such as promoters, polyadenylation signals, additional restriction enzyme sites, multiple cloning sites, other coding segments, and the like, such that their overall length may vary considerably. It is therefore contemplated that a nucleic acid fragment
20 of almost any length may be employed, with the total length preferably being limited by the ease of preparation and use in the intended recombinant DNA protocol. For example, illustrative polynucleotide segments with total lengths of about 10,000, about 5000, about 3000, about 2,000, about 1,000, about 500, about 200, about 100, about 50 base pairs in length, and the like, (including all intermediate lengths) are contemplated
25 to be useful in many implementations of this invention.

When comparing polynucleotide sequences, two sequences are said to be "identical" if the sequence of nucleotides in the two sequences is the same when aligned for maximum correspondence, as described below. Comparisons between two sequences are typically performed by comparing the sequences over a comparison
30 window to identify and compare local regions of sequence similarity. A "comparison

window" as used herein, refers to a segment of at least about 20 contiguous positions, usually 30 to about 75, preferably 40 to about 50, in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned.

- 5 Optimal alignment of sequences for comparison may be conducted using the Megalign program in the Lasergene suite of bioinformatics software (DNASTAR, Inc., Madison, WI), using default parameters. This program embodies several alignment schemes described in the following references: Dayhoff, M.O. (1978) A model of evolutionary change in proteins – Matrices for detecting distant relationships.
- 10 In Dayhoff, M.O. (ed.) Atlas of Protein Sequence and Structure, National Biomedical Research Foundation, Washington DC Vol. 5, Suppl. 3, pp. 345-358; Hein J. (1990) Unified Approach to Alignment and Phylogenies pp. 626-645 *Methods in Enzymology* vol. 183, Academic Press, Inc., San Diego, CA; Higgins, D.G. and Sharp, P.M. (1989) *CABIOS* 5:151-153; Myers, E.W. and Muller W. (1988) *CABIOS* 4:11-17; Robinson,
- 15 E.D. (1971) *Comb. Theor* 11:105; Santou, N. Nes, M. (1987) *Mol. Biol. Evol.* 4:406-425; Sneath, P.H.A. and Sokal, R.R. (1973) *Numerical Taxonomy – the Principles and Practice of Numerical Taxonomy*, Freeman Press, San Francisco, CA; Wilbur, W.J. and Lipman, D.J. (1983) *Proc. Natl. Acad. Sci. USA* 80:726-730.

- Alternatively, optimal alignment of sequences for comparison may be
- 20 conducted by the local identity algorithm of Smith and Waterman (1981) *Add. APL. Math* 2:482, by the identity alignment algorithm of Needleman and Wunsch (1970) *J. Mol. Biol.* 48:443, by the search for similarity methods of Pearson and Lipman (1988) *Proc. Natl. Acad. Sci. USA* 85: 2444, by computerized implementations of these algorithms (GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics
- 25 Software Package, Genetics Computer Group (GCG), 575 Science Dr., Madison, WI), or by inspection.

- One preferred example of algorithms that are suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul et al. (1977) *Nucl. Acids Res.* 25:3389-3402
- 30 and Altschul et al. (1990) *J. Mol. Biol.* 215:403-410, respectively. BLAST and BLAST

2.0 can be used, for example with the parameters described herein, to determine percent sequence identity for the polynucleotides of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information. In one illustrative example, cumulative scores can be calculated using, for
5 nucleotide sequences, the parameters M (reward score for a pair of matching residues; always >0) and N (penalty score for mismatching residues; always <0). Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments;
10 or the end of either sequence is reached. The BLAST algorithm parameters W, T and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff (1989) *Proc. Natl. Acad. Sci. USA* 89:10915) alignments, (B) of 50, expectation (E) of 10, M=5, N=-4 and
15 a comparison of both strands.

Preferably, the "percentage of sequence identity" is determined by comparing two optimally aligned sequences over a window of comparison of at least 20 positions, wherein the portion of the polynucleotide sequence in the comparison window may comprise additions or deletions (*i.e.*, gaps) of 20 percent or less, usually 5
20 to 15 percent, or 10 to 12 percent, as compared to the reference sequences (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid bases occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the
25 reference sequence (*i.e.*, the window size) and multiplying the results by 100 to yield the percentage of sequence identity.

It will be appreciated by those of ordinary skill in the art that, as a result of the degeneracy of the genetic code, there are many nucleotide sequences that encode a polypeptide as described herein. Some of these polynucleotides bear minimal
30 homology to the nucleotide sequence of any native gene. Nonetheless, polynucleotides

that vary due to differences in codon usage are specifically contemplated by the present invention. Further, alleles of the genes comprising the polynucleotide sequences provided herein are within the scope of the present invention. Alleles are endogenous genes that are altered as a result of one or more mutations, such as deletions, additions
5 and/or substitutions of nucleotides. The resulting mRNA and protein may, but need not, have an altered structure or function. Alleles may be identified using standard techniques (such as hybridization, amplification and/or database sequence comparison).

Therefore, in another embodiment of the invention, a mutagenesis approach, such as site-specific mutagenesis, is employed for the preparation of
10 immunogenic variants and/or derivatives of the polypeptides described herein. By this approach, specific modifications in a polypeptide sequence can be made through mutagenesis of the underlying polynucleotides that encode them. These techniques provides a straightforward approach to prepare and test sequence variants, for example, incorporating one or more of the foregoing considerations, by introducing one or more
15 nucleotide sequence changes into the polynucleotide.

Site-specific mutagenesis allows the production of mutants through the use of specific oligonucleotide sequences which encode the DNA sequence of the desired mutation, as well as a sufficient number of adjacent nucleotides, to provide a primer sequence of sufficient size and sequence complexity to form a stable duplex on
20 both sides of the deletion junction being traversed. Mutations may be employed in a selected polynucleotide sequence to improve, alter, decrease, modify, or otherwise change the properties of the polynucleotide itself, and/or alter the properties, activity, composition, stability, or primary sequence of the encoded polypeptide.

In certain embodiments of the present invention, the inventors
25 contemplate the mutagenesis of the disclosed polynucleotide sequences to alter one or more properties of the encoded polypeptide, such as the immunogenicity of a polypeptide vaccine. The techniques of site-specific mutagenesis are well-known in the art, and are widely used to create variants of both polypeptides and polynucleotides. For example, site-specific mutagenesis is often used to alter a specific portion of a DNA
30 molecule. In such embodiments, a primer comprising typically about 14 to about 25

nucleotides or so in length is employed, with about 5 to about 10 residues on both sides of the junction of the sequence being altered.

As will be appreciated by those of skill in the art, site-specific mutagenesis techniques have often employed a phage vector that exists in both a single stranded and double stranded form. Typical vectors useful in site-directed mutagenesis include vectors such as the M13 phage. These phage are readily commercially-available and their use is generally well-known to those skilled in the art. Double-stranded plasmids are also routinely employed in site directed mutagenesis that eliminates the step of transferring the gene of interest from a plasmid to a phage.

10 In general, site-directed mutagenesis in accordance herewith is performed by first obtaining a single-stranded vector or melting apart of two strands of a double-stranded vector that includes within its sequence a DNA sequence that encodes the desired peptide. An oligonucleotide primer bearing the desired mutated sequence is prepared, generally synthetically. This primer is then annealed with the single-stranded
15 vector, and subjected to DNA polymerizing enzymes such as *E. coli* polymerase I Klenow fragment, in order to complete the synthesis of the mutation-bearing strand. Thus, a heteroduplex is formed wherein one strand encodes the original non-mutated sequence and the second strand bears the desired mutation. This heteroduplex vector is then used to transform appropriate cells, such as *E. coli* cells, and clones are selected
20 which include recombinant vectors bearing the mutated sequence arrangement.

The preparation of sequence variants of the selected peptide-encoding DNA segments using site-directed mutagenesis provides a means of producing potentially useful species and is not meant to be limiting as there are other ways in which sequence variants of peptides and the DNA sequences encoding them may be
25 obtained. For example, recombinant vectors encoding the desired peptide sequence may be treated with mutagenic agents, such as hydroxylamine, to obtain sequence variants. Specific details regarding these methods and protocols are found in the teachings of Maloy *et al.*, 1994; Segal, 1976; Prokop and Bajpai, 1991; Kuby, 1994; and Maniatis *et al.*, 1982, each incorporated herein by reference, for that purpose.

As used herein, the term "oligonucleotide directed mutagenesis procedure" refers to template-dependent processes and vector-mediated propagation which result in an increase in the concentration of a specific nucleic acid molecule relative to its initial concentration, or in an increase in the concentration of a detectable
5 signal, such as amplification. As used herein, the term "oligonucleotide directed mutagenesis procedure" is intended to refer to a process that involves the template-dependent extension of a primer molecule. The term template dependent process refers to nucleic acid synthesis of an RNA or a DNA molecule wherein the sequence of the newly synthesized strand of nucleic acid is dictated by the well-known
10 rules of complementary base pairing (see, for example, Watson, 1987). Typically, vector mediated methodologies involve the introduction of the nucleic acid fragment into a DNA or RNA vector, the clonal amplification of the vector, and the recovery of the amplified nucleic acid fragment. Examples of such methodologies are provided by U. S. Patent No. 4,237,224, specifically incorporated herein by reference in its entirety.

15 In another approach for the production of polypeptide variants of the present invention, recursive sequence recombination, as described in U.S. Patent No. 5,837,458, may be employed. In this approach, iterative cycles of recombination and screening or selection are performed to "evolve" individual polynucleotide variants of the invention having, for example, enhanced immunogenic activity.

20 In other embodiments of the present invention, the polynucleotide sequences provided herein can be advantageously used as probes or primers for nucleic acid hybridization. As such, it is contemplated that nucleic acid segments that comprise a sequence region of at least about 15 contiguous nucleotides that has the same sequence as, or is complementary to, a 15 nucleotide long contiguous sequence
25 disclosed herein will find particular utility. Longer contiguous identical or complementary sequences, *e.g.*, those of about 20, 30, 40, 50, 100, 200, 500, 1000 (including all intermediate lengths) and even up to full length sequences will also be of use in certain embodiments.

The ability of such nucleic acid probes to specifically hybridize to a
30 sequence of interest will enable them to be of use in detecting the presence of

complementary sequences in a given sample. However, other uses are also envisioned, such as the use of the sequence information for the preparation of mutant species primers, or primers for use in preparing other genetic constructions.

Polynucleotide molecules having sequence regions consisting of
5 contiguous nucleotide stretches of 10-14, 15-20, 30, 50, or even of 100-200 nucleotides or so (including intermediate lengths as well), identical or complementary to a polynucleotide sequence disclosed herein, are particularly contemplated as hybridization probes for use in, *e.g.*, Southern and Northern blotting. This would allow a gene product, or fragment thereof, to be analyzed, both in diverse cell types and also in
10 various bacterial cells. The total size of fragment, as well as the size of the complementary stretch(es), will ultimately depend on the intended use or application of the particular nucleic acid segment. Smaller fragments will generally find use in hybridization embodiments, wherein the length of the contiguous complementary region may be varied, such as between about 15 and about 100 nucleotides, but larger
15 contiguous complementarity stretches may be used, according to the length complementary sequences one wishes to detect.

The use of a hybridization probe of about 15-25 nucleotides in length allows the formation of a duplex molecule that is both stable and selective. Molecules having contiguous complementary sequences over stretches greater than 15 bases in
20 length are generally preferred, though, in order to increase stability and selectivity of the hybrid, and thereby improve the quality and degree of specific hybrid molecules obtained. One will generally prefer to design nucleic acid molecules having gene-complementary stretches of 15 to 25 contiguous nucleotides, or even longer where desired.

25 Hybridization probes may be selected from any portion of any of the sequences disclosed herein. All that is required is to review the sequences set forth herein, or to any continuous portion of the sequences, from about 15-25 nucleotides in length up to and including the full length sequence, that one wishes to utilize as a probe or primer. The choice of probe and primer sequences may be governed by various

factors. For example, one may wish to employ primers from towards the termini of the total sequence.

Small polynucleotide segments or fragments may be readily prepared by, for example, directly synthesizing the fragment by chemical means, as is commonly practiced using an automated oligonucleotide synthesizer. Also, fragments may be obtained by application of nucleic acid reproduction technology, such as the PCRTM technology of U. S. Patent 4,683,202 (incorporated herein by reference), by introducing selected sequences into recombinant vectors for recombinant production, and by other recombinant DNA techniques generally known to those of skill in the art of molecular biology.

The nucleotide sequences of the invention may be used for their ability to selectively form duplex molecules with complementary stretches of the entire gene or gene fragments of interest. Depending on the application envisioned, one will typically desire to employ varying conditions of hybridization to achieve varying degrees of selectivity of probe towards target sequence. For applications requiring high selectivity, one will typically desire to employ relatively stringent conditions to form the hybrids, *e.g.*, one will select relatively low salt and/or high temperature conditions, such as provided by a salt concentration of from about 0.02 M to about 0.15 M salt at temperatures of from about 50°C to about 70°C. Such selective conditions tolerate little, if any, mismatch between the probe and the template or target strand, and would be particularly suitable for isolating related sequences.

Of course, for some applications, for example, where one desires to prepare mutants employing a mutant primer strand hybridized to an underlying template, less stringent (reduced stringency) hybridization conditions will typically be needed in order to allow formation of the heteroduplex. In these circumstances, one may desire to employ salt conditions such as those of from about 0.15 M to about 0.9 M salt, at temperatures ranging from about 20°C to about 55°C. Cross-hybridizing species can thereby be readily identified as positively hybridizing signals with respect to control hybridizations. In any case, it is generally appreciated that conditions can be rendered more stringent by the addition of increasing amounts of formamide, which serves to

destabilize the hybrid duplex in the same manner as increased temperature. Thus, hybridization conditions can be readily manipulated, and thus will generally be a method of choice depending on the desired results.

According to another embodiment of the present invention,
5 polynucleotide compositions comprising antisense oligonucleotides are provided. Antisense oligonucleotides have been demonstrated to be effective and targeted inhibitors of protein synthesis, and, consequently, provide a therapeutic approach by which a disease can be treated by inhibiting the synthesis of proteins that contribute to the disease. The efficacy of antisense oligonucleotides for inhibiting protein synthesis
10 is well established. For example, the synthesis of polygalacturonase and the muscarine type 2 acetylcholine receptor are inhibited by antisense oligonucleotides directed to their respective mRNA sequences (U. S. Patent 5,739,119 and U. S. Patent 5,759,829). Further, examples of antisense inhibition have been demonstrated with the nuclear protein cyclin, the multiple drug resistance gene (MDG1), ICAM-1, E-selectin, STK-1,
15 striatal GABA_A receptor and human EGF (Jaskulski *et al.*, Science. 1988 Jun 10;240(4858):1544-6; Vasanthakumar and Ahmed, Cancer Commun. 1989;1(4):225-32; Peris *et al.*, Brain Res Mol Brain Res. 1998 Jun 15;57(2):310-20; U. S. Patent 5,801,154; U.S. Patent 5,789,573; U. S. Patent 5,718,709 and U.S. Patent 5,610,288). Antisense constructs have also been described that inhibit and can be used to treat a
20 variety of abnormal cellular proliferations, *e.g.* cancer (U. S. Patent 5,747,470; U. S. Patent 5,591,317 and U. S. Patent 5,783,683).

Therefore, in certain embodiments, the present invention provides oligonucleotide sequences that comprise all, or a portion of, any sequence that is capable of specifically binding to polynucleotide sequence described herein, or a
25 complement thereof. In one embodiment, the antisense oligonucleotides comprise DNA or derivatives thereof. In another embodiment, the oligonucleotides comprise RNA or derivatives thereof. In a third embodiment, the oligonucleotides are modified DNAs comprising a phosphorothioated modified backbone. In a fourth embodiment, the oligonucleotide sequences comprise peptide nucleic acids or derivatives thereof. In
30 each case, preferred compositions comprise a sequence region that is complementary,

and more preferably substantially-complementary, and even more preferably, completely complementary to one or more portions of polynucleotides disclosed herein. Selection of antisense compositions specific for a given gene sequence is based upon analysis of the chosen target sequence and determination of secondary structure, T_m ,
5 binding energy, and relative stability. Antisense compositions may be selected based upon their relative inability to form dimers, hairpins, or other secondary structures that would reduce or prohibit specific binding to the target mRNA in a host cell. Highly preferred target regions of the mRNA, are those which are at or near the AUG translation initiation codon, and those sequences which are substantially complementary
10 to 5' regions of the mRNA. These secondary structure analyses and target site selection considerations can be performed, for example, using v.4 of the OLIGO primer analysis software and/or the BLASTN 2.0.5 algorithm software (Altschul *et al.*, Nucleic Acids Res. 1997 Sep 1;25(17):3389-402).

The use of an antisense delivery method employing a short peptide
15 vector, termed MPG (27 residues), is also contemplated. The MPG peptide contains a hydrophobic domain derived from the fusion sequence of HIV gp41 and a hydrophilic domain from the nuclear localization sequence of SV40 T-antigen (Morris *et al.*, Nucleic Acids Res. 1997 Jul 15;25(14):2730-6). It has been demonstrated that several molecules of the MPG peptide coat the antisense oligonucleotides and can be delivered
20 into cultured mammalian cells in less than 1 hour with relatively high efficiency (90%). Further, the interaction with MPG strongly increases both the stability of the oligonucleotide to nuclease and the ability to cross the plasma membrane.

According to another embodiment of the invention, the polynucleotide compositions described herein are used in the design and preparation of ribozyme
25 molecules for inhibiting expression of the tumor polypeptides and proteins of the present invention in tumor cells. Ribozymes are RNA-protein complexes that cleave nucleic acids in a site-specific fashion. Ribozymes have specific catalytic domains that possess endonuclease activity (Kim and Cech, Proc Natl Acad Sci U S A. 1987 Dec;84(24):8788-92; Forster and Symons, Cell. 1987 Apr 24;49(2):211-20). For
30 example, a large number of ribozymes accelerate phosphoester transfer reactions with a

high degree of specificity, often cleaving only one of several phosphoesters in an oligonucleotide substrate (Cech *et al.*, Cell. 1981 Dec;27(3 Pt 2):487-96; Michel and Westhof, J Mol Biol. 1990 Dec 5;216(3):585-610; Reinhold-Hurek and Shub, Nature. 1992 May 14;357(6374):173-6). This specificity has been attributed to the requirement
5 that the substrate bind via specific base-pairing interactions to the internal guide sequence ("IGS") of the ribozyme prior to chemical reaction.

Six basic varieties of naturally-occurring enzymatic RNAs are known presently. Each can catalyze the hydrolysis of RNA phosphodiester bonds *in trans* (and thus can cleave other RNA molecules) under physiological conditions. In general,
10 enzymatic nucleic acids act by first binding to a target RNA. Such binding occurs through the target binding portion of a enzymatic nucleic acid which is held in close proximity to an enzymatic portion of the molecule that acts to cleave the target RNA. Thus, the enzymatic nucleic acid first recognizes and then binds a target RNA through complementary base-pairing, and once bound to the correct site, acts enzymatically to
15 cut the target RNA. Strategic cleavage of such a target RNA will destroy its ability to direct synthesis of an encoded protein. After an enzymatic nucleic acid has bound and cleaved its RNA target, it is released from that RNA to search for another target and can repeatedly bind and cleave new targets.

The enzymatic nature of a ribozyme is advantageous over many
20 technologies, such as antisense technology (where a nucleic acid molecule simply binds to a nucleic acid target to block its translation) since the concentration of ribozyme necessary to affect a therapeutic treatment is lower than that of an antisense oligonucleotide. This advantage reflects the ability of the ribozyme to act enzymatically. Thus, a single ribozyme molecule is able to cleave many molecules of
25 target RNA. In addition, the ribozyme is a highly specific inhibitor, with the specificity of inhibition depending not only on the base pairing mechanism of binding to the target RNA, but also on the mechanism of target RNA cleavage. Single mismatches, or base-substitutions, near the site of cleavage can completely eliminate catalytic activity of a ribozyme. Similar mismatches in antisense molecules do not prevent their action
30 (Woolf *et al.*, Proc Natl Acad Sci U S A. 1992 Aug 15;89(16):7305-9). Thus, the

specificity of action of a ribozyme is greater than that of an antisense oligonucleotide binding the same RNA site.

The enzymatic nucleic acid molecule may be formed in a hammerhead, hairpin, a hepatitis δ virus, group I intron or RNaseP RNA (in association with an RNA
5 guide sequence) or Neurospora VS RNA motif. Examples of hammerhead motifs are described by Rossi *et al.* Nucleic Acids Res. 1992 Sep 11;20(17):4559-65. Examples of hairpin motifs are described by Hampel *et al.* (Eur. Pat. Appl. Publ. No. EP 0360257), Hampel and Tritz, Biochemistry 1989 Jun 13;28(12):4929-33; Hampel *et al.*, Nucleic
10 Acids Res. 1990 Jan 25;18(2):299-304 and U. S. Patent 5,631,359. An example of the hepatitis δ virus motif is described by Perrotta and Been, Biochemistry. 1992 Dec 1;31(47):11843-52; an example of the RNaseP motif is described by Guerrier-Takada *et al.*, Cell. 1983 Dec;35(3 Pt 2):849-57; Neurospora VS RNA ribozyme motif is described by Collins (Saville and Collins, Cell. 1990 May 18;61(4):685-96; Saville and Collins, Proc Natl Acad Sci U S A. 1991 Oct 1;88(19):8826-30; Collins and Olive,
15 Biochemistry. 1993 Mar 23;32(11):2795-9); and an example of the Group I intron is described in (U. S. Patent 4,987,071). All that is important in an enzymatic nucleic acid molecule of this invention is that it has a specific substrate binding site which is complementary to one or more of the target gene RNA regions, and that it have nucleotide sequences within or surrounding that substrate binding site which impart an
20 RNA cleaving activity to the molecule. Thus the ribozyme constructs need not be limited to specific motifs mentioned herein.

Ribozymes may be designed as described in Int. Pat. Appl. Publ. No. WO 93/23569 and Int. Pat. Appl. Publ. No. WO 94/02595, each specifically incorporated herein by reference) and synthesized to be tested *in vitro* and *in vivo*, as
25 described. Such ribozymes can also be optimized for delivery. While specific examples are provided, those in the art will recognize that equivalent RNA targets in other species can be utilized when necessary.

Ribozyme activity can be optimized by altering the length of the ribozyme binding arms, or chemically synthesizing ribozymes with modifications that
30 prevent their degradation by serum ribonucleases (see *e.g.*, Int. Pat. Appl. Publ. No. WO

92/07065; Int. Pat. Appl. Publ. No. WO 93/15187; Int. Pat. Appl. Publ. No. WO 91/03162; Eur. Pat. Appl. Publ. No. 92110298.4; U. S. Patent 5,334,711; and Int. Pat. Appl. Publ. No. WO 94/13688, which describe various chemical modifications that can be made to the sugar moieties of enzymatic RNA molecules), modifications which enhance their efficacy in cells, and removal of stem II bases to shorten RNA synthesis times and reduce chemical requirements.

Sullivan *et al.* (Int. Pat. Appl. Publ. No. WO 94/02595) describes the general methods for delivery of enzymatic RNA molecules. Ribozymes may be administered to cells by a variety of methods known to those familiar to the art, including, but not restricted to, encapsulation in liposomes, by iontophoresis, or by incorporation into other vehicles, such as hydrogels, cyclodextrins, biodegradable nanocapsules, and bioadhesive microspheres. For some indications, ribozymes may be directly delivered *ex vivo* to cells or tissues with or without the aforementioned vehicles. Alternatively, the RNA/vehicle combination may be locally delivered by direct inhalation, by direct injection or by use of a catheter, infusion pump or stent. Other routes of delivery include, but are not limited to, intravascular, intramuscular, subcutaneous or joint injection, aerosol inhalation, oral (tablet or pill form), topical, systemic, ocular, intraperitoneal and/or intrathecal delivery. More detailed descriptions of ribozyme delivery and administration are provided in Int. Pat. Appl. Publ. No. WO 94/02595 and Int. Pat. Appl. Publ. No. WO 93/23569, each specifically incorporated herein by reference.

Another means of accumulating high concentrations of a ribozyme(s) within cells is to incorporate the ribozyme-encoding sequences into a DNA expression vector. Transcription of the ribozyme sequences are driven from a promoter for eukaryotic RNA polymerase I (pol I), RNA polymerase II (pol II), or RNA polymerase III (pol III). Transcripts from pol II or pol III promoters will be expressed at high levels in all cells; the levels of a given pol II promoter in a given cell type will depend on the nature of the gene regulatory sequences (enhancers, silencers, *etc.*) present nearby. Prokaryotic RNA polymerase promoters may also be used, providing that the prokaryotic RNA polymerase enzyme is expressed in the appropriate cells. Ribozymes

expressed from such promoters have been shown to function in mammalian cells. Such transcription units can be incorporated into a variety of vectors for introduction into mammalian cells, including but not restricted to, plasmid DNA vectors, viral DNA vectors (such as adenovirus or adeno-associated vectors), or viral RNA vectors (such as retroviral, semliki forest virus, sindbis virus vectors).

In another embodiment of the invention, peptide nucleic acids (PNAs) compositions are provided. PNA is a DNA mimic in which the nucleobases are attached to a pseudopeptide backbone (Good and Nielsen, *Antisense Nucleic Acid Drug Dev.* 1997 7(4) 431-37). PNA is able to be utilized in a number of methods that traditionally have used RNA or DNA. Often PNA sequences perform better in techniques than the corresponding RNA or DNA sequences and have utilities that are not inherent to RNA or DNA. A review of PNA including methods of making, characteristics of, and methods of using, is provided by Corey (*Trends Biotechnol* 1997 Jun;15(6):224-9). As such, in certain embodiments, one may prepare PNA sequences that are complementary to one or more portions of the ACE mRNA sequence, and such PNA compositions may be used to regulate, alter, decrease, or reduce the translation of ACE-specific mRNA, and thereby alter the level of ACE activity in a host cell to which such PNA compositions have been administered.

PNAs have 2-aminoethyl-glycine linkages replacing the normal phosphodiester backbone of DNA (Nielsen *et al.*, *Science* 1991 Dec 6;254(5037):1497-500; Hanvey *et al.*, *Science*. 1992 Nov 27;258(5087):1481-5; Hyrup and Nielsen, *Bioorg Med Chem.* 1996 Jan;4(1):5-23). This chemistry has three important consequences: firstly, in contrast to DNA or phosphorothioate oligonucleotides, PNAs are neutral molecules; secondly, PNAs are achiral, which avoids the need to develop a stereoselective synthesis; and thirdly, PNA synthesis uses standard Boc or Fmoc protocols for solid-phase peptide synthesis, although other methods, including a modified Merrifield method, have been used.

PNA monomers or ready-made oligomers are commercially available from PerSeptive Biosystems (Framingham, MA). PNA syntheses by either Boc or Fmoc protocols are straightforward using manual or automated protocols (Norton *et al.*,

Bioorg Med Chem. 1995 Apr;3(4):437-45). The manual protocol lends itself to the production of chemically modified PNAs or the simultaneous synthesis of families of closely related PNAs.

As with peptide synthesis, the success of a particular PNA synthesis will
5 depend on the properties of the chosen sequence. For example, while in theory PNAs can incorporate any combination of nucleotide bases, the presence of adjacent purines can lead to deletions of one or more residues in the product. In expectation of this difficulty, it is suggested that, in producing PNAs with adjacent purines, one should repeat the coupling of residues likely to be added inefficiently. This should be followed
10 by the purification of PNAs by reverse-phase high-pressure liquid chromatography, providing yields and purity of product similar to those observed during the synthesis of peptides.

Modifications of PNAs for a given application may be accomplished by coupling amino acids during solid-phase synthesis or by attaching compounds that
15 contain a carboxylic acid group to the exposed N-terminal amine. Alternatively, PNAs can be modified after synthesis by coupling to an introduced lysine or cysteine. The ease with which PNAs can be modified facilitates optimization for better solubility or for specific functional requirements. Once synthesized, the identity of PNAs and their derivatives can be confirmed by mass spectrometry. Several studies have made and
20 utilized modifications of PNAs (for example, Norton *et al.*, Bioorg Med Chem. 1995 Apr;3(4):437-45; Petersen *et al.*, J Pept Sci. 1995 May-Jun;1(3):175-83; Orum *et al.*, Biotechniques. 1995 Sep;19(3):472-80; Footer *et al.*, Biochemistry. 1996 Aug 20;35(33):10673-9; Griffith *et al.*, Nucleic Acids Res. 1995 Aug 11;23(15):3003-8; Pardridge *et al.*, Proc Natl Acad Sci U S A. 1995 Jun 6;92(12):5592-6; Boffa *et al.*,
25 Proc Natl Acad Sci U S A. 1995 Mar 14;92(6):1901-5; Gambacorti-Passerini *et al.*, Blood. 1996 Aug 15;88(4):1411-7; Armitage *et al.*, Proc Natl Acad Sci U S A. 1997 Nov 11;94(23):12320-5; Seeger *et al.*, Biotechniques. 1997 Sep;23(3):512-7). U.S. Patent No. 5,700,922 discusses PNA-DNA-PNA chimeric molecules and their uses in diagnostics, modulating protein in organisms, and treatment of conditions susceptible to
30 therapeutics.

Methods of characterizing the antisense binding properties of PNAs are discussed in Rose (Anal Chem. 1993 Dec 15;65(24):3545-9) and Jensen *et al.* (Biochemistry. 1997 Apr 22;36(16):5072-7). Rose uses capillary gel electrophoresis to determine binding of PNAs to their complementary oligonucleotide, measuring the relative binding kinetics and stoichiometry. Similar types of measurements were made
5 by Jensen *et al.* using BIAcore™ technology.

Other applications of PNAs that have been described and will be apparent to the skilled artisan include use in DNA strand invasion, antisense inhibition, mutational analysis, enhancers of transcription, nucleic acid purification, isolation of
10 transcriptionally active genes, blocking of transcription factor binding, genome cleavage, biosensors, *in situ* hybridization, and the like.

Polynucleotide Identification, Characterization and Expression

Polynucleotide compositions of the present invention may be identified, prepared and/or manipulated using any of a variety of well established techniques (see
15 generally, Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989, and other like references). For example, a polynucleotide may be identified, as described in more detail below, by screening a microarray of cDNAs for tumor-associated expression (*i.e.*, expression that is at least two fold greater in a tumor than in normal tissue, as determined using a
20 representative assay provided herein). Such screens may be performed, for example, using the microarray technology of Affymetrix, Inc. (Santa Clara, CA) according to the manufacturer's instructions (and essentially as described by Schena et al., *Proc. Natl. Acad. Sci. USA* 93:10614-10619, 1996 and Heller et al., *Proc. Natl. Acad. Sci. USA* 94:2150-2155, 1997). Alternatively, polynucleotides may be amplified from cDNA
25 prepared from cells expressing the proteins described herein, such as tumor cells.

Many template dependent processes are available to amplify a target sequences of interest present in a sample. One of the best known amplification methods is the polymerase chain reaction (PCR™) which is described in detail in U.S. Patent Nos. 4,683,195, 4,683,202 and 4,800,159, each of which is incorporated herein by

reference in its entirety. Briefly, in PCR™, two primer sequences are prepared which are complementary to regions on opposite complementary strands of the target sequence. An excess of deoxynucleoside triphosphates is added to a reaction mixture along with a DNA polymerase (*e.g.*, *Taq* polymerase). If the target sequence is present
5 in a sample, the primers will bind to the target and the polymerase will cause the primers to be extended along the target sequence by adding on nucleotides. By raising and lowering the temperature of the reaction mixture, the extended primers will dissociate from the target to form reaction products, excess primers will bind to the target and to the reaction product and the process is repeated. Preferably reverse
10 transcription and PCR™ amplification procedure may be performed in order to quantify the amount of mRNA amplified. Polymerase chain reaction methodologies are well known in the art.

Any of a number of other template dependent processes, many of which are variations of the PCR™ amplification technique, are readily known and available in
15 the art. Illustratively, some such methods include the ligase chain reaction (referred to as LCR), described, for example, in Eur. Pat. Appl. Publ. No. 320,308 and U.S. Patent No. 4,883,750; Qbeta Replicase, described in PCT Intl. Pat. Appl. Publ. No. PCT/US87/00880; Strand Displacement Amplification (SDA) and Repair Chain Reaction (RCR). Still other amplification methods are described in Great Britain Pat.
20 Appl. No. 2 202 328, and in PCT Intl. Pat. Appl. Publ. No. PCT/US89/01025. Other nucleic acid amplification procedures include transcription-based amplification systems (TAS) (PCT Intl. Pat. Appl. Publ. No. WO 88/10315), including nucleic acid sequence based amplification (NASBA) and 3SR. Eur. Pat. Appl. Publ. No. 329,822 describes a nucleic acid amplification process involving cyclically synthesizing single-stranded
25 RNA ("ssRNA"), ssDNA, and double-stranded DNA (dsDNA). PCT Intl. Pat. Appl. Publ. No. WO 89/06700 describes a nucleic acid sequence amplification scheme based on the hybridization of a promoter/primer sequence to a target single-stranded DNA ("ssDNA") followed by transcription of many RNA copies of the sequence. Other amplification methods such as "RACE" (Frohman, 1990), and "one-sided PCR" (Ohara,
30 1989) are also well-known to those of skill in the art.

An amplified portion of a polynucleotide of the present invention may be used to isolate a full length gene from a suitable library (e.g., a tumor cDNA library) using well known techniques. Within such techniques, a library (cDNA or genomic) is screened using one or more polynucleotide probes or primers suitable for amplification.

5 Preferably, a library is size-selected to include larger molecules. Random primed libraries may also be preferred for identifying 5' and upstream regions of genes. Genomic libraries are preferred for obtaining introns and extending 5' sequences.

For hybridization techniques, a partial sequence may be labeled (e.g., by nick-translation or end-labeling with ³²P) using well known techniques. A bacterial or

10 bacteriophage library is then generally screened by hybridizing filters containing denatured bacterial colonies (or lawns containing phage plaques) with the labeled probe (see Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989). Hybridizing colonies or plaques are selected and expanded, and the DNA is isolated for further analysis. cDNA clones may

15 be analyzed to determine the amount of additional sequence by, for example, PCR using a primer from the partial sequence and a primer from the vector. Restriction maps and partial sequences may be generated to identify one or more overlapping clones. The complete sequence may then be determined using standard techniques, which may involve generating a series of deletion clones. The resulting overlapping sequences can

20 then assembled into a single contiguous sequence. A full length cDNA molecule can be generated by ligating suitable fragments, using well known techniques.

Alternatively, amplification techniques, such as those described above, can be useful for obtaining a full length coding sequence from a partial cDNA sequence. One such amplification technique is inverse PCR (see Triglia et al., *Nucl. Acids Res.*

25 16:8186, 1988), which uses restriction enzymes to generate a fragment in the known region of the gene. The fragment is then circularized by intramolecular ligation and used as a template for PCR with divergent primers derived from the known region. Within an alternative approach, sequences adjacent to a partial sequence may be retrieved by amplification with a primer to a linker sequence and a primer specific to a

30 known region. The amplified sequences are typically subjected to a second round of

amplification with the same linker primer and a second primer specific to the known region. A variation on this procedure, which employs two primers that initiate extension in opposite directions from the known sequence, is described in WO 96/38591. Another such technique is known as "rapid amplification of cDNA ends" or RACE. This technique involves the use of an internal primer and an external primer, which hybridizes to a polyA region or vector sequence, to identify sequences that are 5' and 3' of a known sequence. Additional techniques include capture PCR (Lagerstrom et al., *PCR Methods Applic. 1*:111-19, 1991) and walking PCR (Parker et al., *Nucl. Acids. Res. 19*:3055-60, 1991). Other methods employing amplification may also be employed to obtain a full length cDNA sequence.

In certain instances, it is possible to obtain a full length cDNA sequence by analysis of sequences provided in an expressed sequence tag (EST) database, such as that available from GenBank. Searches for overlapping ESTs may generally be performed using well known programs (e.g., NCBI BLAST searches), and such ESTs may be used to generate a contiguous full length sequence. Full length DNA sequences may also be obtained by analysis of genomic fragments.

In other embodiments of the invention, polynucleotide sequences or fragments thereof which encode polypeptides of the invention, or fusion proteins or functional equivalents thereof, may be used in recombinant DNA molecules to direct expression of a polypeptide in appropriate host cells. Due to the inherent degeneracy of the genetic code, other DNA sequences that encode substantially the same or a functionally equivalent amino acid sequence may be produced and these sequences may be used to clone and express a given polypeptide.

As will be understood by those of skill in the art, it may be advantageous in some instances to produce polypeptide-encoding nucleotide sequences possessing non-naturally occurring codons. For example, codons preferred by a particular prokaryotic or eukaryotic host can be selected to increase the rate of protein expression or to produce a recombinant RNA transcript having desirable properties, such as a half-life which is longer than that of a transcript generated from the naturally occurring sequence.

Moreover, the polynucleotide sequences of the present invention can be engineered using methods generally known in the art in order to alter polypeptide encoding sequences for a variety of reasons, including but not limited to, alterations which modify the cloning, processing, and/or expression of the gene product. For example, DNA shuffling by random fragmentation and PCR reassembly of gene fragments and synthetic oligonucleotides may be used to engineer the nucleotide sequences. In addition, site-directed mutagenesis may be used to insert new restriction sites, alter glycosylation patterns, change codon preference, produce splice variants, or introduce mutations, and so forth.

In another embodiment of the invention, natural, modified, or recombinant nucleic acid sequences may be ligated to a heterologous sequence to encode a fusion protein. For example, to screen peptide libraries for inhibitors of polypeptide activity, it may be useful to encode a chimeric protein that can be recognized by a commercially available antibody. A fusion protein may also be engineered to contain a cleavage site located between the polypeptide-encoding sequence and the heterologous protein sequence, so that the polypeptide may be cleaved and purified away from the heterologous moiety.

Sequences encoding a desired polypeptide may be synthesized, in whole or in part, using chemical methods well known in the art (see Caruthers, M. H. et al. (1980) *Nucl. Acids Res. Symp. Ser.* 215-223, Horn, T. et al. (1980) *Nucl. Acids Res. Symp. Ser.* 225-232). Alternatively, the protein itself may be produced using chemical methods to synthesize the amino acid sequence of a polypeptide, or a portion thereof. For example, peptide synthesis can be performed using various solid-phase techniques (Roberge, J. Y. et al. (1995) *Science* 269:202-204) and automated synthesis may be achieved, for example, using the ABI 431A Peptide Synthesizer (Perkin Elmer, Palo Alto, CA).

A newly synthesized peptide may be substantially purified by preparative high performance liquid chromatography (e.g., Creighton, T. (1983) *Proteins, Structures and Molecular Principles*, WH Freeman and Co., New York, N.Y.) or other comparable techniques available in the art. The composition of the synthetic peptides may be

confirmed by amino acid analysis or sequencing (e.g., the Edman degradation procedure). Additionally, the amino acid sequence of a polypeptide, or any part thereof, may be altered during direct synthesis and/or combined using chemical methods with sequences from other proteins, or any part thereof, to produce a variant polypeptide.

5 In order to express a desired polypeptide, the nucleotide sequences encoding the polypeptide, or functional equivalents, may be inserted into appropriate expression vector, i.e., a vector which contains the necessary elements for the transcription and translation of the inserted coding sequence. Methods which are well known to those skilled in the art may be used to construct expression vectors containing
10 sequences encoding a polypeptide of interest and appropriate transcriptional and translational control elements. These methods include *in vitro* recombinant DNA techniques, synthetic techniques, and *in vivo* genetic recombination. Such techniques are described, for example, in Sambrook, J. et al. (1989) Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, Plainview, N.Y., and Ausubel, F. M. et al. (1989) Current Protocols in Molecular Biology, John Wiley & Sons, New York.
15 N.Y.

A variety of expression vector/host systems may be utilized to contain and express polynucleotide sequences. These include, but are not limited to, microorganisms such as bacteria transformed with recombinant bacteriophage, plasmid,
20 or cosmid DNA expression vectors; yeast transformed with yeast expression vectors; insect cell systems infected with virus expression vectors (e.g., baculovirus); plant cell systems transformed with virus expression vectors (e.g., cauliflower mosaic virus, CaMV; tobacco mosaic virus, TMV) or with bacterial expression vectors (e.g., Ti or pBR322 plasmids); or animal cell systems.

25 The "control elements" or "regulatory sequences" present in an expression vector are those non-translated regions of the vector--enhancers, promoters, 5' and 3' untranslated regions--which interact with host cellular proteins to carry out transcription and translation. Such elements may vary in their strength and specificity. Depending on the vector system and host utilized, any number of suitable transcription
30 and translation elements, including constitutive and inducible promoters, may be used.

For example, when cloning in bacterial systems, inducible promoters such as the hybrid lacZ promoter of the PBLUESCRIPT phagemid (Stratagene, La Jolla, Calif.) or PSPORT1 plasmid (Gibco BRL, Gaithersburg, MD) and the like may be used. In mammalian cell systems, promoters from mammalian genes or from mammalian viruses
5 are generally preferred. If it is necessary to generate a cell line that contains multiple copies of the sequence encoding a polypeptide, vectors based on SV40 or EBV may be advantageously used with an appropriate selectable marker.

In bacterial systems, any of a number of expression vectors may be selected depending upon the use intended for the expressed polypeptide. For example,
10 when large quantities are needed, for example for the induction of antibodies, vectors which direct high level expression of fusion proteins that are readily purified may be used. Such vectors include, but are not limited to, the multifunctional *E. coli* cloning and expression vectors such as BLUESCRIPT (Stratagene), in which the sequence encoding the polypeptide of interest may be ligated into the vector in frame with
15 sequences for the amino-terminal Met and the subsequent 7 residues of .beta.-galactosidase so that a hybrid protein is produced; pIN vectors (Van Heeke, G. and S. M. Schuster (1989) *J. Biol. Chem.* 264:5503-5509); and the like. pGEX Vectors (Promega, Madison, Wis.) may also be used to express foreign polypeptides as fusion proteins with glutathione S-transferase (GST). In general, such fusion proteins are
20 soluble and can easily be purified from lysed cells by adsorption to glutathione-agarose beads followed by elution in the presence of free glutathione. Proteins made in such systems may be designed to include heparin, thrombin, or factor XA protease cleavage sites so that the cloned polypeptide of interest can be released from the GST moiety at will.

25 In the yeast, *Saccharomyces cerevisiae*, a number of vectors containing constitutive or inducible promoters such as alpha factor, alcohol oxidase, and PGH may be used. For reviews, see Ausubel et al. (supra) and Grant et al. (1987) *Methods Enzymol.* 153:516-544.

In cases where plant expression vectors are used, the expression of
30 sequences encoding polypeptides may be driven by any of a number of promoters. For

example, viral promoters such as the 35S and 19S promoters of CaMV may be used alone or in combination with the omega leader sequence from TMV (Takamatsu, N. (1987) *EMBO J.* 6:307-311. Alternatively, plant promoters such as the small subunit of RUBISCO or heat shock promoters may be used (Coruzzi, G. et al. (1984) *EMBO J.* 3:1671-1680; Broglie, R. et al. (1984) *Science* 224:838-843; and Winter, J. et al. (1991) *Results Probl. Cell Differ.* 17:85-105). These constructs can be introduced into plant cells by direct DNA transformation or pathogen-mediated transfection. Such techniques are described in a number of generally available reviews (see, for example, Hobbs, S. or Murry, L. E. in McGraw Hill Yearbook of Science and Technology (1992) McGraw Hill, New York, N.Y.; pp. 191-196).

An insect system may also be used to express a polypeptide of interest. For example, in one such system, Autographa californica nuclear polyhedrosis virus (AcNPV) is used as a vector to express foreign genes in *Spodoptera frugiperda* cells or in *Trichoplusia* larvae. The sequences encoding the polypeptide may be cloned into a non-essential region of the virus, such as the polyhedrin gene, and placed under control of the polyhedrin promoter. Successful insertion of the polypeptide-encoding sequence will render the polyhedrin gene inactive and produce recombinant virus lacking coat protein. The recombinant viruses may then be used to infect, for example, *S. frugiperda* cells or *Trichoplusia* larvae in which the polypeptide of interest may be expressed (Engelhard, E. K. et al. (1994) *Proc. Natl. Acad. Sci.* 91 :3224-3227).

In mammalian host cells, a number of viral-based expression systems are generally available. For example, in cases where an adenovirus is used as an expression vector, sequences encoding a polypeptide of interest may be ligated into an adenovirus transcription/translation complex consisting of the late promoter and tripartite leader sequence. Insertion in a non-essential E1 or E3 region of the viral genome may be used to obtain a viable virus which is capable of expressing the polypeptide in infected host cells (Logan, J. and Shenk, T. (1984) *Proc. Natl. Acad. Sci.* 81:3655-3659). In addition, transcription enhancers, such as the Rous sarcoma virus (RSV) enhancer, may be used to increase expression in mammalian host cells.

Specific initiation signals may also be used to achieve more efficient translation of sequences encoding a polypeptide of interest. Such signals include the ATG initiation codon and adjacent sequences. In cases where sequences encoding the polypeptide, its initiation codon, and upstream sequences are inserted into the appropriate expression vector, no additional transcriptional or translational control signals may be needed. However, in cases where only coding sequence, or a portion thereof, is inserted, exogenous translational control signals including the ATG initiation codon should be provided. Furthermore, the initiation codon should be in the correct reading frame to ensure translation of the entire insert. Exogenous translational elements and initiation codons may be of various origins, both natural and synthetic. The efficiency of expression may be enhanced by the inclusion of enhancers which are appropriate for the particular cell system which is used, such as those described in the literature (Scharf, D. et al. (1994) *Results Probl. Cell Differ.* 20:125-162).

In addition, a host cell strain may be chosen for its ability to modulate the expression of the inserted sequences or to process the expressed protein in the desired fashion. Such modifications of the polypeptide include, but are not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation, and acylation. Post-translational processing which cleaves a "prepro" form of the protein may also be used to facilitate correct insertion, folding and/or function. Different host cells such as CHO, COS, HeLa, MDCK, HEK293, and WI38, which have specific cellular machinery and characteristic mechanisms for such post-translational activities, may be chosen to ensure the correct modification and processing of the foreign protein.

For long-term, high-yield production of recombinant proteins, stable expression is generally preferred. For example, cell lines which stably express a polynucleotide of interest may be transformed using expression vectors which may contain viral origins of replication and/or endogenous expression elements and a selectable marker gene on the same or on a separate vector. Following the introduction of the vector, cells may be allowed to grow for 1-2 days in an enriched media before they are switched to selective media. The purpose of the selectable marker is to confer resistance to selection, and its presence allows growth and recovery of cells which

successfully express the introduced sequences. Resistant clones of stably transformed cells may be proliferated using tissue culture techniques appropriate to the cell type.

Any number of selection systems may be used to recover transformed cell lines. These include, but are not limited to, the herpes simplex virus thymidine kinase (Wigler, M. et al. (1977) *Cell* 11:223-32) and adenine phosphoribosyltransferase (Lowy, I. et al. (1990) *Cell* 22:817-23) genes which can be employed in tk.sup.- or aprt.sup.- cells, respectively. Also, antimetabolite, antibiotic or herbicide resistance can be used as the basis for selection; for example, dhfr which confers resistance to methotrexate (Wigler, M. et al. (1980) *Proc. Natl. Acad. Sci.* 77:3567-70); npt, which confers resistance to the aminoglycosides, neomycin and G-418 (Colbere-Garapin, F. et al (1981) *J. Mol. Biol.* 150:1-14); and als or pat, which confer resistance to chlorsulfuron and phosphinotricin acetyltransferase, respectively (Murry, *supra*). Additional selectable genes have been described, for example, trpB, which allows cells to utilize indole in place of tryptophan, or hisD, which allows cells to utilize histinol in place of histidine (Hartman, S. C. and R. C. Mulligan (1988) *Proc. Natl. Acad. Sci.* 85:8047-51). The use of visible markers has gained popularity with such markers as anthocyanins, beta-glucuronidase and its substrate GUS, and luciferase and its substrate luciferin, being widely used not only to identify transformants, but also to quantify the amount of transient or stable protein expression attributable to a specific vector system (Rhodes, C. A. et al. (1995) *Methods Mol. Biol.* 55:121-131).

Although the presence/absence of marker gene expression suggests that the gene of interest is also present, its presence and expression may need to be confirmed. For example, if the sequence encoding a polypeptide is inserted within a marker gene sequence, recombinant cells containing sequences can be identified by the absence of marker gene function. Alternatively, a marker gene can be placed in tandem with a polypeptide-encoding sequence under the control of a single promoter. Expression of the marker gene in response to induction or selection usually indicates expression of the tandem gene as well.

Alternatively, host cells that contain and express a desired polynucleotide sequence may be identified by a variety of procedures known to those of

skill in the art. These procedures include, but are not limited to, DNA-DNA or DNA-RNA hybridizations and protein bioassay or immunoassay techniques which include, for example, membrane, solution, or chip based technologies for the detection and/or quantification of nucleic acid or protein.

5 A variety of protocols for detecting and measuring the expression of polynucleotide-encoded products, using either polyclonal or monoclonal antibodies specific for the product are known in the art. Examples include enzyme-linked immunosorbent assay (ELISA), radioimmunoassay (RIA), and fluorescence activated cell sorting (FACS). A two-site, monoclonal-based immunoassay utilizing monoclonal
10 antibodies reactive to two non-interfering epitopes on a given polypeptide may be preferred for some applications, but a competitive binding assay may also be employed. These and other assays are described, among other places, in Hampton, R. et al. (1990; *Serological Methods, a Laboratory Manual*, APS Press, St Paul, Minn.) and Maddox, D. E. et al. (1983; *J. Exp. Med.* 158:1211-1216).

15 A wide variety of labels and conjugation techniques are known by those skilled in the art and may be used in various nucleic acid and amino acid assays. Means for producing labeled hybridization or PCR probes for detecting sequences related to polynucleotides include oligolabeling, nick translation, end-labeling or PCR amplification using a labeled nucleotide. Alternatively, the sequences, or any portions
20 thereof may be cloned into a vector for the production of an mRNA probe. Such vectors are known in the art, are commercially available, and may be used to synthesize RNA probes in vitro by addition of an appropriate RNA polymerase such as T7, T3, or SP6 and labeled nucleotides. These procedures may be conducted using a variety of commercially available kits. Suitable reporter molecules or labels, which may be used
25 include radionuclides, enzymes, fluorescent, chemiluminescent, or chromogenic agents as well as substrates, cofactors, inhibitors, magnetic particles, and the like.

Host cells transformed with a polynucleotide sequence of interest may be cultured under conditions suitable for the expression and recovery of the protein from cell culture. The protein produced by a recombinant cell may be secreted or contained
30 intracellularly depending on the sequence and/or the vector used. As will be understood

by those of skill in the art, expression vectors containing polynucleotides of the invention may be designed to contain signal sequences which direct secretion of the encoded polypeptide through a prokaryotic or eukaryotic cell membrane. Other recombinant constructions may be used to join sequences encoding a polypeptide of interest to nucleotide sequence encoding a polypeptide domain which will facilitate purification of soluble proteins. Such purification facilitating domains include, but are not limited to, metal chelating peptides such as histidine-tryptophan modules that allow purification on immobilized metals, protein A domains that allow purification on immobilized immunoglobulin, and the domain utilized in the FLAGS extension/affinity purification system (Immunex Corp., Seattle, Wash.). The inclusion of cleavable linker sequences such as those specific for Factor XA or enterokinase (Invitrogen, San Diego, Calif.) between the purification domain and the encoded polypeptide may be used to facilitate purification. One such expression vector provides for expression of a fusion protein containing a polypeptide of interest and a nucleic acid encoding 6 histidine residues preceding a thioredoxin or an enterokinase cleavage site. The histidine residues facilitate purification on IMLAC (immobilized metal ion affinity chromatography) as described in Porath, J. et al. (1992, *Prot. Exp. Purif.* 3:263-281) while the enterokinase cleavage site provides a means for purifying the desired polypeptide from the fusion protein. A discussion of vectors which contain fusion proteins is provided in Kroll, D. J. et al. (1993; *DNA Cell Biol.* 12:441-453).

In addition to recombinant production methods, polypeptides of the invention, and fragments thereof, may be produced by direct peptide synthesis using solid-phase techniques (Merrifield J. (1963) *J. Am. Chem. Soc.* 85:2149-2154). Protein synthesis may be performed using manual techniques or by automation. Automated synthesis may be achieved, for example, using Applied Biosystems 431A Peptide Synthesizer (Perkin Elmer). Alternatively, various fragments may be chemically synthesized separately and combined using chemical methods to produce the full length molecule.

Antibody Compositions, Fragments Thereof and Other Binding Agents

According to another aspect, the present invention further provides binding agents, such as antibodies and antigen-binding fragments thereof, that exhibit immunological binding to a tumor polypeptide disclosed herein, or to a portion, variant
5 or derivative thereof. An antibody, or antigen-binding fragment thereof, is said to "specifically bind," "immunologically bind," and/or is "immunologically reactive" to a polypeptide of the invention if it reacts at a detectable level (within, for example, an ELISA assay) with the polypeptide, and does not react detectably with unrelated polypeptides under similar conditions.

10 Immunological binding, as used in this context, generally refers to the non-covalent interactions of the type which occur between an immunoglobulin molecule and an antigen for which the immunoglobulin is specific. The strength, or affinity of immunological binding interactions can be expressed in terms of the dissociation constant (K_d) of the interaction, wherein a smaller K_d represents a greater
15 affinity. Immunological binding properties of selected polypeptides can be quantified using methods well known in the art. One such method entails measuring the rates of antigen-binding site/antigen complex formation and dissociation, wherein those rates depend on the concentrations of the complex partners, the affinity of the interaction, and on geometric parameters that equally influence the rate in both directions. Thus, both
20 the "on rate constant" (K_{on}) and the "off rate constant" (K_{off}) can be determined by calculation of the concentrations and the actual rates of association and dissociation. The ratio of K_{off}/K_{on} enables cancellation of all parameters not related to affinity, and is thus equal to the dissociation constant K_d . See, generally, Davies et al. (1990) Annual Rev. Biochem. 59:439-473.

25 An "antigen-binding site," or "binding portion" of an antibody refers to the part of the immunoglobulin molecule that participates in antigen binding. The antigen binding site is formed by amino acid residues of the N-terminal variable ("V") regions of the heavy ("H") and light ("L") chains. Three highly divergent stretches within the V regions of the heavy and light chains are referred to as "hypervariable
30 regions" which are interposed between more conserved flanking stretches known as

"framework regions," or "FRs". Thus the term "FR" refers to amino acid sequences which are naturally found between and adjacent to hypervariable regions in immunoglobulins. In an antibody molecule, the three hypervariable regions of a light chain and the three hypervariable regions of a heavy chain are disposed relative to each other in three dimensional space to form an antigen-binding surface. The antigen-binding surface is complementary to the three-dimensional surface of a bound antigen, and the three hypervariable regions of each of the heavy and light chains are referred to as "complementarity-determining regions," or "CDRs."

Binding agents may be further capable of differentiating between patients with and without a cancer, such as prostate cancer, using the representative assays provided herein. For example, antibodies or other binding agents that bind to a tumor protein will preferably generate a signal indicating the presence of a cancer in at least about 20% of patients with the disease, more preferably at least about 30% of patients. Alternatively, or in addition, the antibody will generate a negative signal indicating the absence of the disease in at least about 90% of individuals without the cancer. To determine whether a binding agent satisfies this requirement, biological samples (e.g., blood, sera, sputum, urine and/or tumor biopsies) from patients with and without a cancer (as determined using standard clinical tests) may be assayed as described herein for the presence of polypeptides that bind to the binding agent. Preferably, a statistically significant number of samples with and without the disease will be assayed. Each binding agent should satisfy the above criteria; however, those of ordinary skill in the art will recognize that binding agents may be used in combination to improve sensitivity.

Any agent that satisfies the above requirements may be a binding agent. For example, a binding agent may be a ribosome, with or without a peptide component, an RNA molecule or a polypeptide. In a preferred embodiment, a binding agent is an antibody or an antigen-binding fragment thereof. Antibodies may be prepared by any of a variety of techniques known to those of ordinary skill in the art. *See, e.g., Harlow and Lane, Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In general, antibodies can be produced by cell culture techniques, including the generation

of monoclonal antibodies as described herein, or via transfection of antibody genes into suitable bacterial or mammalian cell hosts, in order to allow for the production of recombinant antibodies. In one technique, an immunogen comprising the polypeptide is initially injected into any of a wide variety of mammals (e.g., mice, rats, rabbits, sheep or goats). In this step, the polypeptides of this invention may serve as the immunogen without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled periodically. Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

Monoclonal antibodies specific for an antigenic polypeptide of interest may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. Immunol.* 6:511-519, 1976, and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the desired specificity (i.e., reactivity with the polypeptide of interest). Such cell lines may be produced, for example, from spleen cells obtained from an animal immunized as described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the spleen cells and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are selected and their culture supernatants tested for binding activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the yield, such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The polypeptides of this invention may be used in the purification process in, for example, an affinity chromatography step.

A number of therapeutically useful molecules are known in the art which comprise antigen-binding sites that are capable of exhibiting immunological binding properties of an antibody molecule. The proteolytic enzyme papain preferentially cleaves IgG molecules to yield several fragments, two of which (the "F(ab)" fragments) each comprise a covalent heterodimer that includes an intact antigen-binding site. The enzyme pepsin is able to cleave IgG molecules to provide several fragments, including the "F(ab')₂" fragment which comprises both antigen-binding sites. An "Fv" fragment can be produced by preferential proteolytic cleavage of an IgM, and on rare occasions IgG or IgA immunoglobulin molecule. Fv fragments are, however, more commonly derived using recombinant techniques known in the art. The Fv fragment includes a non-covalent V_H::V_L heterodimer including an antigen-binding site which retains much of the antigen recognition and binding capabilities of the native antibody molecule. Inbar et al. (1972) Proc. Nat. Acad. Sci. USA 69:2659-2662; Hochman et al. (1976) Biochem 15:2706-2710; and Ehrlich et al. (1980) Biochem 19:4091-4096.

A single chain Fv ("sFv") polypeptide is a covalently linked V_H::V_L heterodimer which is expressed from a gene fusion including V_H- and V_L-encoding genes linked by a peptide-encoding linker. Huston et al. (1988) Proc. Nat. Acad. Sci. USA 85(16):5879-5883. A number of methods have been described to discern chemical structures for converting the naturally aggregated--but chemically separated--light and heavy polypeptide chains from an antibody V region into an sFv molecule which will fold into a three dimensional structure substantially similar to the structure of an

antigen-binding site. See, *e.g.*, U.S. Pat. Nos. 5,091,513 and 5,132,405, to Huston et al.; and U.S. Pat. No. 4,946,778, to Ladner et al.

Each of the above-described molecules includes a heavy chain and a light chain CDR set, respectively interposed between a heavy chain and a light chain FR set which provide support to the CDRS and define the spatial relationship of the CDRs relative to each other. As used herein, the term "CDR set" refers to the three hypervariable regions of a heavy or light chain V region. Proceeding from the N-terminus of a heavy or light chain, these regions are denoted as "CDR1," "CDR2," and "CDR3" respectively. An antigen-binding site, therefore, includes six CDRs, comprising the CDR set from each of a heavy and a light chain V region. A polypeptide comprising a single CDR, (*e.g.*, a CDR1, CDR2 or CDR3) is referred to herein as a "molecular recognition unit." Crystallographic analysis of a number of antigen-antibody complexes has demonstrated that the amino acid residues of CDRs form extensive contact with bound antigen, wherein the most extensive antigen contact is with the heavy chain CDR3. Thus, the molecular recognition units are primarily responsible for the specificity of an antigen-binding site.

As used herein, the term "FR set" refers to the four flanking amino acid sequences which frame the CDRs of a CDR set of a heavy or light chain V region. Some FR residues may contact bound antigen; however, FRs are primarily responsible for folding the V region into the antigen-binding site, particularly the FR residues directly adjacent to the CDRS. Within FRs, certain amino residues and certain structural features are very highly conserved. In this regard, all V region sequences contain an internal disulfide loop of around 90 amino acid residues. When the V regions fold into a binding-site, the CDRs are displayed as projecting loop motifs which form an antigen-binding surface. It is generally recognized that there are conserved structural regions of FRs which influence the folded shape of the CDR loops into certain "canonical" structures—regardless of the precise CDR amino acid sequence. Further, certain FR residues are known to participate in non-covalent interdomain contacts which stabilize the interaction of the antibody heavy and light chains.

A number of "humanized" antibody molecules comprising an antigen-binding site derived from a non-human immunoglobulin have been described, including chimeric antibodies having rodent V regions and their associated CDRs fused to human constant domains (Winter et al. (1991) Nature 349:293-299; Lobuglio et al. (1989) Proc. Nat. Acad. Sci. USA 86:4220-4224; Shaw et al. (1987) J Immunol. 138:4534-4538; and Brown et al. (1987) Cancer Res. 47:3577-3583), rodent CDRs grafted into a human supporting FR prior to fusion with an appropriate human antibody constant domain (Riechmann et al. (1988) Nature 332:323-327; Verhoeyen et al. (1988) Science 239:1534-1536; and Jones et al. (1986) Nature 321:522-525), and rodent CDRs supported by recombinantly veneered rodent FRs (European Patent Publication No. 519,596, published Dec. 23, 1992). These "humanized" molecules are designed to minimize unwanted immunological response toward rodent antihuman antibody molecules which limits the duration and effectiveness of therapeutic applications of those moieties in human recipients.

As used herein, the terms "veneered FRs" and "recombinantly veneered FRs" refer to the selective replacement of FR residues from, *e.g.*, a rodent heavy or light chain V region, with human FR residues in order to provide a xenogeneic molecule comprising an antigen-binding site which retains substantially all of the native FR polypeptide folding structure. Veneering techniques are based on the understanding that the ligand binding characteristics of an antigen-binding site are determined primarily by the structure and relative disposition of the heavy and light chain CDR sets within the antigen-binding surface. Davies et al. (1990) Ann. Rev. Biochem. 59:439-473. Thus, antigen binding specificity can be preserved in a humanized antibody only wherein the CDR structures, their interaction with each other, and their interaction with the rest of the V region domains are carefully maintained. By using veneering techniques, exterior (*e.g.*, solvent-accessible) FR residues which are readily encountered by the immune system are selectively replaced with human residues to provide a hybrid molecule that comprises either a weakly immunogenic, or substantially non-immunogenic veneered surface.

The process of veneering makes use of the available sequence data for human antibody variable domains compiled by Kabat et al., in Sequences of Proteins of Immunological Interest, 4th ed., (U.S. Dept. of Health and Human Services, U.S. Government Printing Office, 1987), updates to the Kabat database, and other accessible U.S. and foreign databases (both nucleic acid and protein). Solvent accessibilities of V region amino acids can be deduced from the known three-dimensional structure for human and murine antibody fragments. There are two general steps in veneering a murine antigen-binding site. Initially, the FRs of the variable domains of an antibody molecule of interest are compared with corresponding FR sequences of human variable domains obtained from the above-identified sources. The most homologous human V regions are then compared residue by residue to corresponding murine amino acids. The residues in the murine FR which differ from the human counterpart are replaced by the residues present in the human moiety using recombinant techniques well known in the art. Residue switching is only carried out with moieties which are at least partially exposed (solvent accessible), and care is exercised in the replacement of amino acid residues which may have a significant effect on the tertiary structure of V region domains, such as proline, glycine and charged amino acids.

In this manner, the resultant "veneered" murine antigen-binding sites are thus designed to retain the murine CDR residues, the residues substantially adjacent to the CDRs, the residues identified as buried or mostly buried (solvent inaccessible), the residues believed to participate in non-covalent (e.g., electrostatic and hydrophobic) contacts between heavy and light chain domains, and the residues from conserved structural regions of the FRs which are believed to influence the "canonical" tertiary structures of the CDR loops. These design criteria are then used to prepare recombinant nucleotide sequences which combine the CDRs of both the heavy and light chain of a murine antigen-binding site into human-appearing FRs that can be used to transfect mammalian cells for the expression of recombinant human antibodies which exhibit the antigen specificity of the murine antibody molecule.

In another embodiment of the invention, monoclonal antibodies of the present invention may be coupled to one or more therapeutic agents. Suitable agents in

this regard include radionuclides, differentiation inducers, drugs, toxins, and derivatives thereof. Preferred radionuclides include ^{90}Y , ^{123}I , ^{125}I , ^{131}I , ^{186}Re , ^{188}Re , ^{211}At , and ^{212}Bi . Preferred drugs include methotrexate, and pyrimidine and purine analogs. Preferred differentiation inducers include phorbol esters and butyric acid. Preferred
5 toxins include ricin, abrin, diphtheria toxin, cholera toxin, gelonin, *Pseudomonas* exotoxin, *Shigella* toxin, and pokeweed antiviral protein.

A therapeutic agent may be coupled (*e.g.*, covalently bonded) to a suitable monoclonal antibody either directly or indirectly (*e.g.*, via a linker group). A direct reaction between an agent and an antibody is possible when each possesses a
10 substituent capable of reacting with the other. For example, a nucleophilic group, such as an amino or sulfhydryl group, on one may be capable of reacting with a carbonyl-containing group, such as an anhydride or an acid halide, or with an alkyl group containing a good leaving group (*e.g.*, a halide) on the other.

Alternatively, it may be desirable to couple a therapeutic agent and an
15 antibody via a linker group. A linker group can function as a spacer to distance an antibody from an agent in order to avoid interference with binding capabilities. A linker group can also serve to increase the chemical reactivity of a substituent on an agent or an antibody, and thus increase the coupling efficiency. An increase in chemical reactivity may also facilitate the use of agents, or functional groups on agents, which
20 otherwise would not be possible.

It will be evident to those skilled in the art that a variety of bifunctional or polyfunctional reagents, both homo- and hetero-functional (such as those described in the catalog of the Pierce Chemical Co., Rockford, IL), may be employed as the linker group. Coupling may be effected, for example, through amino groups, carboxyl groups,
25 sulfhydryl groups or oxidized carbohydrate residues. There are numerous references describing such methodology, *e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.

Where a therapeutic agent is more potent when free from the antibody portion of the immunoconjugates of the present invention, it may be desirable to use a linker group which is cleavable during or upon internalization into a cell. A number of
30 different cleavable linker groups have been described. The mechanisms for the

intracellular release of an agent from these linker groups include cleavage by reduction of a disulfide bond (*e.g.*, U.S. Patent No. 4,489,710, to Spitler), by irradiation of a photolabile bond (*e.g.*, U.S. Patent No. 4,625,014, to Senter et al.), by hydrolysis of derivatized amino acid side chains (*e.g.*, U.S. Patent No. 4,638,045, to Kohn et al.), by
5 serum complement-mediated hydrolysis (*e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.), and acid-catalyzed hydrolysis (*e.g.*, U.S. Patent No. 4,569,789, to Blattler et al.).

It may be desirable to couple more than one agent to an antibody. In one embodiment, multiple molecules of an agent are coupled to one antibody molecule. In another embodiment, more than one type of agent may be coupled to one antibody.
10 Regardless of the particular embodiment, immunoconjugates with more than one agent may be prepared in a variety of ways. For example, more than one agent may be coupled directly to an antibody molecule, or linkers that provide multiple sites for attachment can be used. Alternatively, a carrier can be used.

A carrier may bear the agents in a variety of ways, including covalent
15 bonding either directly or via a linker group. Suitable carriers include proteins such as albumins (*e.g.*, U.S. Patent No. 4,507,234, to Kato et al.), peptides and polysaccharides such as aminodextran (*e.g.*, U.S. Patent No. 4,699,784, to Shih et al.). A carrier may also bear an agent by noncovalent bonding or by encapsulation, such as within a liposome vesicle (*e.g.*, U.S. Patent Nos. 4,429,008 and 4,873,088). Carriers specific for
20 radionuclide agents include radiohalogenated small molecules and chelating compounds. For example, U.S. Patent No. 4,735,792 discloses representative radiohalogenated small molecules and their synthesis. A radionuclide chelate may be formed from chelating compounds that include those containing nitrogen and sulfur atoms as the donor atoms for binding the metal, or metal oxide, radionuclide. For
25 example, U.S. Patent No. 4,673,562, to Davison et al. discloses representative chelating compounds and their synthesis.

T Cell Compositions

The present invention, in another aspect, provides T cells specific for a tumor polypeptide disclosed herein, or for a variant or derivative thereof. Such cells

may generally be prepared *in vitro* or *ex vivo*, using standard procedures. For example, T cells may be isolated from bone marrow, peripheral blood, or a fraction of bone marrow or peripheral blood of a patient, using a commercially available cell separation system, such as the Isolex™ System, available from Nexell Therapeutics, Inc. (Irvine, CA; see also U.S. Patent No. 5,240,856; U.S. Patent No. 5,215,926; WO 89/06280; WO 91/16116 and WO 92/07243). Alternatively, T cells may be derived from related or unrelated humans, non-human mammals, cell lines or cultures.

T cells may be stimulated with a polypeptide, polynucleotide encoding a polypeptide and/or an antigen presenting cell (APC) that expresses such a polypeptide. Such stimulation is performed under conditions and for a time sufficient to permit the generation of T cells that are specific for the polypeptide of interest. Preferably, a tumor polypeptide or polynucleotide of the invention is present within a delivery vehicle, such as a microsphere, to facilitate the generation of specific T cells.

T cells are considered to be specific for a polypeptide of the present invention if the T cells specifically proliferate, secrete cytokines or kill target cells coated with the polypeptide or expressing a gene encoding the polypeptide. T cell specificity may be evaluated using any of a variety of standard techniques. For example, within a chromium release assay or proliferation assay, a stimulation index of more than two fold increase in lysis and/or proliferation, compared to negative controls, indicates T cell specificity. Such assays may be performed, for example, as described in Chen et al., *Cancer Res.* 54:1065-1070, 1994. Alternatively, detection of the proliferation of T cells may be accomplished by a variety of known techniques. For example, T cell proliferation can be detected by measuring an increased rate of DNA synthesis (*e.g.*, by pulse-labeling cultures of T cells with tritiated thymidine and measuring the amount of tritiated thymidine incorporated into DNA). Contact with a tumor polypeptide (100 ng/ml - 100 µg/ml, preferably 200 ng/ml - 25 µg/ml) for 3 - 7 days will typically result in at least a two fold increase in proliferation of the T cells. Contact as described above for 2-3 hours should result in activation of the T cells, as measured using standard cytokine assays in which a two fold increase in the level of cytokine release (*e.g.*, TNF or IFN-γ) is indicative of T cell activation (*see* Coligan et

al., Current Protocols in Immunology, vol. 1, Wiley Interscience (Greene 1998)). T cells that have been activated in response to a tumor polypeptide, polynucleotide or polypeptide-expressing APC may be CD4⁺ and/or CD8⁺. Tumor polypeptide-specific T cells may be expanded using standard techniques. Within preferred embodiments, the T
5 cells are derived from a patient, a related donor or an unrelated donor, and are administered to the patient following stimulation and expansion.

For therapeutic purposes, CD4⁺ or CD8⁺ T cells that proliferate in response to a tumor polypeptide, polynucleotide or APC can be expanded in number either *in vitro* or *in vivo*. Proliferation of such T cells *in vitro* may be accomplished in a
10 variety of ways. For example, the T cells can be re-exposed to a tumor polypeptide, or a short peptide corresponding to an immunogenic portion of such a polypeptide, with or without the addition of T cell growth factors, such as interleukin-2, and/or stimulator cells that synthesize a tumor polypeptide. Alternatively, one or more T cells that proliferate in the presence of the tumor polypeptide can be expanded in number by
15 cloning. Methods for cloning cells are well known in the art, and include limiting dilution.

Pharmaceutical Compositions

In additional embodiments, the present invention concerns formulation of one or more of the polynucleotide, polypeptide, T-cell and/or antibody compositions
20 disclosed herein in pharmaceutically-acceptable carriers for administration to a cell or an animal, either alone, or in combination with one or more other modalities of therapy.

It will be understood that, if desired, a composition as disclosed herein may be administered in combination with other agents as well, such as, *e.g.*, other proteins or polypeptides or various pharmaceutically-active agents. In fact, there is
25 virtually no limit to other components that may also be included, given that the additional agents do not cause a significant adverse effect upon contact with the target cells or host tissues. The compositions may thus be delivered along with various other agents as required in the particular instance. Such compositions may be purified from host cells or other biological sources, or alternatively may be chemically synthesized as

described herein. Likewise, such compositions may further comprise substituted or derivatized RNA or DNA compositions.

Therefore, in another aspect of the present invention, pharmaceutical compositions are provided comprising one or more of the polynucleotide, polypeptide, antibody, and/or T-cell compositions described herein in combination with a physiologically acceptable carrier. In certain preferred embodiments, the pharmaceutical compositions of the invention comprise immunogenic polynucleotide and/or polypeptide compositions of the invention for use in prophylactic and therapeutic vaccine applications. Vaccine preparation is generally described in, for example, M.F. Powell and M.J. Newman, eds., "Vaccine Design (the subunit and adjuvant approach)," Plenum Press (NY, 1995). Generally, such compositions will comprise one or more polynucleotide and/or polypeptide compositions of the present invention in combination with one or more immunostimulants.

It will be apparent that any of the pharmaceutical compositions described herein can contain pharmaceutically acceptable salts of the polynucleotides and polypeptides of the invention. Such salts can be prepared, for example, from pharmaceutically acceptable non-toxic bases, including organic bases (e.g., salts of primary, secondary and tertiary amines and basic amino acids) and inorganic bases (e.g., sodium, potassium, lithium, ammonium, calcium and magnesium salts).

In another embodiment, illustrative immunogenic compositions, e.g., vaccine compositions, of the present invention comprise DNA encoding one or more of the polypeptides as described above, such that the polypeptide is generated *in situ*. As noted above, the polynucleotide may be administered within any of a variety of delivery systems known to those of ordinary skill in the art. Indeed, numerous gene delivery techniques are well known in the art, such as those described by Rolland, *Crit. Rev. Therap. Drug Carrier Systems* 15:143-198, 1998, and references cited therein. Appropriate polynucleotide expression systems will, of course, contain the necessary regulatory DNA regulatory sequences for expression in a patient (such as a suitable promoter and terminating signal). Alternatively, bacterial delivery systems may involve

the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an immunogenic portion of the polypeptide on its cell surface or secretes such an epitope.

Therefore, in certain embodiments, polynucleotides encoding immunogenic polypeptides described herein are introduced into suitable mammalian host cells for expression using any of a number of known viral-based systems. In one illustrative embodiment, retroviruses provide a convenient and effective platform for gene delivery systems. A selected nucleotide sequence encoding a polypeptide of the present invention can be inserted into a vector and packaged in retroviral particles using techniques known in the art. The recombinant virus can then be isolated and delivered to a subject. A number of illustrative retroviral systems have been described (e.g., U.S. Pat. No. 5,219,740; Miller and Rosman (1989) *BioTechniques* 7:980-990; Miller, A. D. (1990) *Human Gene Therapy* 1:5-14; Scarpa et al. (1991) *Virology* 180:849-852; Burns et al. (1993) *Proc. Natl. Acad. Sci. USA* 90:8033-8037; and Boris-Lawrie and Temin (1993) *Cur. Opin. Genet. Develop.* 3:102-109.

In addition, a number of illustrative adenovirus-based systems have also been described. Unlike retroviruses which integrate into the host genome, adenoviruses persist extrachromosomally thus minimizing the risks associated with insertional mutagenesis (Haj-Ahmad and Graham (1986) *J. Virol.* 57:267-274; Bett et al. (1993) *J. Virol.* 67:5911-5921; Mittereder et al. (1994) *Human Gene Therapy* 5:717-729; Seth et al. (1994) *J. Virol.* 68:933-940; Barr et al. (1994) *Gene Therapy* 1:51-58; Berkner, K. L. (1988) *BioTechniques* 6:616-629; and Rich et al. (1993) *Human Gene Therapy* 4:461-476).

Various adeno-associated virus (AAV) vector systems have also been developed for polynucleotide delivery. AAV vectors can be readily constructed using techniques well known in the art. See, e.g., U.S. Pat. Nos. 5,173,414 and 5,139,941; International Publication Nos. WO 92/01070 and WO 93/03769; Lebkowski et al. (1988) *Molec. Cell. Biol.* 8:3988-3996; Vincent et al. (1990) *Vaccines 90* (Cold Spring Harbor Laboratory Press); Carter, B. J. (1992) *Current Opinion in Biotechnology* 3:533-539; Muzyczka, N. (1992) *Current Topics in Microbiol. and Immunol.* 158:97-129;

Kotin, R. M. (1994) Human Gene Therapy 5:793-801; Shelling and Smith (1994) Gene Therapy 1:165-169; and Zhou et al. (1994) J. Exp. Med. 179:1867-1875.

Additional viral vectors useful for delivering the polynucleotides encoding polypeptides of the present invention by gene transfer include those derived from the pox family of viruses, such as vaccinia virus and avian poxvirus. By way of example, vaccinia virus recombinants expressing the novel molecules can be constructed as follows. The DNA encoding a polypeptide is first inserted into an appropriate vector so that it is adjacent to a vaccinia promoter and flanking vaccinia DNA sequences, such as the sequence encoding thymidine kinase (TK). This vector is then used to transfect cells which are simultaneously infected with vaccinia. Homologous recombination serves to insert the vaccinia promoter plus the gene encoding the polypeptide of interest into the viral genome. The resulting TK.sup.(-) recombinant can be selected by culturing the cells in the presence of 5-bromodeoxyuridine and picking viral plaques resistant thereto.

A vaccinia-based infection/transfection system can be conveniently used to provide for inducible, transient expression or coexpression of one or more polypeptides described herein in host cells of an organism. In this particular system, cells are first infected in vitro with a vaccinia virus recombinant that encodes the bacteriophage T7 RNA polymerase. This polymerase displays exquisite specificity in that it only transcribes templates bearing T7 promoters. Following infection, cells are transfected with the polynucleotide or polynucleotides of interest, driven by a T7 promoter. The polymerase, expressed in the cytoplasm from the vaccinia virus recombinant transcribes the transfected DNA into RNA which is then translated into polypeptide by the host translational machinery. The method provides for high level, transient, cytoplasmic production of large quantities of RNA and its translation products. See, e.g., Elroy-Stein and Moss, Proc. Natl. Acad. Sci. USA (1990) 87:6743-6747; Fuerst et al. Proc. Natl. Acad. Sci. USA (1986) 83:8122-8126.

Alternatively, avipoxviruses, such as the fowlpox and canarypox viruses, can also be used to deliver the coding sequences of interest. Recombinant avipox viruses, expressing immunogens from mammalian pathogens, are known to confer

protective immunity when administered to non-avian species. The use of an Avipox vector is particularly desirable in human and other mammalian species since members of the Avipox genus can only productively replicate in susceptible avian species and therefore are not infective in mammalian cells. Methods for producing recombinant
5 Avipoxviruses are known in the art and employ genetic recombination, as described above with respect to the production of vaccinia viruses. See, *e.g.*, WO 91/12882; WO 89/03429; and WO 92/03545.

Any of a number of alphavirus vectors can also be used for delivery of polynucleotide compositions of the present invention, such as those vectors described in
10 U.S. Patent Nos. 5,843,723; 6,015,686; 6,008,035 and 6,015,694. Certain vectors based on Venezuelan Equine Encephalitis (VEE) can also be used, illustrative examples of which can be found in U.S. Patent Nos. 5,505,947 and 5,643,576.

Moreover, molecular conjugate vectors, such as the adenovirus chimeric vectors described in Michael et al. *J. Biol. Chem.* (1993) 268:6866-6869 and Wagner et
15 al. *Proc. Natl. Acad. Sci. USA* (1992) 89:6099-6103, can also be used for gene delivery under the invention.

Additional illustrative information on these and other known viral-based delivery systems can be found, for example, in Fisher-Hoch et al., *Proc. Natl. Acad. Sci. USA* 86:317-321, 1989; Flexner et al., *Ann. N.Y. Acad. Sci.* 569:86-103, 1989; Flexner
20 et al., *Vaccine* 8:17-21, 1990; U.S. Patent Nos. 4,603,112, 4,769,330, and 5,017,487; WO 89/01973; U.S. Patent No. 4,777,127; GB 2,200,651; EP 0,345,242; WO 91/02805; Berkner, *Biotechniques* 6:616-627, 1988; Rosenfeld et al., *Science* 252:431-434, 1991; Kolls et al., *Proc. Natl. Acad. Sci. USA* 91:215-219, 1994; Kass-Eisler et al., *Proc. Natl. Acad. Sci. USA* 90:11498-11502, 1993; Guzman et al.,
25 *Circulation* 88:2838-2848, 1993; and Guzman et al., *Cir. Res.* 73:1202-1207, 1993.

In certain embodiments, a polynucleotide may be integrated into the genome of a target cell. This integration may be in a specific location and orientation via homologous recombination (gene replacement) or it may be integrated in a random, non-specific location (gene augmentation). In yet further embodiments, the
30 polynucleotide may be stably maintained in the cell as a separate, episomal segment of

DNA. Such polynucleotide segments or "episomes" encode sequences sufficient to permit maintenance and replication independent of or in synchronization with the host cell cycle. The manner in which the expression construct is delivered to a cell and where in the cell the polynucleotide remains is dependent on the type of expression
5 construct employed.

In another embodiment of the invention, a polynucleotide is administered/delivered as "naked" DNA, for example as described in Ulmer et al., *Science* 259:1745-1749, 1993 and reviewed by Cohen, *Science* 259:1691-1692, 1993. The uptake of naked DNA may be increased by coating the DNA onto biodegradable
10 beads, which are efficiently transported into the cells.

In still another embodiment, a composition of the present invention can be delivered via a particle bombardment approach, many of which have been described. In one illustrative example, gas-driven particle acceleration can be achieved with devices such as those manufactured by Powderject Pharmaceuticals PLC (Oxford, UK)
15 and Powderject Vaccines Inc. (Madison, WI), some examples of which are described in U.S. Patent Nos. 5,846,796; 6,010,478; 5,865,796; 5,584,807; and EP Patent No. 0500 799. This approach offers a needle-free delivery approach wherein a dry powder formulation of microscopic particles, such as polynucleotide or polypeptide particles, are accelerated to high speed within a helium gas jet generated by a hand held device,
20 propelling the particles into a target tissue of interest.

In a related embodiment, other devices and methods that may be useful for gas-driven needle-less injection of compositions of the present invention include those provided by Bioject, Inc. (Portland, OR), some examples of which are described in U.S. Patent Nos. 4,790,824; 5,064,413; 5,312,335; 5,383,851; 5,399,163; 5,520,639
25 and 5,993,412.

According to another embodiment, the pharmaceutical compositions described herein will comprise one or more immunostimulants in addition to the immunogenic polynucleotide, polypeptide, antibody, T-cell and/or APC compositions of this invention. An immunostimulant refers to essentially any substance that enhances
30 or potentiates an immune response (antibody and/or cell-mediated) to an exogenous

antigen. One preferred type of immunostimulant comprises an adjuvant. Many adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis* derived proteins.

5 Certain adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated

10 sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF, interleukin-2, -7, -12, and other like growth factors, may also be used as adjuvants.

Within certain embodiments of the invention, the adjuvant composition

15 is preferably one that induces an immune response predominantly of the Th1 type. High levels of Th1-type cytokines (e.g., IFN- γ , TNF α , IL-2 and IL-12) tend to favor the induction of cell mediated immune responses to an administered antigen. In contrast, high levels of Th2-type cytokines (e.g., IL-4, IL-5, IL-6 and IL-10) tend to favor the induction of humoral immune responses. Following application of a vaccine as

20 provided herein, a patient will support an immune response that includes Th1- and Th2-type responses. Within a preferred embodiment, in which a response is predominantly Th1-type, the level of Th1-type cytokines will increase to a greater extent than the level of Th2-type cytokines. The levels of these cytokines may be readily assessed using standard assays. For a review of the families of cytokines, see Mosmann and Coffman,

25 *Ann. Rev. Immunol.* 7:145-173, 1989.

Certain preferred adjuvants for eliciting a predominantly Th1-type response include, for example, a combination of monophosphoryl lipid A, preferably 3-de-O-acylated monophosphoryl lipid A, together with an aluminum salt. MPL[®] adjuvants are available from Corixa Corporation (Seattle, WA; see, for example, US

30 Patent Nos. 4,436,727; 4,877,611; 4,866,034 and 4,912,094). CpG-containing

oligonucleotides (in which the CpG dinucleotide is unmethylated) also induce a predominantly Th1 response. Such oligonucleotides are well known and are described, for example, in WO 96/02555, WO 99/33488 and U.S. Patent Nos. 6,008,200 and 5,856,462. Immunostimulatory DNA sequences are also described, for example, by

5 Sato et al., *Science* 273:352, 1996. Another preferred adjuvant comprises a saponin, such as Quil A, or derivatives thereof, including QS21 and QS7 (Aquila Biopharmaceuticals Inc., Framingham, MA); Escin; Digitonin; or *Gypsophila* or *Chenopodium quinoa* saponins. Other preferred formulations include more than one saponin in the adjuvant combinations of the present invention, for example

10 combinations of at least two of the following group comprising QS21, QS7, Quil A, β -escin, or digitonin.

Alternatively the saponin formulations may be combined with vaccine vehicles composed of chitosan or other polycationic polymers, polylactide and polylactide-co-glycolide particles, poly-N-acetyl glucosamine-based polymer matrix,

15 particles composed of polysaccharides or chemically modified polysaccharides, liposomes and lipid-based particles, particles composed of glycerol monoesters, etc. The saponins may also be formulated in the presence of cholesterol to form particulate structures such as liposomes or ISCOMs. Furthermore, the saponins may be formulated together with a polyoxyethylene ether or ester, in either a non-particulate solution or

20 suspension, or in a particulate structure such as a paucilamellar liposome or ISCOM. The saponins may also be formulated with excipients such as Carbopol^R to increase viscosity, or may be formulated in a dry powder form with a powder excipient such as lactose.

In one preferred embodiment, the adjuvant system includes the

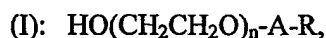
25 combination of a monophosphoryl lipid A and a saponin derivative, such as the combination of QS21 and 3D-MPL[®] adjuvant, as described in WO 94/00153, or a less reactogenic composition where the QS21 is quenched with cholesterol, as described in WO 96/33739. Other preferred formulations comprise an oil-in-water emulsion and tocopherol. Another particularly preferred adjuvant formulation employing QS21, 3D-

MPL[®] adjuvant and tocopherol in an oil-in-water emulsion is described in WO 95/17210.

Another enhanced adjuvant system involves the combination of a CpG-containing oligonucleotide and a saponin derivative particularly the combination of
5 CpG and QS21 is disclosed in WO 00/09159. Preferably the formulation additionally comprises an oil in water emulsion and tocopherol.

Additional illustrative adjuvants for use in the pharmaceutical compositions of the invention include Montanide ISA 720 (Seppic, France), SAF (Chiron, California, United States), ISCOMS (CSL), MF-59 (Chiron), the SBAS series
10 of adjuvants (e.g., SBAS-2 or SBAS-4, available from SmithKline Beecham, Rixensart, Belgium), Detox (Enhanzyn[®]; Corixa, Hamilton, MT), RC-529 (Corixa, Hamilton, MT) and other aminoalkyl glucosaminide 4-phosphates (AGPs), such as those described in pending U.S. Patent Application Serial Nos. 08/853,826 and 09/074,720, the disclosures of which are incorporated herein by reference in their entireties, and polyoxyethylene
15 ether adjuvants such as those described in WO 99/52549A1.

Other preferred adjuvants include adjuvant molecules of the general formula



wherein, n is 1-50, A is a bond or $-\text{C}(\text{O})-$, R is C_{1-50} alkyl or Phenyl C_{1-50} alkyl.

20 One embodiment of the present invention consists of a vaccine formulation comprising a polyoxyethylene ether of general formula (I), wherein n is between 1 and 50, preferably 4-24, most preferably 9; the R component is C_{1-50} , preferably $\text{C}_4\text{-C}_{20}$ alkyl and most preferably C_{12} alkyl, and A is a bond. The concentration of the polyoxyethylene ethers should be in the range 0.1-20%, preferably
25 from 0.1-10%, and most preferably in the range 0.1-1%. Preferred polyoxyethylene ethers are selected from the following group: polyoxyethylene-9-lauryl ether, polyoxyethylene-9-stearyl ether, polyoxyethylene-8-stearyl ether, polyoxyethylene-4-lauryl ether, polyoxyethylene-35-lauryl ether, and polyoxyethylene-23-lauryl ether. Polyoxyethylene ethers such as polyoxyethylene lauryl ether are described in the Merck
30 index (12th edition: entry 7717). These adjuvant molecules are described in WO

99/52549. The polyoxyethylene ether according to the general formula (I) above may, if desired, be combined with another adjuvant. For example, a preferred adjuvant combination is preferably with CpG as described in the pending UK patent application GB 9820956.2.

5 According to another embodiment of this invention, an immunogenic composition described herein is delivered to a host via antigen presenting cells (APCs), such as dendritic cells, macrophages, B cells, monocytes and other cells that may be engineered to be efficient APCs. Such cells may, but need not, be genetically modified to increase the capacity for presenting the antigen, to improve activation and/or
10 maintenance of the T cell response, to have anti-tumor effects *per se* and/or to be immunologically compatible with the receiver (*i.e.*, matched HLA haplotype). APCs may generally be isolated from any of a variety of biological fluids and organs, including tumor and peritumoral tissues, and may be autologous, allogeneic, syngeneic or xenogeneic cells.

15 Certain preferred embodiments of the present invention use dendritic cells or progenitors thereof as antigen-presenting cells. Dendritic cells are highly potent APCs (Banchereau and Steinman, *Nature* 392:245-251, 1998) and have been shown to be effective as a physiological adjuvant for eliciting prophylactic or therapeutic antitumor immunity (*see* Timmerman and Levy, *Ann. Rev. Med.* 50:507-529, 1999). In
20 general, dendritic cells may be identified based on their typical shape (stellate *in situ*, with marked cytoplasmic processes (dendrites) visible *in vitro*), their ability to take up, process and present antigens with high efficiency and their ability to activate naïve T cell responses. Dendritic cells may, of course, be engineered to express specific cell-surface receptors or ligands that are not commonly found on dendritic cells *in vivo* or *ex*
25 *vivo*, and such modified dendritic cells are contemplated by the present invention. As an alternative to dendritic cells, secreted vesicles antigen-loaded dendritic cells (called exosomes) may be used within a vaccine (*see* Zitvogel et al., *Nature Med.* 4:594-600, 1998).

 Dendritic cells and progenitors may be obtained from peripheral blood,
30 bone marrow, tumor-infiltrating cells, peritumoral tissues-infiltrating cells, lymph

nodes, spleen, skin, umbilical cord blood or any other suitable tissue or fluid. For example, dendritic cells may be differentiated *ex vivo* by adding a combination of cytokines such as GM-CSF, IL-4, IL-13 and/or TNF α to cultures of monocytes harvested from peripheral blood. Alternatively, CD34 positive cells harvested from
5 peripheral blood, umbilical cord blood or bone marrow may be differentiated into dendritic cells by adding to the culture medium combinations of GM-CSF, IL-3, TNF α , CD40 ligand, LPS, flt3 ligand and/or other compound(s) that induce differentiation, maturation and proliferation of dendritic cells.

Dendritic cells are conveniently categorized as "immature" and "mature"
10 cells, which allows a simple way to discriminate between two well characterized phenotypes. However, this nomenclature should not be construed to exclude all possible intermediate stages of differentiation. Immature dendritic cells are characterized as APC with a high capacity for antigen uptake and processing, which correlates with the high expression of Fc γ receptor and mannose receptor. The mature
15 phenotype is typically characterized by a lower expression of these markers, but a high expression of cell surface molecules responsible for T cell activation such as class I and class II MHC, adhesion molecules (*e.g.*, CD54 and CD11) and costimulatory molecules (*e.g.*, CD40, CD80, CD86 and 4-1BB).

APCs may generally be transfected with a polynucleotide of the
20 invention (or portion or other variant thereof) such that the encoded polypeptide, or an immunogenic portion thereof, is expressed on the cell surface. Such transfection may take place *ex vivo*, and a pharmaceutical composition comprising such transfected cells may then be used for therapeutic purposes, as described herein. Alternatively, a gene delivery vehicle that targets a dendritic or other antigen presenting cell may be
25 administered to a patient, resulting in transfection that occurs *in vivo*. *In vivo* and *ex vivo* transfection of dendritic cells, for example, may generally be performed using any methods known in the art, such as those described in WO 97/24447, or the gene gun approach described by Mahvi et al., *Immunology and cell Biology* 75:456-460, 1997. Antigen loading of dendritic cells may be achieved by incubating dendritic cells or
30 progenitor cells with the tumor polypeptide, DNA (naked or within a plasmid vector) or

RNA; or with antigen-expressing recombinant bacterium or viruses (*e.g.*, vaccinia, fowlpox, adenovirus or lentivirus vectors). Prior to loading, the polypeptide may be covalently conjugated to an immunological partner that provides T cell help (*e.g.*, a carrier molecule). Alternatively, a dendritic cell may be pulsed with a non-conjugated
5 immunological partner, separately or in the presence of the polypeptide.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will typically vary depending on the mode of administration. Compositions of the present invention may be formulated for any appropriate manner of administration,
10 including for example, topical, oral, nasal, mucosal, intravenous, intracranial, intraperitoneal, subcutaneous and intramuscular administration.

Carriers for use within such pharmaceutical compositions are biocompatible, and may also be biodegradable. In certain embodiments, the formulation preferably provides a relatively constant level of active component release.
15 In other embodiments, however, a more rapid rate of release immediately upon administration may be desired. The formulation of such compositions is well within the level of ordinary skill in the art using known techniques. Illustrative carriers useful in this regard include microparticles of poly(lactide-co-glycolide), polyacrylate, latex, starch, cellulose, dextran and the like. Other illustrative delayed-release carriers
20 include supramolecular biovectors, which comprise a non-liquid hydrophilic core (*e.g.*, a cross-linked polysaccharide or oligosaccharide) and, optionally, an external layer comprising an amphiphilic compound, such as a phospholipid (*see e.g.*, U.S. Patent No. 5,151,254 and PCT applications WO 94/20078, WO/94/23701 and WO 96/06638). The amount of active compound contained within a sustained release formulation depends
25 upon the site of implantation, the rate and expected duration of release and the nature of the condition to be treated or prevented.

In another illustrative embodiment, biodegradable microspheres (*e.g.*, polylactate polyglycolate) are employed as carriers for the compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S.
30 Patent Nos. 4,897,268; 5,075,109; 5,928,647; 5,811,128; 5,820,883; 5,853,763;

5,814,344, 5,407,609 and 5,942,252. Modified hepatitis B core protein carrier systems, such as described in WO/99 40934, and references cited therein, will also be useful for many applications. Another illustrative carrier/delivery system employs a carrier comprising particulate-protein complexes, such as those described in U.S. Patent No. 5,928,647, which are capable of inducing a class I-restricted cytotoxic T lymphocyte responses in a host.

The pharmaceutical compositions of the invention will often further comprise one or more buffers (*e.g.*, neutral buffered saline or phosphate buffered saline), carbohydrates (*e.g.*, glucose, mannose, sucrose or dextrans), mannitol, proteins, polypeptides or amino acids such as glycine, antioxidants, bacteriostats, chelating agents such as EDTA or glutathione, adjuvants (*e.g.*, aluminum hydroxide), solutes that render the formulation isotonic, hypotonic or weakly hypertonic with the blood of a recipient, suspending agents, thickening agents and/or preservatives. Alternatively, compositions of the present invention may be formulated as a lyophilizate.

The pharmaceutical compositions described herein may be presented in unit-dose or multi-dose containers, such as sealed ampoules or vials. Such containers are typically sealed in such a way to preserve the sterility and stability of the formulation until use. In general, formulations may be stored as suspensions, solutions or emulsions in oily or aqueous vehicles. Alternatively, a pharmaceutical composition may be stored in a freeze-dried condition requiring only the addition of a sterile liquid carrier immediately prior to use.

The development of suitable dosing and treatment regimens for using the particular compositions described herein in a variety of treatment regimens, including *e.g.*, oral, parenteral, intravenous, intranasal, and intramuscular administration and formulation, is well known in the art, some of which are briefly discussed below for general purposes of illustration.

In certain applications, the pharmaceutical compositions disclosed herein may be delivered *via* oral administration to an animal. As such, these compositions may be formulated with an inert diluent or with an assimilable edible carrier, or they

may be enclosed in hard- or soft-shell gelatin capsule, or they may be compressed into tablets, or they may be incorporated directly with the food of the diet.

The active compounds may even be incorporated with excipients and used in the form of ingestible tablets, buccal tables, troches, capsules, elixirs, suspensions, syrups, wafers, and the like (see, for example, Mathiowitz *et al.*, Nature 1997 Mar 27;386(6623):410-4; Hwang *et al.*, Crit Rev Ther Drug Carrier Syst 1998;15(3):243-84; U. S. Patent 5,641,515; U. S. Patent 5,580,579 and U. S. Patent 5,792,451). Tablets, troches, pills, capsules and the like may also contain any of a variety of additional components, for example, a binder, such as gum tragacanth, acacia, cornstarch, or gelatin; excipients, such as dicalcium phosphate; a disintegrating agent, such as corn starch, potato starch, alginic acid and the like; a lubricant, such as magnesium stearate; and a sweetening agent, such as sucrose, lactose or saccharin may be added or a flavoring agent, such as peppermint, oil of wintergreen, or cherry flavoring. When the dosage unit form is a capsule, it may contain, in addition to materials of the above type, a liquid carrier. Various other materials may be present as coatings or to otherwise modify the physical form of the dosage unit. For instance, tablets, pills, or capsules may be coated with shellac, sugar, or both. Of course, any material used in preparing any dosage unit form should be pharmaceutically pure and substantially non-toxic in the amounts employed. In addition, the active compounds may be incorporated into sustained-release preparation and formulations.

Typically, these formulations will contain at least about 0.1% of the active compound or more, although the percentage of the active ingredient(s) may, of course, be varied and may conveniently be between about 1 or 2% and about 60% or 70% or more of the weight or volume of the total formulation. Naturally, the amount of active compound(s) in each therapeutically useful composition may be prepared in such a way that a suitable dosage will be obtained in any given unit dose of the compound. Factors such as solubility, bioavailability, biological half-life, route of administration, product shelf life, as well as other pharmacological considerations will be contemplated by one skilled in the art of preparing such pharmaceutical formulations, and as such, a variety of dosages and treatment regimens may be desirable.

For oral administration, the compositions of the present invention may alternatively be incorporated with one or more excipients in the form of a mouthwash, dentifrice, buccal tablet, oral spray, or sublingual orally-administered formulation. Alternatively, the active ingredient may be incorporated into an oral solution such as
5 one containing sodium borate, glycerin and potassium bicarbonate, or dispersed in a dentifrice, or added in a therapeutically-effective amount to a composition that may include water, binders, abrasives, flavoring agents, foaming agents, and humectants. Alternatively the compositions may be fashioned into a tablet or solution form that may be placed under the tongue or otherwise dissolved in the mouth.

10 In certain circumstances it will be desirable to deliver the pharmaceutical compositions disclosed herein parenterally, intravenously, intramuscularly, or even intraperitoneally. Such approaches are well known to the skilled artisan, some of which are further described, for example, in U. S. Patent 5,543,158; U. S. Patent 5,641,515 and U. S. Patent 5,399,363. In certain embodiments, solutions of the active compounds
15 as free base or pharmacologically acceptable salts may be prepared in water suitably mixed with a surfactant, such as hydroxypropylcellulose. Dispersions may also be prepared in glycerol, liquid polyethylene glycols, and mixtures thereof and in oils. Under ordinary conditions of storage and use, these preparations generally will contain a preservative to prevent the growth of microorganisms.

20 Illustrative pharmaceutical forms suitable for injectable use include sterile aqueous solutions or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersions (for example, see U. S. Patent 5,466,468). In all cases the form must be sterile and must be fluid to the extent that easy syringability exists. It must be stable under the conditions of manufacture and
25 storage and must be preserved against the contaminating action of microorganisms, such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (e.g., glycerol, propylene glycol, and liquid polyethylene glycol, and the like), suitable mixtures thereof, and/or vegetable oils. Proper fluidity may be maintained, for example, by the use of a coating, such as
30 lecithin, by the maintenance of the required particle size in the case of dispersion and/or

by the use of surfactants. The prevention of the action of microorganisms can be facilitated by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, sorbic acid, thimerosal, and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars or sodium chloride.

5 Prolonged absorption of the injectable compositions can be brought about by the use in the compositions of agents delaying absorption, for example, aluminum monostearate and gelatin.

In one embodiment, for parenteral administration in an aqueous solution, the solution should be suitably buffered if necessary and the liquid diluent first rendered

10 isotonic with sufficient saline or glucose. These particular aqueous solutions are especially suitable for intravenous, intramuscular, subcutaneous and intraperitoneal administration. In this connection, a sterile aqueous medium that can be employed will be known to those of skill in the art in light of the present disclosure. For example, one dosage may be dissolved in 1 ml of isotonic NaCl solution and either added to 1000 ml

15 of hypodermoclysis fluid or injected at the proposed site of infusion, (see for example, "Remington's Pharmaceutical Sciences" 15th Edition, pages 1035-1038 and 1570-1580). Some variation in dosage will necessarily occur depending on the condition of the subject being treated. Moreover, for human administration, preparations will of course preferably meet sterility, pyrogenicity, and the general safety and purity

20 standards as required by FDA Office of Biologics standards.

In another embodiment of the invention, the compositions disclosed herein may be formulated in a neutral or salt form. Illustrative pharmaceutically-acceptable salts include the acid addition salts (formed with the free amino groups of the protein) and which are formed with inorganic acids such as, for

25 example, hydrochloric or phosphoric acids, or such organic acids as acetic, oxalic, tartaric, mandelic, and the like. Salts formed with the free carboxyl groups can also be derived from inorganic bases such as, for example, sodium, potassium, ammonium, calcium, or ferric hydroxides, and such organic bases as isopropylamine, trimethylamine, histidine, procaine and the like. Upon formulation, solutions will be

administered in a manner compatible with the dosage formulation and in such amount as is therapeutically effective.

The carriers can further comprise any and all solvents, dispersion media, vehicles, coatings, diluents, antibacterial and antifungal agents, isotonic and absorption
5 delaying agents, buffers, carrier solutions, suspensions, colloids, and the like. The use of such media and agents for pharmaceutical active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the active ingredient, its use in the therapeutic compositions is contemplated. Supplementary active ingredients can also be incorporated into the compositions. The phrase
10 "pharmaceutically-acceptable" refers to molecular entities and compositions that do not produce an allergic or similar untoward reaction when administered to a human.

In certain embodiments, the pharmaceutical compositions may be delivered by intranasal sprays, inhalation, and/or other aerosol delivery vehicles. Methods for delivering genes, nucleic acids, and peptide compositions directly to the
15 lungs *via* nasal aerosol sprays has been described, *e.g.*, in U. S. Patent 5,756,353 and U. S. Patent 5,804,212. Likewise, the delivery of drugs using intranasal microparticle resins (Takenaga *et al.*, J Controlled Release 1998 Mar 2;52(1-2):81-7) and lysophosphatidyl-glycerol compounds (U. S. Patent 5,725,871) are also well-known in the pharmaceutical arts. Likewise, illustrative transmucosal drug delivery in the form of
20 a polytetrafluoroethylene support matrix is described in U. S. Patent 5,780,045.

In certain embodiments, liposomes, nanocapsules, microparticles, lipid particles, vesicles, and the like, are used for the introduction of the compositions of the present invention into suitable host cells/organisms. In particular, the compositions of the present invention may be formulated for delivery either encapsulated in a lipid
25 particle, a liposome, a vesicle, a nanosphere, or a nanoparticle or the like. Alternatively, compositions of the present invention can be bound, either covalently or non-covalently, to the surface of such carrier vehicles.

The formation and use of liposome and liposome-like preparations as potential drug carriers is generally known to those of skill in the art (see for example,
30 Lasic, Trends Biotechnol 1998 Jul;16(7):307-21; Takakura, Nippon Rinsho 1998

Mar;56(3):691-5; Chandran *et al.*, Indian J Exp Biol. 1997 Aug;35(8):801-9; Margalit, Crit Rev Ther Drug Carrier Syst. 1995;12(2-3):233-61; U.S. Patent 5,567,434; U.S. Patent 5,552,157; U.S. Patent 5,565,213; U.S. Patent 5,738,868 and U.S. Patent 5,795,587, each specifically incorporated herein by reference in its entirety).

5 Liposomes have been used successfully with a number of cell types that are normally difficult to transfect by other procedures, including T cell suspensions, primary hepatocyte cultures and PC 12 cells (Renneisen *et al.*, J Biol Chem. 1990 Sep 25;265(27):16337-42; Muller *et al.*, DNA Cell Biol. 1990 Apr;9(3):221-9). In addition, liposomes are free of the DNA length constraints that are typical of viral-based delivery
10 systems. Liposomes have been used effectively to introduce genes, various drugs, radiotherapeutic agents, enzymes, viruses, transcription factors, allosteric effectors and the like, into a variety of cultured cell lines and animals. Furthermore, the use of liposomes does not appear to be associated with autoimmune responses or unacceptable toxicity after systemic delivery.

15 In certain embodiments, liposomes are formed from phospholipids that are dispersed in an aqueous medium and spontaneously form multilamellar concentric bilayer vesicles (also termed multilamellar vesicles (MLVs)).

 Alternatively, in other embodiments, the invention provides for pharmaceutically-acceptable nanocapsule formulations of the compositions of the
20 present invention. Nanocapsules can generally entrap compounds in a stable and reproducible way (see, for example, Quintanar-Guerrero *et al.*, Drug Dev Ind Pharm. 1998 Dec;24(12):1113-28). To avoid side effects due to intracellular polymeric overloading, such ultrafine particles (sized around 0.1 μ m) may be designed using polymers able to be degraded *in vivo*. Such particles can be made as described, for
25 example, by Couvreur *et al.*, Crit Rev Ther Drug Carrier Syst. 1988;5(1):1-20; zur Muhlen *et al.*, Eur J Pharm Biopharm. 1998 Mar;45(2):149-55; Zambaux *et al.* J Controlled Release. 1998 Jan 2;50(1-3):31-40; and U. S. Patent 5,145,684.

Cancer Therapeutic Methods

In further aspects of the present invention, the pharmaceutical compositions described herein may be used for the treatment of cancer, particularly for the immunotherapy of prostate cancer. Within such methods, the pharmaceutical compositions described herein are administered to a patient, typically a warm-blooded animal, preferably a human. A patient may or may not be afflicted with cancer. Accordingly, the above pharmaceutical compositions may be used to prevent the development of a cancer or to treat a patient afflicted with a cancer. Pharmaceutical compositions and vaccines may be administered either prior to or following surgical removal of primary tumors and/or treatment such as administration of radiotherapy or conventional chemotherapeutic drugs. As discussed above, administration of the pharmaceutical compositions may be by any suitable method, including administration by intravenous, intraperitoneal, intramuscular, subcutaneous, intranasal, intradermal, anal, vaginal, topical and oral routes.

Within certain embodiments, immunotherapy may be active immunotherapy, in which treatment relies on the *in vivo* stimulation of the endogenous host immune system to react against tumors with the administration of immune response-modifying agents (such as polypeptides and polynucleotides as provided herein).

Within other embodiments, immunotherapy may be passive immunotherapy, in which treatment involves the delivery of agents with established tumor-immune reactivity (such as effector cells or antibodies) that can directly or indirectly mediate antitumor effects and does not necessarily depend on an intact host immune system. Examples of effector cells include T cells as discussed above, T lymphocytes (such as CD8⁺ cytotoxic T lymphocytes and CD4⁺ T-helper tumor-infiltrating lymphocytes), killer cells (such as Natural Killer cells and lymphokine-activated killer cells), B cells and antigen-presenting cells (such as dendritic cells and macrophages) expressing a polypeptide provided herein. T cell receptors and antibody receptors specific for the polypeptides recited herein may be cloned, expressed and transferred into other vectors or effector cells for adoptive immunotherapy. The

polypeptides provided herein may also be used to generate antibodies or anti-idiotypic antibodies (as described above and in U.S. Patent No. 4,918,164) for passive immunotherapy.

Effector cells may generally be obtained in sufficient quantities for adoptive immunotherapy by growth *in vitro*, as described herein. Culture conditions for expanding single antigen-specific effector cells to several billion in number with retention of antigen recognition *in vivo* are well known in the art. Such *in vitro* culture conditions typically use intermittent stimulation with antigen, often in the presence of cytokines (such as IL-2) and non-dividing feeder cells. As noted above, immunoreactive polypeptides as provided herein may be used to rapidly expand antigen-specific T cell cultures in order to generate a sufficient number of cells for immunotherapy. In particular, antigen-presenting cells, such as dendritic, macrophage, monocyte, fibroblast and/or B cells, may be pulsed with immunoreactive polypeptides or transfected with one or more polynucleotides using standard techniques well known in the art. For example, antigen-presenting cells can be transfected with a polynucleotide having a promoter appropriate for increasing expression in a recombinant virus or other expression system. Cultured effector cells for use in therapy must be able to grow and distribute widely, and to survive long term *in vivo*. Studies have shown that cultured effector cells can be induced to grow *in vivo* and to survive long term in substantial numbers by repeated stimulation with antigen supplemented with IL-2 (see, for example, Cheever et al., *Immunological Reviews* 157:177, 1997).

Alternatively, a vector expressing a polypeptide recited herein may be introduced into antigen presenting cells taken from a patient and clonally propagated *ex vivo* for transplant back into the same patient. Transfected cells may be reintroduced into the patient using any means known in the art, preferably in sterile form by intravenous, intracavitary, intraperitoneal or intratumor administration.

Routes and frequency of administration of the therapeutic compositions described herein, as well as dosage, will vary from individual to individual, and may be readily established using standard techniques. In general, the pharmaceutical compositions and vaccines may be administered by injection (e.g., intracutaneous,

intramuscular, intravenous or subcutaneous), intranasally (*e.g.*, by aspiration) or orally. Preferably, between 1 and 10 doses may be administered over a 52 week period. Preferably, 6 doses are administered, at intervals of 1 month, and booster vaccinations may be given periodically thereafter. Alternate protocols may be appropriate for
5 individual patients. A suitable dose is an amount of a compound that, when administered as described above, is capable of promoting an anti-tumor immune response, and is at least 10-50% above the basal (*i.e.*, untreated) level. Such response can be monitored by measuring the anti-tumor antibodies in a patient or by vaccine-dependent generation of cytolytic effector cells capable of killing the patient's tumor
10 cells *in vitro*. Such vaccines should also be capable of causing an immune response that leads to an improved clinical outcome (*e.g.*, more frequent remissions, complete or partial or longer disease-free survival) in vaccinated patients as compared to non-vaccinated patients. In general, for pharmaceutical compositions and vaccines comprising one or more polypeptides, the amount of each polypeptide present in a dose
15 ranges from about 25 µg to 5 mg per kg of host. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.1 mL to about 5 mL.

In general, an appropriate dosage and treatment regimen provides the active compound(s) in an amount sufficient to provide therapeutic and/or prophylactic benefit. Such a response can be monitored by establishing an improved clinical
20 outcome (*e.g.*, more frequent remissions, complete or partial, or longer disease-free survival) in treated patients as compared to non-treated patients. Increases in preexisting immune responses to a tumor protein generally correlate with an improved clinical outcome. Such immune responses may generally be evaluated using standard proliferation, cytotoxicity or cytokine assays, which may be performed using samples
25 obtained from a patient before and after treatment.

Cancer Detection and Diagnostic Compositions, Methods and Kits

In general, a cancer may be detected in a patient based on the presence of one or more prostate tumor proteins and/or polynucleotides encoding such proteins in a biological sample (for example, blood, sera, sputum urine and/or tumor biopsies)

obtained from the patient. In other words, such proteins may be used as markers to indicate the presence or absence of a cancer such as prostate cancer. In addition, such proteins may be useful for the detection of other cancers. The binding agents provided herein generally permit detection of the level of antigen that binds to the agent in the biological sample. Polynucleotide primers and probes may be used to detect the level of mRNA encoding a tumor protein, which is also indicative of the presence or absence of a cancer. In general, a prostate tumor sequence should be present at a level that is at least three fold higher in tumor tissue than in normal tissue

There are a variety of assay formats known to those of ordinary skill in the art for using a binding agent to detect polypeptide markers in a sample. *See, e.g.,* Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In general, the presence or absence of a cancer in a patient may be determined by (a) contacting a biological sample obtained from a patient with a binding agent; (b) detecting in the sample a level of polypeptide that binds to the binding agent; and (c) comparing the level of polypeptide with a predetermined cut-off value.

In a preferred embodiment, the assay involves the use of binding agent immobilized on a solid support to bind to and remove the polypeptide from the remainder of the sample. The bound polypeptide may then be detected using a detection reagent that contains a reporter group and specifically binds to the binding agent/polypeptide complex. Such detection reagents may comprise, for example, a binding agent that specifically binds to the polypeptide or an antibody or other agent that specifically binds to the binding agent, such as an anti-immunoglobulin, protein G, protein A or a lectin. Alternatively, a competitive assay may be utilized, in which a polypeptide is labeled with a reporter group and allowed to bind to the immobilized binding agent after incubation of the binding agent with the sample. The extent to which components of the sample inhibit the binding of the labeled polypeptide to the binding agent is indicative of the reactivity of the sample with the immobilized binding agent. Suitable polypeptides for use within such assays include full length prostate tumor proteins and polypeptide portions thereof to which the binding agent binds, as described above.

The solid support may be any material known to those of ordinary skill in the art to which the tumor protein may be attached. For example, the solid support may be a test well in a microtiter plate or a nitrocellulose or other suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681. The binding agent may be immobilized on the solid support using a variety of techniques known to those of skill in the art, which are amply described in the patent and scientific literature. In the context of the present invention, the term "immobilization" refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the agent and functional groups on the support or may be a linkage by way of a cross-linking agent). Immobilization by adsorption to a well in a microtiter plate or to a membrane is preferred. In such cases, adsorption may be achieved by contacting the binding agent, in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and about 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of binding agent ranging from about 10 ng to about 10 μ g, and preferably about 100 ng to about 1 μ g, is sufficient to immobilize an adequate amount of binding agent.

Covalent attachment of binding agent to a solid support may generally be achieved by first reacting the support with a bifunctional reagent that will react with both the support and a functional group, such as a hydroxyl or amino group, on the binding agent. For example, the binding agent may be covalently attached to supports having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the binding partner (*see, e.g.,* Pierce Immunotechnology Catalog and Handbook, 1991, at A12-A13).

In certain embodiments, the assay is a two-antibody sandwich assay. This assay may be performed by first contacting an antibody that has been immobilized

on a solid support, commonly the well of a microtiter plate, with the sample, such that polypeptides within the sample are allowed to bind to the immobilized antibody. Unbound sample is then removed from the immobilized polypeptide-antibody complexes and a detection reagent (preferably a second antibody capable of binding to a different site on the polypeptide) containing a reporter group is added. The amount of detection reagent that remains bound to the solid support is then determined using a method appropriate for the specific reporter group.

More specifically, once the antibody is immobilized on the support as described above, the remaining protein binding sites on the support are typically blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin or Tween 20™ (Sigma Chemical Co., St. Louis, MO). The immobilized antibody is then incubated with the sample, and polypeptide is allowed to bind to the antibody. The sample may be diluted with a suitable diluent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact time (*i.e.*, incubation time) is a period of time that is sufficient to detect the presence of polypeptide within a sample obtained from an individual with prostate cancer. Preferably, the contact time is sufficient to achieve a level of binding that is at least about 95% of that achieved at equilibrium between bound and unbound polypeptide. Those of ordinary skill in the art will recognize that the time necessary to achieve equilibrium may be readily determined by assaying the level of binding that occurs over a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

Unbound sample may then be removed by washing the solid support with an appropriate buffer, such as PBS containing 0.1% Tween 20™. The second antibody, which contains a reporter group, may then be added to the solid support. Preferred reporter groups include those groups recited above.

The detection reagent is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound polypeptide. An appropriate amount of time may generally be determined by assaying the level of binding that occurs over a period of time. Unbound detection reagent is then removed

and bound detection reagent is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups and fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction products.

10 To determine the presence or absence of a cancer, such as prostate cancer, the signal detected from the reporter group that remains bound to the solid support is generally compared to a signal that corresponds to a predetermined cut-off value. In one preferred embodiment, the cut-off value for the detection of a cancer is the average mean signal obtained when the immobilized antibody is incubated with
15 samples from patients without the cancer. In general, a sample generating a signal that is three standard deviations above the predetermined cut-off value is considered positive for the cancer. In an alternate preferred embodiment, the cut-off value is determined using a Receiver Operator Curve, according to the method of Sackett et al., *Clinical Epidemiology: A Basic Science for Clinical Medicine*, Little Brown and Co., 1985,
20 p. 106-7. Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (*i.e.*, sensitivity) and false positive rates (100%-specificity) that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on the plot that is the closest to the upper left-hand corner (*i.e.*, the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a
25 signal that is higher than the cut-off value determined by this method may be considered positive. Alternatively, the cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for a cancer.

In a related embodiment, the assay is performed in a flow-through or strip test format, wherein the binding agent is immobilized on a membrane, such as nitrocellulose. In the flow-through test, polypeptides within the sample bind to the immobilized binding agent as the sample passes through the membrane. A second, labeled binding agent then binds to the binding agent-polypeptide complex as a solution containing the second binding agent flows through the membrane. The detection of bound second binding agent may then be performed as described above. In the strip test format, one end of the membrane to which binding agent is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing second binding agent and to the area of immobilized binding agent. Concentration of second binding agent at the area of immobilized antibody indicates the presence of a cancer. Typically, the concentration of second binding agent at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of binding agent immobilized on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of polypeptide that would be sufficient to generate a positive signal in the two-antibody sandwich assay, in the format discussed above. Preferred binding agents for use in such assays are antibodies and antigen-binding fragments thereof. Preferably, the amount of antibody immobilized on the membrane ranges from about 25 ng to about 1 μ g, and more preferably from about 50 ng to about 500 ng. Such tests can typically be performed with a very small amount of biological sample.

Of course, numerous other assay protocols exist that are suitable for use with the tumor proteins or binding agents of the present invention. The above descriptions are intended to be exemplary only. For example, it will be apparent to those of ordinary skill in the art that the above protocols may be readily modified to use tumor polypeptides to detect antibodies that bind to such polypeptides in a biological sample. The detection of such tumor protein specific antibodies may correlate with the presence of a cancer.

A cancer may also, or alternatively, be detected based on the presence of T cells that specifically react with a tumor protein in a biological sample. Within certain methods, a biological sample comprising CD4⁺ and/or CD8⁺ T cells isolated from a patient is incubated with a tumor polypeptide, a polynucleotide encoding such a polypeptide and/or an APC that expresses at least an immunogenic portion of such a polypeptide, and the presence or absence of specific activation of the T cells is detected. Suitable biological samples include, but are not limited to, isolated T cells. For example, T cells may be isolated from a patient by routine techniques (such as by Ficoll/Hypaque density gradient centrifugation of peripheral blood lymphocytes). T cells may be incubated *in vitro* for 2-9 days (typically 4 days) at 37°C with polypeptide (e.g., 5 - 25 µg/ml). It may be desirable to incubate another aliquot of a T cell sample in the absence of tumor polypeptide to serve as a control. For CD4⁺ T cells, activation is preferably detected by evaluating proliferation of the T cells. For CD8⁺ T cells, activation is preferably detected by evaluating cytolytic activity. A level of proliferation that is at least two fold greater and/or a level of cytolytic activity that is at least 20% greater than in disease-free patients indicates the presence of a cancer in the patient.

As noted above, a cancer may also, or alternatively, be detected based on the level of mRNA encoding a tumor protein in a biological sample. For example, at least two oligonucleotide primers may be employed in a polymerase chain reaction (PCR) based assay to amplify a portion of a tumor cDNA derived from a biological sample, wherein at least one of the oligonucleotide primers is specific for (*i.e.*, hybridizes to) a polynucleotide encoding the tumor protein. The amplified cDNA is then separated and detected using techniques well known in the art, such as gel electrophoresis. Similarly, oligonucleotide probes that specifically hybridize to a polynucleotide encoding a tumor protein may be used in a hybridization assay to detect the presence of polynucleotide encoding the tumor protein in a biological sample.

To permit hybridization under assay conditions, oligonucleotide primers and probes should comprise an oligonucleotide sequence that has at least about 60%, preferably at least about 75% and more preferably at least about 90%, identity to a portion of a polynucleotide encoding a tumor protein of the invention that is at least 10

nucleotides, and preferably at least 20 nucleotides, in length. Preferably, oligonucleotide primers and/or probes hybridize to a polynucleotide encoding a polypeptide described herein under moderately stringent conditions, as defined above. Oligonucleotide primers and/or probes which may be usefully employed in the

5 diagnostic methods described herein preferably are at least 10-40 nucleotides in length. In a preferred embodiment, the oligonucleotide primers comprise at least 10 contiguous nucleotides, more preferably at least 15 contiguous nucleotides, of a DNA molecule having a sequence as disclosed herein. Techniques for both PCR based assays and hybridization assays are well known in the art (*see, for example, Mullis et al., Cold*

10 *Spring Harbor Symp. Quant. Biol.*, 51:263, 1987; Erlich ed., *PCR Technology*, Stockton Press, NY, 1989).

One preferred assay employs RT-PCR, in which PCR is applied in conjunction with reverse transcription. Typically, RNA is extracted from a biological sample, such as biopsy tissue, and is reverse transcribed to produce cDNA molecules.

15 PCR amplification using at least one specific primer generates a cDNA molecule, which may be separated and visualized using, for example, gel electrophoresis. Amplification may be performed on biological samples taken from a test patient and from an individual who is not afflicted with a cancer. The amplification reaction may be performed on several dilutions of cDNA spanning two orders of magnitude. A two-fold

20 or greater increase in expression in several dilutions of the test patient sample as compared to the same dilutions of the non-cancerous sample is typically considered positive.

In another embodiment, the compositions described herein may be used as markers for the progression of cancer. In this embodiment, assays as described above

25 for the diagnosis of a cancer may be performed over time, and the change in the level of reactive polypeptide(s) or polynucleotide(s) evaluated. For example, the assays may be performed every 24-72 hours for a period of 6 months to 1 year, and thereafter performed as needed. In general, a cancer is progressing in those patients in whom the level of polypeptide or polynucleotide detected increases over time. In contrast, the

cancer is not progressing when the level of reactive polypeptide or polynucleotide either remains constant or decreases with time.

Certain *in vivo* diagnostic assays may be performed directly on a tumor. One such assay involves contacting tumor cells with a binding agent. The bound
5 binding agent may then be detected directly or indirectly via a reporter group. Such binding agents may also be used in histological applications. Alternatively, polynucleotide probes may be used within such applications.

As noted above, to improve sensitivity, multiple tumor protein markers may be assayed within a given sample. It will be apparent that binding agents specific
10 for different proteins provided herein may be combined within a single assay. Further, multiple primers or probes may be used concurrently. The selection of tumor protein markers may be based on routine experiments to determine combinations that results in optimal sensitivity. In addition, or alternatively, assays for tumor proteins provided herein may be combined with assays for other known tumor antigens.

15 The present invention further provides kits for use within any of the above diagnostic methods. Such kits typically comprise two or more components necessary for performing a diagnostic assay. Components may be compounds, reagents, containers and/or equipment. For example, one container within a kit may contain a monoclonal antibody or fragment thereof that specifically binds to a tumor protein.
20 Such antibodies or fragments may be provided attached to a support material, as described above. One or more additional containers may enclose elements, such as reagents or buffers, to be used in the assay. Such kits may also, or alternatively, contain a detection reagent as described above that contains a reporter group suitable for direct or indirect detection of antibody binding.

25 Alternatively, a kit may be designed to detect the level of mRNA encoding a tumor protein in a biological sample. Such kits generally comprise at least one oligonucleotide probe or primer, as described above, that hybridizes to a polynucleotide encoding a tumor protein. Such an oligonucleotide may be used, for example, within a PCR or hybridization assay. Additional components that may be

present within such kits include a second oligonucleotide and/or a diagnostic reagent or container to facilitate the detection of a polynucleotide encoding a tumor protein.

The following Examples are offered by way of illustration and not by way of limitation.

5

EXAMPLES

EXAMPLE 1

ISOLATION AND CHARACTERIZATION OF PROSTATE-SPECIFIC POLYPEPTIDES

10

This Example describes the isolation of certain prostate-specific polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library was constructed from prostate tumor poly A⁺ RNA using a Superscript Plasmid System for cDNA Synthesis and Plasmid Cloning kit (BRL Life Technologies, Gaithersburg, MD 20897) following the manufacturer's protocol. Specifically, prostate tumor tissues were homogenized with polytron (Kinematica, Switzerland) and total RNA was extracted using Trizol reagent (BRL Life Technologies) as directed by the manufacturer. The poly A⁺ RNA was then purified using a Qiagen oligotex spin column mRNA purification kit (Qiagen, 20 Santa Clarita, CA 91355) according to the manufacturer's protocol. First-strand cDNA was synthesized using the NotI/Oligo-dT18 primer. Double-stranded cDNA was synthesized, ligated with EcoRI/BAXI adaptors (Invitrogen, San Diego, CA) and digested with NotI. Following size fractionation with Chroma Spin-1000 columns (Clontech, Palo Alto, CA), the cDNA was ligated into the EcoRI/NotI site of 25 pCDNA3.1 (Invitrogen) and transformed into ElectroMax *E. coli* DH10B cells (BRL Life Technologies) by electroporation.

Using the same procedure, a normal human pancreas cDNA expression library was prepared from a pool of six tissue specimens (Clontech). The cDNA libraries were characterized by determining the number of independent colonies, the 30 percentage of clones that carried insert, the average insert size and by sequence analysis.

The prostate tumor library contained 1.64×10^7 independent colonies, with 70% of clones having an insert and the average insert size being 1745 base pairs. The normal pancreas cDNA library contained 3.3×10^6 independent colonies, with 69% of clones having inserts and the average insert size being 1120 base pairs. For both libraries, sequence analysis showed that the majority of clones had a full length cDNA sequence and were synthesized from mRNA, with minimal rRNA and mitochondrial DNA contamination.

cDNA library subtraction was performed using the above prostate tumor and normal pancreas cDNA libraries, as described by Hara *et al.* (*Blood*, 84:189-199, 1994) with some modifications. Specifically, a prostate tumor-specific subtracted cDNA library was generated as follows. Normal pancreas cDNA library (70 µg) was digested with EcoRI, NotI, and SfuI, followed by a filling-in reaction with DNA polymerase Klenow fragment. After phenol-chloroform extraction and ethanol precipitation, the DNA was dissolved in 100 µl of H₂O, heat-denatured and mixed with 100 µl (100 µg) of Photoprobe biotin (Vector Laboratories, Burlingame, CA). As recommended by the manufacturer, the resulting mixture was irradiated with a 270 W sunlamp on ice for 20 minutes. Additional Photoprobe biotin (50 µl) was added and the biotinylation reaction was repeated. After extraction with butanol five times, the DNA was ethanol-precipitated and dissolved in 23 µl H₂O to form the driver DNA.

To form the tracer DNA, 10 µg prostate tumor cDNA library was digested with BamHI and XhoI, phenol chloroform extracted and passed through Chroma spin-400 columns (Clontech). Following ethanol precipitation, the tracer DNA was dissolved in 5 µl H₂O. Tracer DNA was mixed with 15 µl driver DNA and 20 µl of 2 x hybridization buffer (1.5 M NaCl/10 mM EDTA/50 mM HEPES pH 7.5/0.2% sodium dodecyl sulfate), overlaid with mineral oil, and heat-denatured completely. The sample was immediately transferred into a 68 °C water bath and incubated for 20 hours (long hybridization [LH]). The reaction mixture was then subjected to a streptavidin treatment followed by phenol/chloroform extraction. This process was repeated three more times. Subtracted DNA was precipitated, dissolved in 12 µl H₂O, mixed with 8 µl driver DNA and 20 µl of 2 x hybridization buffer, and subjected to a hybridization at 68

⁰C for 2 hours (short hybridization [SH]). After removal of biotinylated double-stranded DNA, subtracted cDNA was ligated into BamHI/XhoI site of chloramphenicol resistant pBCSK⁺ (Stratagene, La Jolla, CA 92037) and transformed into ElectroMax *E. coli* DH10B cells by electroporation to generate a prostate tumor specific subtracted
5 cDNA library (referred to as "prostate subtraction 1").

To analyze the subtracted cDNA library, plasmid DNA was prepared from 100 independent clones, randomly picked from the subtracted prostate tumor specific library and grouped based on insert size. Representative cDNA clones were further characterized by DNA sequencing with a Perkin Elmer/Applied Biosystems
10 Division Automated Sequencer Model 373A (Foster City, CA). Six cDNA clones, hereinafter referred to as F1-13, F1-12, F1-16, H1-1, H1-9 and H1-4, were shown to be abundant in the subtracted prostate-specific cDNA library. The determined 3' and 5' cDNA sequences for F1-12 are provided in SEQ ID NO: 2 and 3, respectively, with determined 3' cDNA sequences for F1-13, F1-16, H1-1, H1-9 and H1-4 being provided
15 in SEQ ID NO: 1 and 4-7, respectively.

The cDNA sequences for the isolated clones were compared to known sequences in the gene bank using the EMBL and GenBank databases (release 96). Four of the prostate tumor cDNA clones, F1-13, F1-16, H1-1, and H1-4, were determined to encode the following previously identified proteins: prostate specific antigen (PSA),
20 human glandular kallikrein, human tumor expression enhanced gene, and mitochondria cytochrome C oxidase subunit II. H1-9 was found to be identical to a previously identified human autonomously replicating sequence. No significant homologies to the cDNA sequence for F1-12 were found.

Subsequent studies led to the isolation of a full-length cDNA sequence
25 for F1-12 (also referred to as P504S). This sequence is provided in SEQ ID NO: 107, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 108. cDNA splice variants of P504S are provided in SEQ ID NO: 600-605.

To clone less abundant prostate tumor specific genes, cDNA library subtraction was performed by subtracting the prostate tumor cDNA library described
30 above with the normal pancreas cDNA library and with the three most abundant genes

in the previously subtracted prostate tumor specific cDNA library: human glandular kallikrein, prostate specific antigen (PSA), and mitochondria cytochrome C oxidase subunit II. Specifically, 1 μ g each of human glandular kallikrein, PSA and mitochondria cytochrome C oxidase subunit II cDNAs in pCDNA3.1 were added to the driver DNA and subtraction was performed as described above to provide a second subtracted cDNA library hereinafter referred to as the "subtracted prostate tumor specific cDNA library with spike".

Twenty-two cDNA clones were isolated from the subtracted prostate tumor specific cDNA library with spike. The determined 3' and 5' cDNA sequences for the clones referred to as J1-17, L1-12, N1-1862, J1-13, J1-19, J1-25, J1-24, K1-58, K1-63, L1-4 and L1-14 are provided in SEQ ID NOS: 8-9, 10-11, 12-13, 14-15, 16-17, 18-19, 20-21, 22-23, 24-25, 26-27 and 28-29, respectively. The determined 3' cDNA sequences for the clones referred to as J1-12, J1-16, J1-21, K1-48, K1-55, L1-2, L1-6, N1-1858, N1-1860, N1-1861, N1-1864 are provided in SEQ ID NOS: 30-40, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to three of the five most abundant DNA species, (J1-17, L1-12 and N1-1862; SEQ ID NOS: 8-9, 10-11 and 12-13, respectively). Of the remaining two most abundant species, one (J1-12; SEQ ID NO:30) was found to be identical to the previously identified human pulmonary surfactant-associated protein, and the other (K1-48; SEQ ID NO:33) was determined to have some homology to *R. norvegicus* mRNA for 2-arylpropionyl-CoA epimerase. Of the 17 less abundant cDNA clones isolated from the subtracted prostate tumor specific cDNA library with spike, four (J1-16, K1-55, L1-6 and N1-1864; SEQ ID NOS:31, 34, 36 and 40, respectively) were found to be identical to previously identified sequences, two (J1-21 and N1-1860; SEQ ID NOS: 32 and 38, respectively) were found to show some homology to non-human sequences, and two (L1-2 and N1-1861; SEQ ID NOS: 35 and 39, respectively) were found to show some homology to known human sequences. No significant homologies were found to the polypeptides J1-13, J1-19, J1-24, J1-25, K1-58, K1-63, L1-4, L1-14 (SEQ ID NOS: 14-15, 16-17, 20-21, 18-19, 22-23, 24-25, 26-27, 28-29, respectively).

Subsequent studies led to the isolation of full length cDNA sequences for J1-17, L1-12 and N1-1862 (SEQ ID NOS: 109-111, respectively). The corresponding predicted amino acid sequences are provided in SEQ ID NOS: 112-114. L1-12 is also referred to as P501S. A cDNA splice variant of P501S is provided in SEQ ID NO: 606.

5 In a further experiment, four additional clones were identified by subtracting a prostate tumor cDNA library with normal prostate cDNA prepared from a pool of three normal prostate poly A+ RNA (referred to as "prostate subtraction 2"). The determined cDNA sequences for these clones, hereinafter referred to as U1-3064, U1-3065, V1-3692 and 1A-3905, are provided in SEQ ID NO: 69-72, respectively.

10 Comparison of the determined sequences with those in the gene bank revealed no significant homologies to U1-3065.

A second subtraction with spike (referred to as "prostate subtraction spike 2") was performed by subtracting a prostate tumor specific cDNA library with spike with normal pancreas cDNA library and further spiked with PSA, J1-17,

15 pulmonary surfactant-associated protein, mitochondrial DNA, cytochrome c oxidase subunit II, N1-1862, autonomously replicating sequence, L1-12 and tumor expression enhanced gene. Four additional clones, hereinafter referred to as V1-3686, R1-2330, 1B-3976 and V1-3679, were isolated. The determined cDNA sequences for these clones are provided in SEQ ID NO:73-76, respectively. Comparison of these sequences

20 with those in the gene bank revealed no significant homologies to V1-3686 and R1-2330.

Further analysis of the three prostate subtractions described above (prostate subtraction 2, subtracted prostate tumor specific cDNA library with spike, and prostate subtraction spike 2) resulted in the identification of sixteen additional clones,

25 referred to as 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1G-4734, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4810, 1I-4811, 1J-4876, 1K-4884 and 1K-4896. The determined cDNA sequences for these clones are provided in SEQ ID NOS: 77-92, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to 1G-4741, 1G-4734, 1I-4807, 1J-4876 and

30 1K-4896 (SEQ ID NOS: 79, 81, 87, 90 and 92, respectively). Further analysis of the

isolated clones led to the determination of extended cDNA sequences for 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4807, 1J-4876, 1K-4884 and 1K-4896, provided in SEQ ID NOS: 179-188 and 191-193, respectively, and to the determination of additional partial cDNA sequences for 1I-4810
5 and 1I-4811, provided in SEQ ID NOS: 189 and 190, respectively.

Additional studies with prostate subtraction spike 2 resulted in the isolation of three more clones. Their sequences were determined as described above and compared to the most recent GenBank. All three clones were found to have homology to known genes, which are Cysteine-rich protein, KIAA0242, and KIAA0280
10 (SEQ ID NO: 317, 319, and 320, respectively). Further analysis of these clones by Synteni microarray (Synteni, Palo Alto, CA) demonstrated that all three clones were over-expressed in most prostate tumors and prostate BPH, as well as in the majority of normal prostate tissues tested, but low expression in all other normal tissues.

An additional subtraction was performed by subtracting a normal
15 prostate cDNA library with normal pancreas cDNA (referred to as "prostate subtraction 3"). This led to the identification of six additional clones referred to as 1G-4761, 1G-4762, 1H-4766, 1H-4770, 1H-4771 and 1H-4772 (SEQ ID NOS: 93-98). Comparison of these sequences with those in the gene bank revealed no significant homologies to 1G-4761 and 1H-4771 (SEQ ID NOS: 93 and 97, respectively). Further analysis of the
20 isolated clones led to the determination of extended cDNA sequences for 1G-4761, 1G-4762, 1H-4766 and 1H-4772 provided in SEQ ID NOS: 194-196 and 199, respectively, and to the determination of additional partial cDNA sequences for 1H-4770 and 1H-4771, provided in SEQ ID NOS: 197 and 198, respectively.

Subtraction of a prostate tumor cDNA library, prepared from a pool of
25 polyA+ RNA from three prostate cancer patients, with a normal pancreas cDNA library (prostate subtraction 4) led to the identification of eight clones, referred to as 1D-4297, 1D-4309, 1D-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280 (SEQ ID NOS: 99-107). These sequences were compared to those in the gene bank as described above. No significant homologies were found to 1D-4283 and 1D-4304 (SEQ ID NOS:
30 103 and 104, respectively). Further analysis of the isolated clones led to the

determination of extended cDNA sequences for 1D-4309, 1D-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280, provided in SEQ ID NOS: 200-206, respectively.

cDNA clones isolated in prostate subtraction 1 and prostate subtraction 2, described above, were colony PCR amplified and their mRNA expression levels in prostate tumor, normal prostate and in various other normal tissues were determined using microarray technology (Synteni, Palo Alto, CA). Briefly, the PCR amplification products were dotted onto slides in an array format, with each product occupying a unique location in the array. mRNA was extracted from the tissue sample to be tested, reverse transcribed, and fluorescent-labeled cDNA probes were generated. The microarrays were probed with the labeled cDNA probes, the slides scanned and fluorescence intensity was measured. This intensity correlates with the hybridization intensity. Two clones (referred to as P509S and P510S) were found to be over-expressed in prostate tumor and normal prostate and expressed at low levels in all other normal tissues tested (liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon). The determined cDNA sequences for P509S and P510S are provided in SEQ ID NO: 223 and 224, respectively. Comparison of these sequences with those in the gene bank as described above, revealed some homology to previously identified ESTs.

Additional studies led to the isolation of the full-length cDNA sequence for P509S. This sequence is provided in SEQ ID NO: 332, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 339. Two variant full-length cDNA sequences for P510S are provided in SEQ ID NO: 535 and 536, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 537 and 538, respectively. Additional splice variants of P510S are provided in SEQ ID NO: 598 and 599.

EXAMPLE 2

DETERMINATION OF TISSUE SPECIFICITY OF PROSTATE-SPECIFIC POLYPEPTIDES

Using gene specific primers, mRNA expression levels for the
5 representative prostate-specific polypeptides F1-16, H1-1, J1-17 (also referred to as P502S), L1-12 (also referred to as P501S), F1-12 (also referred to as P504S) and N1-1862 (also referred to as P503S) were examined in a variety of normal and tumor tissues using RT-PCR.

Briefly, total RNA was extracted from a variety of normal and tumor
10 tissues using Trizol reagent as described above. First strand synthesis was carried out using 1-2 μ g of total RNA with SuperScript II reverse transcriptase (BRL Life Technologies) at 42 °C for one hour. The cDNA was then amplified by PCR with gene-specific primers. To ensure the semi-quantitative nature of the RT-PCR, β -actin was used as an internal control for each of the tissues examined. First, serial dilutions of the
15 first strand cDNAs were prepared and RT-PCR assays were performed using β -actin specific primers. A dilution was then chosen that enabled the linear range amplification of the β -actin template and which was sensitive enough to reflect the differences in the initial copy numbers. Using these conditions, the β -actin levels were determined for each reverse transcription reaction from each tissue. DNA contamination was
20 minimized by DNase treatment and by assuring a negative PCR result when using first strand cDNA that was prepared without adding reverse transcriptase.

mRNA Expression levels were examined in four different types of tumor tissue (prostate tumor from 2 patients, breast tumor from 3 patients, colon tumor, lung tumor), and sixteen different normal tissues, including prostate, colon, kidney, liver,
25 lung, ovary, pancreas, skeletal muscle, skin, stomach, testes, bone marrow and brain. F1-16 was found to be expressed at high levels in prostate tumor tissue, colon tumor and normal prostate, and at lower levels in normal liver, skin and testes, with expression being undetectable in the other tissues examined. H1-1 was found to be expressed at high levels in prostate tumor, lung tumor, breast tumor, normal prostate, normal colon
30 and normal brain, at much lower levels in normal lung, pancreas, skeletal muscle, skin,

small intestine, bone marrow, and was not detected in the other tissues tested. J1-17 (P502S) and L1-12 (P501S) appear to be specifically over-expressed in prostate, with both genes being expressed at high levels in prostate tumor and normal prostate but at low to undetectable levels in all the other tissues examined. N1-1862 (P503S) was found to be over-expressed in 60% of prostate tumors and detectable in normal colon and kidney. The RT-PCR results thus indicate that F1-16, H1-1, J1-17 (P502S), N1-1862 (P503S) and L1-12 (P501S) are either prostate specific or are expressed at significantly elevated levels in prostate.

Further RT-PCR studies showed that F1-12 (P504S) is over-expressed in 60% of prostate tumors, detectable in normal kidney but not detectable in all other tissues tested. Similarly, R1-2330 was shown to be over-expressed in 40% of prostate tumors, detectable in normal kidney and liver, but not detectable in all other tissues tested. U1-3064 was found to be over-expressed in 60% of prostate tumors, and also expressed in breast and colon tumors, but was not detectable in normal tissues.

RT-PCR characterization of R1-2330, U1-3064 and 1D-4279 showed that these three antigens are over-expressed in prostate and/or prostate tumors.

Northern analysis with four prostate tumors, two normal prostate samples, two BPH prostates, and normal colon, kidney, liver, lung, pancreas, skeletal muscle, brain, stomach, testes, small intestine and bone marrow, showed that L1-12 (P501S) is over-expressed in prostate tumors and normal prostate, while being undetectable in other normal tissues tested. J1-17 (P502S) was detected in two prostate tumors and not in the other tissues tested. N1-1862 (P503S) was found to be over-expressed in three prostate tumors and to be expressed in normal prostate, colon and kidney, but not in other tissues tested. F1-12 (P504S) was found to be highly expressed in two prostate tumors and to be undetectable in all other tissues tested.

The microarray technology described above was used to determine the expression levels of representative antigens described herein in prostate tumor, breast tumor and the following normal tissues: prostate, liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon. L1-12 (P501S) was found to be

over-expressed in normal prostate and prostate tumor, with some expression being detected in normal skeletal muscle. Both J1-12 and F1-12 (P504S) were found to be over-expressed in prostate tumor, with expression being lower or undetectable in all other tissues tested. N1-1862 (P503S) was found to be expressed at high levels in prostate tumor and normal prostate, and at low levels in normal large intestine and normal colon, with expression being undetectable in all other tissues tested. R1-2330 was found to be over-expressed in prostate tumor and normal prostate, and to be expressed at lower levels in all other tissues tested. 1D-4279 was found to be over-expressed in prostate tumor and normal prostate, expressed at lower levels in normal spinal cord, and to be undetectable in all other tissues tested.

Further microarray analysis to specifically address the extent to which P501S (SEQ ID NO: 110) was expressed in breast tumor revealed moderate over-expression not only in breast tumor, but also in metastatic breast tumor (2/31), with negligible to low expression in normal tissues. This data suggests that P501S may be over-expressed in various breast tumors as well as in prostate tumors.

The expression levels of 32 ESTs (expressed sequence tags) described by Vasmatazis *et al.* (*Proc. Natl. Acad. Sci. USA* 95:300-304, 1998) in a variety of tumor and normal tissues were examined by microarray technology as described above. Two of these clones (referred to as P1000C and P1001C) were found to be over-expressed in prostate tumor and normal prostate, and expressed at low to undetectable levels in all other tissues tested (normal aorta, thymus, resting and activated PBMC, epithelial cells, spinal cord, adrenal gland, fetal tissues, skin, salivary gland, large intestine, bone marrow, liver, lung, dendritic cells, stomach, lymph nodes, brain, heart, small intestine, skeletal muscle, colon and kidney. The determined cDNA sequences for P1000C and P1001C are provided in SEQ ID NO: 384 and 472, respectively. The sequence of P1001C was found to show some homology to the previously isolated Human mRNA for JM27 protein. Subsequent comparison of the sequence of SEQ ID NO: 384 with sequences in the public databases, led to the identification of a full-length cDNA sequence of P1000C (SEQ ID NO: 786), which encodes a 492 amino acid sequence. Analysis of the amino acid sequence using the PSORT II program led to the

identification of a putative transmembrane domain from amino acids 84-100. The cDNA sequence of the open reading frame of P1000C, including the stop codon, is provided in SEQ ID NO: 787, with the open reading frame without the stop codon being provided in SEQ ID NO: 788. The full-length amino acid sequence of P1000C is
5 provided in SEQ ID NO: 789. SEQ ID NO: 790 and 791 represent amino acids 1-100 and 100-492 of P1000C, respectively.

The expression of the polypeptide encoded by the full length cDNA sequence for F1-12 (also referred to as P504S; SEQ ID NO: 108) was investigated by immunohistochemical analysis. Rabbit-anti-P504S polyclonal antibodies were
10 generated against the full length P504S protein by standard techniques. Subsequent isolation and characterization of the polyclonal antibodies were also performed by techniques well known in the art. Immunohistochemical analysis showed that the P504S polypeptide was expressed in 100% of prostate carcinoma samples tested (n=5).

The rabbit-anti-P504S polyclonal antibody did not appear to label benign
15 prostate cells with the same cytoplasmic granular staining, but rather with light nuclear staining. Analysis of normal tissues revealed that the encoded polypeptide was found to be expressed in some, but not all normal human tissues. Positive cytoplasmic staining with rabbit-anti-P504S polyclonal antibody was found in normal human kidney, liver, brain, colon and lung-associated macrophages, whereas heart and bone marrow were
20 negative.

This data indicates that the P504S polypeptide is present in prostate cancer tissues, and that there are qualitative and quantitative differences in the staining between benign prostatic hyperplasia tissues and prostate cancer tissues, suggesting that this polypeptide may be detected selectively in prostate tumors and therefore be useful
25 in the diagnosis of prostate cancer.

EXAMPLE 3

ISOLATION AND CHARACTERIZATION OF PROSTATE-SPECIFIC
POLYPEPTIDES BY PCR-BASED SUBTRACTION

5 A cDNA subtraction library, containing cDNA from normal prostate
subtracted with ten other normal tissue cDNAs (brain, heart, kidney, liver, lung, ovary,
placenta, skeletal muscle, spleen and thymus) and then submitted to a first round of
PCR amplification, was purchased from Clontech. This library was subjected to a
second round of PCR amplification, following the manufacturer's protocol. The
10 resulting cDNA fragments were subcloned into the vector pT7 Blue T-vector (Novagen,
Madison, WI) and transformed into XL-1 Blue MRF' *E. coli* (Stratagene). DNA was
isolated from independent clones and sequenced using a Perkin Elmer/Applied
Biosystems Division Automated Sequencer Model 373A.

Fifty-nine positive clones were sequenced. Comparison of the DNA
15 sequences of these clones with those in the gene bank, as described above, revealed no
significant homologies to 25 of these clones, hereinafter referred to as P5, P8, P9, P18,
P20, P30, P34, P36, P38, P39, P42, P49, P50, P53, P55, P60, P64, P65, P73, P75, P76,
P79 and P84. The determined cDNA sequences for these clones are provided in SEQ
ID NO: 41-45, 47-52 and 54-65, respectively. P29, P47, P68, P80 and P82 (SEQ ID
20 NO: 46, 53 and 66-68, respectively) were found to show some degree of homology to
previously identified DNA sequences. To the best of the inventors' knowledge, none of
these sequences have been previously shown to be present in prostate.

Further studies employing the sequence of SEQ ID NO: 67 as a probe in
standard full-length cloning methods, resulted in the isolation of three cDNA sequences
25 which appear to be splice variants of P80 (also known as P704P). These sequences are
provided in SEQ ID NO: 620-622.

Further studies using the PCR-based methodology described above
resulted in the isolation of more than 180 additional clones, of which 23 clones were
found to show no significant homologies to known sequences. The determined cDNA
30 sequences for these clones are provided in SEQ ID NO: 115-123, 127, 131, 137, 145,

147-151, 153, 156-158 and 160. Twenty-three clones (SEQ ID NO: 124-126, 128-130, 132-136, 138-144, 146, 152, 154, 155 and 159) were found to show some homology to previously identified ESTs. An additional ten clones (SEQ ID NO: 161-170) were found to have some degree of homology to known genes. Larger cDNA clones
5 containing the P20 sequence represent splice variants of a gene referred to as P703P. The determined DNA sequence for the variants referred to as DE1, DE13 and DE14 are provided in SEQ ID NOS: 171, 175 and 177, respectively, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 172, 176 and 178, respectively. The determined cDNA sequence for an extended spliced form of P703 is
10 provided in SEQ ID NO: 225. The DNA sequences for the splice variants referred to as DE2 and DE6 are provided in SEQ ID NOS: 173 and 174, respectively.

mRNA Expression levels for representative clones in tumor tissues (prostate (n=5), breast (n=2), colon and lung) normal tissues (prostate (n=5), colon, kidney, liver, lung (n=2), ovary (n=2), skeletal muscle, skin, stomach, small intestine
15 and brain), and activated and non-activated PBMC was determined by RT-PCR as described above. Expression was examined in one sample of each tissue type unless otherwise indicated.

P9 was found to be highly expressed in normal prostate and prostate tumor compared to all normal tissues tested except for normal colon which showed
20 comparable expression. P20, a portion of the P703P gene, was found to be highly expressed in normal prostate and prostate tumor, compared to all twelve normal tissues tested. A modest increase in expression of P20 in breast tumor (n=2), colon tumor and lung tumor was seen compared to all normal tissues except lung (1 of 2). Increased expression of P18 was found in normal prostate, prostate tumor and breast tumor
25 compared to other normal tissues except lung and stomach. A modest increase in expression of P5 was observed in normal prostate compared to most other normal tissues. However, some elevated expression was seen in normal lung and PBMC. Elevated expression of P5 was also observed in prostate tumors (2 of 5), breast tumor and one lung tumor sample. For P30, similar expression levels were seen in normal
30 prostate and prostate tumor, compared to six of twelve other normal tissues tested.

Increased expression was seen in breast tumors, one lung tumor sample and one colon tumor sample, and also in normal PBMC. P29 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5 of 5) compared to the majority of normal tissues. However, substantial expression of P29 was observed in normal colon and
5 normal lung (2 of 2). P80 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5 of 5) compared to all other normal tissues tested, with increased expression also being seen in colon tumor.

Further studies resulted in the isolation of twelve additional clones, hereinafter referred to as 10-d8, 10-h10, 11-c8, 7-g6, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3, 8-
10 h11, 9-f12 and 9-f3. The determined DNA sequences for 10-d8, 10-h10, 11-c8, 8-d4, 8-d9, 8-h11, 9-f12 and 9-f3 are provided in SEQ ID NO: 207, 208, 209, 216, 217, 220, 221 and 222, respectively. The determined forward and reverse DNA sequences for 7-g6, 8-b5, 8-b6 and 8-g3 are provided in SEQ ID NO: 210 and 211; 212 and 213; 214 and 215; and 218 and 219, respectively. Comparison of these sequences with those in
15 the gene bank revealed no significant homologies to the sequence of 9-f3. The clones 10-d8, 11-c8 and 8-h11 were found to show some homology to previously isolated ESTs, while 10-h10, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3 and 9-f12 were found to show some homology to previously identified genes. Further characterization of 7-G6 and 8-G3 showed identity to the known genes PAP and PSA, respectively.

20 mRNA expression levels for these clones were determined using the micro-array technology described above. The clones 7-G6, 8-G3, 8-B5, 8-B6, 8-D4, 8-D9, 9-F3, 9-F12, 9-H3, 10-A2, 10-A4, 11-C9 and 11-F2 were found to be over-expressed in prostate tumor and normal prostate, with expression in other tissues tested being low or undetectable. Increased expression of 8-F11 was seen in prostate tumor
25 and normal prostate, bladder, skeletal muscle and colon. Increased expression of 10-H10 was seen in prostate tumor and normal prostate, bladder, lung, colon, brain and large intestine. Increased expression of 9-B1 was seen in prostate tumor, breast tumor, and normal prostate, salivary gland, large intestine and skin, with increased expression of 11-C8 being seen in prostate tumor, and normal prostate and large intestine.

An additional cDNA fragment derived from the PCR-based normal prostate subtraction, described above, was found to be prostate specific by both microarray technology and RT-PCR. The determined cDNA sequence of this clone (referred to as 9-A11) is provided in SEQ ID NO: 226. Comparison of this sequence with those
5 in the public databases revealed 99% identity to the known gene HOXB13.

Further studies led to the isolation of the clones 8-C6 and 8-H7. The determined cDNA sequences for these clones are provided in SEQ ID NO: 227 and 228, respectively. These sequences were found to show some homology to previously isolated ESTs.

10 PCR and hybridization-based methodologies were employed to obtain longer cDNA sequences for clone P20 (also referred to as P703P), yielding three additional cDNA fragments that progressively extend the 5' end of the gene. These fragments, referred to as P703PDE5, P703P6.26, and P703PX-23 (SEQ ID NO: 326, 328 and 330, with the predicted corresponding amino acid sequences being provided in
15 SEQ ID NO: 327, 329 and 331, respectively) contain additional 5' sequence. P703PDE5 was recovered by screening of a cDNA library (#141-26) with a portion of P703P as a probe. P703P6.26 was recovered from a mixture of three prostate tumor cDNAs and P703PX_23 was recovered from cDNA library (#438-48). Together, the additional sequences include all of the putative mature serine protease along with part of
20 the putative signal sequence. The full-length cDNA sequence for P703P is provided in SEQ ID NO: 524, with the corresponding amino acid sequence being provided in SEQ ID NO: 525.

Using computer algorithms, the following regions of P703P were predicted to represent potential HLA A2-binding CTL epitopes: amino acids 164-172
25 of SEQ ID NO: 525 (SEQ ID NO: 723); amino acids 160-168 of SEQ ID NO: 525 (SEQ ID NO: 724); amino acids 239-247 of SEQ ID NO: 525 (SEQ ID NO: 725); amino acids 118-126 of SEQ ID NO: 525 (SEQ ID NO: 726); amino acids 112-120 of SEQ ID NO: 525 (SEQ ID NO: 727); amino acids 155-164 of SEQ ID NO: 525 (SEQ ID NO: 728); amino acids 117-126 of SEQ ID NO: 525 (SEQ ID NO: 729); amino acids
30 164-173 of SEQ ID NO: 525 (SEQ ID NO: 730); amino acids 154-163 of SEQ ID NO:

525 (SEQ ID NO: 731); amino acids 163-172 of SEQ ID NO: 525 (SEQ ID NO: 732); amino acids 58-66 of SEQ ID NO: 525 (SEQ ID NO: 733); and amino acids 59-67 of SEQ ID NO: 525 (SEQ ID NO: 734).

P703P was found to show some homology to previously identified proteases, such as thrombin. The thrombin receptor has been shown to be preferentially expressed in highly metastatic breast carcinoma cells and breast carcinoma biopsy samples. Introduction of thrombin receptor antisense cDNA has been shown to inhibit the invasion of metastatic breast carcinoma cells in culture. Antibodies against thrombin receptor inhibit thrombin receptor activation and thrombin-induced platelet activation. Furthermore, peptides that resemble the receptor's tethered ligand domain inhibit platelet aggregation by thrombin. P703P may play a role in prostate cancer through a protease-activated receptor on the cancer cell or on stromal cells. The potential trypsin-like protease activity of P703P may either activate a protease-activated receptor on the cancer cell membrane to promote tumorigenesis or activate a protease-activated receptor on the adjacent cells (such as stromal cells) to secrete growth factors and/or proteases (such as matrix metalloproteinases) that could promote tumor angiogenesis, invasion and metastasis. P703P may thus promote tumor progression and/or metastasis through the activation of protease-activated receptor. Polypeptides and antibodies that block the P703P-receptor interaction may therefore be usefully employed in the treatment of prostate cancer.

To determine whether P703P expression increases with increased severity of Gleason grade, an indicator of tumor stage, quantitative PCR analysis was performed on prostate tumor samples with a range of Gleason scores from 5 to > 8. The mean level of P703P expression increased with increasing Gleason score, indicating that P703P expression may correlate with increased disease severity.

Further studies using a PCR-based subtraction library of a prostate tumor pool subtracted against a pool of normal tissues (referred to as JP: PCR subtraction) resulted in the isolation of thirteen additional clones, seven of which did not share any significant homology to known GenBank sequences. The determined cDNA sequences for these seven clones (P711P, P712P, novel 23, P774P, P775P, P710P and P768P) are

provided in SEQ ID NO: 307-311, 313 and 315, respectively. The remaining six clones (SEQ ID NO: 316 and 321-325) were shown to share some homology to known genes. By microarray analysis, all thirteen clones showed three or more fold over-expression in prostate tissues, including prostate tumors, BPH and normal prostate as compared to normal non-prostate tissues. Clones P711P, P712P, novel 23 and P768P showed over-expression in most prostate tumors and BPH tissues tested (n=29), and in the majority of normal prostate tissues (n=4), but background to low expression levels in all normal tissues. Clones P774P, P775P and P710P showed comparatively lower expression and expression in fewer prostate tumors and BPH samples, with negative to low expression in normal prostate.

Further studies led to the isolation of an extended cDNA sequence for P712P (SEQ ID NO: 552). The amino acid sequences encoded by 16 predicted open reading frames present within the sequence of SEQ ID NO: 552 are provided in SEQ ID NO: 553-568.

The full-length cDNA for P711P was obtained by employing the partial sequence of SEQ ID NO: 307 to screen a prostate cDNA library. Specifically, a directionally cloned prostate cDNA library was prepared using standard techniques. One million colonies of this library were plated onto LB/Amp plates. Nylon membrane filters were used to lift these colonies, and the cDNAs which were picked up by these filters were denatured and cross-linked to the filters by UV light. The P711P cDNA fragment of SEQ ID NO: 307 was radio-labeled and used to hybridize with these filters. Positive clones were selected, and cDNAs were prepared and sequenced using an automatic Perkin Elmer/Applied Biosystems sequencer. The determined full-length sequence of P711P is provided in SEQ ID NO: 382, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 383.

Using PCR and hybridization-based methodologies, additional cDNA sequence information was derived for two clones described above, 11-C9 and 9-F3, herein after referred to as P707P and P714P, respectively (SEQ ID NO: 333 and 334). After comparison with the most recent GenBank, P707P was found to be a splice variant of the known gene HoxB13. In contrast, no significant homologies to P714P

were found. Further studies employing the sequence of SEQ ID NO: 334 as a probe in standard full-length cloning methods, resulted in an extended cDNA sequence for P714P. This sequence is provided in SEQ ID NO: 619. This sequence was found to show some homology to the gene that encodes human ribosomal L23A protein.

5 Clones 8-B3, P89, P98, P130 and P201 (as disclosed in U.S. Patent Application No. 09/020,956, filed February 9, 1998) were found to be contained within one contiguous sequence, referred to as P705P (SEQ ID NO: 335, with the predicted amino acid sequence provided in SEQ ID NO: 336), which was determined to be a splice variant of the known gene NKX 3.1.

10 Further studies on P775P resulted in the isolation of four additional sequences (SEQ ID NO: 473-476) which are all splice variants of the P775P gene. The sequence of SEQ ID NO: 474 was found to contain two open reading frames (ORFs). The predicted amino acid sequences encoded by these ORFs are provided in SEQ ID NO: 477 and 478. The cDNA sequence of SEQ ID NO: 475 was found to contain an
15 ORF which encodes the amino acid sequence of SEQ ID NO: 479. The cDNA sequence of SEQ ID NO: 473 was found to contain four ORFs. The predicted amino acid sequences encoded by these ORFs are provided in SEQ ID NO: 480-483. Additional splice variants of P775P are provided in SEQ ID NO: 593-597.

Subsequent studies led to the identification of a genomic region on
20 chromosome 22q11.2, known as the Cat Eye Syndrome region, that contains the five prostate genes P704P, P712P, P774P, P775P and B305D. The relative location of each of these five genes within the genomic region is shown in Fig. 10. This region may therefore be associated with malignant tumors, and other potential tumor genes may be contained within this region. These studies also led to the identification of a potential
25 open reading frame (ORF) for P775P (provided in SEQ ID NO: 533), which encodes the amino acid sequence of SEQ ID NO: 534.

Comparison of the clone of SEQ ID NO: 325 (referred to as P558S) with sequences in the GenBank and GeneSeq DNA databases showed that P558S is identical to the prostate-specific transglutaminase gene, which is known to have two forms. The
30 full-length sequences for the two forms are provided in SEQ ID NO: 630 and 631, with

the corresponding amino acid sequences being provided in SEQ ID NO: 632 and 633, respectively. The cDNA sequence of SEQ ID NO: 631 has a 15 pair base insert, resulting in a 5 amino acid insert in the corresponding amino acid sequence (SEQ ID NO: 633). This insert is not present in the sequence of SEQ ID NO: 630.

5 Further studies on P768P (SEQ ID NO: 315) led to the identification of the putative full-length open reading frame (ORF). The cDNA sequence of the ORF with stop codon is provided in SEQ ID NO: 764. The cDNA sequence of the ORF without stop codon is provided in SEQ ID NO: 765, with the corresponding amino acid sequence being provided in SEQ ID NO: 766. This sequence was found to show 86%
10 identity to a rat calcium transporter protein, indicating that P768P may represent a human calcium transporter protein. The locations of transmembrane domains within P768P were predicted using the PSORT II computer algorithm. Six transmembrane domains were predicted at amino acid positions 118-134, 172-188, 211-227, 230-246, 282-298 and 348-364. The amino acid sequences of SEQ ID NO: 767-772 represent
15 amino acids 1-134, 135-188, 189-227, 228-246, 247-298 and 299-511 of P768P, respectively.

EXAMPLE 4

SYNTHESIS OF POLYPEPTIDES

20 Polypeptides may be synthesized on a Perkin Elmer/Applied Biosystems 430A peptide synthesizer using Fmoc chemistry with HPTU (O-Benzotriazole-N,N,N',N'-tetramethyluronium hexafluorophosphate) activation. A Gly-Cys-Gly sequence may be attached to the amino terminus of the peptide to provide a method of
25 conjugation, binding to an immobilized surface, or labeling of the peptide. Cleavage of the peptides from the solid support may be carried out using the following cleavage mixture: trifluoroacetic acid:ethanedithiol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for 2 hours, the peptides may be precipitated in cold methyl-t-butyl-ether. The peptide pellets may then be dissolved in water containing 0.1% trifluoroacetic acid
30 (TFA) and lyophilized prior to purification by C18 reverse phase HPLC. A gradient of

0%-60% acetonitrile (containing 0.1% TFA) in water (containing 0.1% TFA) may be used to elute the peptides. Following lyophilization of the pure fractions, the peptides may be characterized using electrospray or other types of mass spectrometry and by amino acid analysis.

5

EXAMPLE 5

FURTHER ISOLATION AND CHARACTERIZATION OF
PROSTATE-SPECIFIC POLYPEPTIDES BY PCR-BASED SUBTRACTION

10 A cDNA library generated from prostate primary tumor mRNA as described above was subtracted with cDNA from normal prostate. The subtraction was performed using a PCR-based protocol (Clontech), which was modified to generate larger fragments. Within this protocol, tester and driver double stranded cDNA were separately digested with five restriction enzymes that recognize six-nucleotide
15 restriction sites (MluI, MscI, PvuII, SalI and StuI). This digestion resulted in an average cDNA size of 600 bp, rather than the average size of 300 bp that results from digestion with RsaI according to the Clontech protocol. This modification did not affect the subtraction efficiency. Two tester populations were then created with different adapters, and the driver library remained without adapters.

20 The tester and driver libraries were then hybridized using excess driver cDNA. In the first hybridization step, driver was separately hybridized with each of the two tester cDNA populations. This resulted in populations of (a) unhybridized tester cDNAs, (b) tester cDNAs hybridized to other tester cDNAs, (c) tester cDNAs hybridized to driver cDNAs and (d) unhybridized driver cDNAs. The two separate
25 hybridization reactions were then combined, and rehybridized in the presence of additional denatured driver cDNA. Following this second hybridization, in addition to populations (a) through (d), a fifth population (e) was generated in which tester cDNA with one adapter hybridized to tester cDNA with the second adapter. Accordingly, the second hybridization step resulted in enrichment of differentially expressed sequences
30 which could be used as templates for PCR amplification with adaptor-specific primers.

The ends were then filled in, and PCR amplification was performed using adaptor-specific primers. Only population (e), which contained tester cDNA that did not hybridize to driver cDNA, was amplified exponentially. A second PCR amplification step was then performed, to reduce background and further enrich
5 differentially expressed sequences.

This PCR-based subtraction technique normalizes differentially expressed cDNAs so that rare transcripts that are overexpressed in prostate tumor tissue may be recoverable. Such transcripts would be difficult to recover by traditional subtraction methods.

10 In addition to genes known to be overexpressed in prostate tumor, seventy-seven further clones were identified. Sequences of these partial cDNAs are provided in SEQ ID NO: 29 to 305. Most of these clones had no significant homology to database sequences. Exceptions were JPTPN23 (SEQ ID NO: 231; similarity to pig valosin-containing protein), JPTPN30 (SEQ ID NO: 234; similarity to rat mRNA for
15 proteasome subunit), JPTPN45 (SEQ ID NO: 243; similarity to rat *norvegicus* cytosolic NADP-dependent isocitrate dehydrogenase), JPTPN46 (SEQ ID NO: 244; similarity to human subclone H8 4 d4 DNA sequence), JP1D6 (SEQ ID NO: 265; similarity to *G. gallus* dynein light chain-A), JP8D6 (SEQ ID NO: 288; similarity to human BAC clone RG016J04), JP8F5 (SEQ ID NO: 289; similarity to human subclone H8 3 b5 DNA
20 sequence), and JP8E9 (SEQ ID NO: 299; similarity to human Alu sequence).

Additional studies using the PCR-based subtraction library consisting of a prostate tumor pool subtracted against a normal prostate pool (referred to as PT-PN PCR subtraction) yielded three additional clones. Comparison of the cDNA sequences of these clones with the most recent release of GenBank revealed no significant
25 homologies to the two clones referred to as P715P and P767P (SEQ ID NO: 312 and 314). The remaining clone was found to show some homology to the known gene KIAA0056 (SEQ ID NO: 318). Using microarray analysis to measure mRNA expression levels in various tissues, all three clones were found to be over-expressed in prostate tumors and BPH tissues. Specifically, clone P715P was over-expressed in most
30 prostate tumors and BPH tissues by a factor of three or greater, with elevated expression

seen in the majority of normal prostate samples and in fetal tissue, but negative to low expression in all other normal tissues. Clone P767P was over-expressed in several prostate tumors and BPH tissues, with moderate expression levels in half of the normal prostate samples, and background to low expression in all other normal tissues tested.

5 Further analysis, by microarray as described above, of the PT-PN PCR subtraction library and of a DNA subtraction library containing cDNA from prostate tumor subtracted with a pool of normal tissue cDNAs, led to the isolation of 27 additional clones (SEQ ID NO: 340-365 and 381) which were determined to be over-expressed in prostate tumor. The clones of SEQ ID NO: 341, 342, 345, 347, 348, 349,
10 351, 355-359, 361, 362 and 364 were also found to be expressed in normal prostate. Expression of all 26 clones in a variety of normal tissues was found to be low or undetectable, with the exception of P544S (SEQ ID NO: 356) which was found to be expressed in small intestine. Of the 26 clones, 11 (SEQ ID NO: 340-349 and 362) were found to show some homology to previously identified sequences. No significant
15 homologies were found to the clones of SEQ ID NO: 350, 351, 353-361, and 363-365.

Comparison of the sequence of SEQ ID NO: 362 with sequences in the GenBank and GeneSeq DNA databases showed that this clone (referred to as P788P) is identical to GeneSeq Accession No. X27262, which encodes a protein found in the GeneSeq protein Accession No. Y00931. The full length cDNA sequence of P788P is
20 provided in SEQ ID NO: 634, with the corresponding predicted amino acid being provided in SEQ ID NO: 635. Subsequently, a full-length cDNA sequence for P788P that contains polymorphisms not found in the sequence of SEQ ID NO: 634, was cloned multiple times by PCR amplification from cDNA prepared from several RNA templates from three individuals. This determined cDNA sequence of this polymorphic variant of
25 P788P is provided in SEQ ID NO: 636, with the corresponding amino acid sequence being provided in SEQ ID NO: 637. The sequence of SEQ ID NO: 637 differs from that of SEQ ID NO: 635 by six amino acid residues. The P788P protein has 7 potential transmembrane domains at the C-terminal portion and is predicted to be a plasma membrane protein with an extracellular N-terminal region.

Further studies on the clone of SEQ ID NO: 352 (referred to as P790P) led to the isolation of the full-length cDNA sequence of SEQ ID NO: 526. The corresponding predicted amino acid is provided in SEQ ID NO: 527. Data from two quantitative PCR experiments indicated that P790P is over-expressed in 11/15 tested prostate tumor samples and is expressed at low levels in spinal cord, with no expression being seen in all other normal samples tested. Data from further PCR experiments and microarray experiments showed over-expression in normal prostate and prostate tumor with little or no expression in other tissues tested. P790P was subsequently found to show significant homology to a previously identified G-protein coupled prostate tissue receptor.

Additional studies on the clone of SEQ ID NO: 354 (referred to as P776P) led to the isolation of an extended cDNA sequence, provided in SEQ ID NO: 569. The determined cDNA sequences of three additional splice variants of P776P are provided in SEQ ID NO: 570-572. The amino acid sequences encoded by two predicted open reading frames (ORFs) contained within SEQ ID NO: 570, one predicted ORF contained within SEQ ID NO: 571, and 11 predicted ORFs contained within SEQ ID NO: 569, are provided in SEQ ID NO: 573-586, respectively. Further studies led to the isolation of the full-length sequence for the clone of SEQ ID NO: 570 (provided in SEQ ID NO: 737). Full-length cloning efforts on the clone of SEQ ID NO: 571 led to the isolation of two sequences (provided in SEQ ID NO: 738 and 739), representing a single clone, that are identical with the exception of a polymorphic insertion/deletion at position 1293. Specifically, the clone of SEQ ID NO: 739 (referred to as clone F1) has a C at position 1293. The clone of SEQ ID NO: 738 (referred to as clone F2) has a single base pair deletion at position 1293. The predicted amino acid sequences encoded by 5 open reading frames located within SEQ ID NO: 737 are provided in SEQ ID NO: 740-744, with the predicted amino acid sequences encoded by the clone of SEQ ID NO: 738 and 739 being provided in SEQ ID NO: 745-750.

Comparison of the cDNA sequences for the clones P767P (SEQ ID NO: 314) and P777P (SEQ ID NO: 350) with sequences in the GenBank human EST database showed that the two clones matched many EST sequences in common,

suggesting that P767P and P777P may represent the same gene. A DNA consensus sequence derived from a DNA sequence alignment of P767P, P777P and multiple EST clones is provided in SEQ ID NO: 587. The amino acid sequences encoded by three putative ORFs located within SEQ ID NO: 587 are provided in SEQ ID NO: 588-590.

5 The clone of SEQ ID NO: 342 (referred to as P789P) was found to show homology to a previously identified gene. The full length cDNA sequence for P789P and the corresponding amino acid sequence are provided in SEQ ID NO: 735 and 736, respectively.

10

EXAMPLE 6

PEPTIDE PRIMING OF MICE AND PROPAGATION OF CTL LINES

6.1. This Example illustrates the preparation of a CTL cell line specific for cells expressing the P502S gene.

15 Mice expressing the transgene for human HLA A2Kb (provided by Dr L. Sherman, The Scripps Research Institute, La Jolla, CA) were immunized with P2S#12 peptide (VLGWVAEL; SEQ ID NO: 306), which is derived from the P502S gene (also referred to herein as J1-17, SEQ ID NO: 8), as described by Theobald et al., *Proc. Natl. Acad. Sci. USA* 92:11993-11997, 1995 with the following modifications. Mice were
20 immunized with 100µg of P2S#12 and 120µg of an I-A^b binding peptide derived from hepatitis B Virus protein emulsified in incomplete Freund's adjuvant. Three weeks later these mice were sacrificed and using a nylon mesh single cell suspensions prepared. Cells were then resuspended at 6×10^6 cells/ml in complete media (RPMI-1640; Gibco BRL, Gaithersburg, MD) containing 10% FCS, 2mM Glutamine (Gibco BRL), sodium
25 pyruvate (Gibco BRL), non-essential amino acids (Gibco BRL), 2×10^{-5} M 2-mercaptoethanol, 50U/ml penicillin and streptomycin, and cultured in the presence of irradiated (3000 rads) P2S#12-pulsed (5mg/ml P2S#12 and 10mg/ml β 2-microglobulin) LPS blasts (A2 transgenic spleens cells cultured in the presence of 7µg/ml dextran sulfate and 25µg/ml LPS for 3 days). Six days later, cells (5×10^5 /ml) were
30 restimulated with 2.5×10^6 /ml peptide pulsed irradiated (20,000 rads) EL4A2Kb cells

(Sherman et al, *Science* 258:815-818, 1992) and 3×10^6 /ml A2 transgenic spleen feeder cells. Cells were cultured in the presence of 20U/ml IL-2. Cells continued to be restimulated on a weekly basis as described, in preparation for cloning the line.

P2S#12 line was cloned by limiting dilution analysis with peptide pulsed
5 EL4 A2Kb tumor cells (1×10^4 cells/ well) as stimulators and A2 transgenic spleen cells as feeders (5×10^5 cells/ well) grown in the presence of 30U/ml IL-2. On day 14, cells were restimulated as before. On day 21, clones that were growing were isolated and maintained in culture. Several of these clones demonstrated significantly higher reactivity (lysis) against human fibroblasts (HLA A2Kb expressing) transduced with
10 P502S than against control fibroblasts. An example is presented in Figure 1.

This data indicates that P2S #12 represents a naturally processed epitope of the P502S protein that is expressed in the context of the human HLA A2Kb molecule.

15 6.2. This Example illustrates the preparation of murine CTL lines and CTL clones specific for cells expressing the P501S gene.

This series of experiments were performed similarly to that described above. Mice were immunized with the P1S#10 peptide (SEQ ID NO: 337), which is
20 derived from the P501S gene (also referred to herein as L1-12, SEQ ID NO: 110). The P1S#10 peptide was derived by analysis of the predicted polypeptide sequence for P501S for potential HLA-A2 binding sequences as defined by published HLA-A2 binding motifs (Parker, KC, et al, *J. Immunol.*, 152:163, 1994). P1S#10 peptide was synthesized as described in Example 4, and empirically tested for HLA-A2 binding
25 using a T cell based competition assay. Predicted A2 binding peptides were tested for their ability to compete HLA-A2 specific peptide presentation to an HLA-A2 restricted CTL clone (D150M58), which is specific for the HLA-A2 binding influenza matrix peptide fluM58. D150M58 CTL secretes TNF in response to self-presentation of peptide fluM58. In the competition assay, test peptides at 100-200 μ g/ml were added to
30 cultures of D150M58 CTL in order to bind HLA-A2 on the CTL. After thirty minutes,

CTL cultured with test peptides, or control peptides, were tested for their antigen dose response to the fluM58 peptide in a standard TNF bioassay. As shown in Figure 3, peptide P1S#10 competes HLA-A2 restricted presentation of fluM58, demonstrating that peptide P1S#10 binds HLA-A2.

- 5 Mice expressing the transgene for human HLA A2Kb were immunized as described by Theobald et al. (*Proc. Natl. Acad. Sci. USA* 92:11993-11997, 1995) with the following modifications. Mice were immunized with 62.5 μ g of P1S #10 and 120 μ g of an I-A^b binding peptide derived from Hepatitis B Virus protein emulsified in incomplete Freund's adjuvant. Three weeks later these mice were sacrificed and single
10 cell suspensions prepared using a nylon mesh. Cells were then resuspended at 6×10^6 cells/ml in complete media (as described above) and cultured in the presence of irradiated (3000 rads) P1S#10-pulsed (2 μ g/ml P1S#10 and 10mg/ml β 2-microglobulin) LPS blasts (A2 transgenic spleens cells cultured in the presence of 7 μ g/ml dextran sulfate and 25 μ g/ml LPS for 3 days). Six days later cells (5×10^5 /ml) were restimulated
15 with 2.5×10^6 /ml peptide-pulsed irradiated (20,000 rads) EL4A2Kb cells, as described above, and 3×10^6 /ml A2 transgenic spleen feeder cells. Cells were cultured in the presence of 20 U/ml IL-2. Cells were restimulated on a weekly basis in preparation for cloning. After three rounds of *in vitro* stimulations, one line was generated that recognized P1S#10-pulsed Jurkat A2Kb targets and P501S-transduced Jurkat targets as
20 shown in Figure 4.

- A P1S#10-specific CTL line was cloned by limiting dilution analysis with peptide pulsed EL4 A2Kb tumor cells (1×10^4 cells/ well) as stimulators and A2 transgenic spleen cells as feeders (5×10^5 cells/ well) grown in the presence of 30U/ml IL-2. On day 14, cells were restimulated as before. On day 21, viable clones were
25 isolated and maintained in culture. As shown in Figure 5, five of these clones demonstrated specific cytolytic reactivity against P501S-transduced Jurkat A2Kb targets. This data indicates that P1S#10 represents a naturally processed epitope of the P501S protein that is expressed in the context of the human HLA-A2.1 molecule.

EXAMPLE 7

PRIMING OF CTL *IN VIVO* USING NAKED DNA IMMUNIZATION

WITH A PROSTATE ANTIGEN

The prostate-specific antigen L1-12, as described above, is also referred
5 to as P501S. HLA A2Kb Tg mice (provided by Dr L. Sherman, The Scripps Research
Institute, La Jolla, CA) were immunized with 100 µg P501S in the vector VR1012
either intramuscularly or intradermally. The mice were immunized three times, with a
two week interval between immunizations. Two weeks after the last immunization,
immune spleen cells were cultured with Jurkat A2Kb-P501S transduced stimulator
10 cells. CTL lines were stimulated weekly. After two weeks of *in vitro* stimulation, CTL
activity was assessed against P501S transduced targets. Two out of 8 mice developed
strong anti-P501S CTL responses. These results demonstrate that P501S contains at
least one naturally processed HLA-A2-restricted CTL epitope.

15

EXAMPLE 8

ABILITY OF HUMAN T CELLS TO RECOGNIZE PROSTATE-SPECIFIC POLYPEPTIDES

This Example illustrates the ability of T cells specific for a prostate
tumor polypeptide to recognize human tumor.

20 Human CD8⁺ T cells were primed *in vitro* to the P2S-12 peptide (SEQ
ID NO: 306) derived from P502S (also referred to as J1-17) using dendritic cells
according to the protocol of Van Tsai et al. (*Critical Reviews in Immunology* 18:65-75,
1998). The resulting CD8⁺ T cell microcultures were tested for their ability to
recognize the P2S-12 peptide presented by autologous fibroblasts or fibroblasts which
25 were transduced to express the P502S gene in a γ -interferon ELISPOT assay (*see*
Lalvani et al., *J. Exp. Med.* 186:859-865, 1997). Briefly, titrating numbers of T cells
were assayed in duplicate on 10⁴ fibroblasts in the presence of 3 µg/ml human β_2 -
microglobulin and 1 µg/ml P2S-12 peptide or control E75 peptide. In addition, T cells
were simultaneously assayed on autologous fibroblasts transduced with the P502S gene
30 or as a control, fibroblasts transduced with HER-2/*neu*. Prior to the assay, the

fibroblasts were treated with 10 ng/ml γ -interferon for 48 hours to upregulate class I MHC expression. One of the microcultures (#5) demonstrated strong recognition of both peptide pulsed fibroblasts as well as transduced fibroblasts in a γ -interferon ELISPOT assay. Figure 2A demonstrates that there was a strong increase in the number of γ -interferon spots with increasing numbers of T cells on fibroblasts pulsed with the P2S-12 peptide (solid bars) but not with the control E75 peptide (open bars). This shows the ability of these T cells to specifically recognize the P2S-12 peptide. As shown in Figure 2B, this microculture also demonstrated an increase in the number of γ -interferon spots with increasing numbers of T cells on fibroblasts transduced to express the P502S gene but not the HER-2/*neu* gene. These results provide additional confirmatory evidence that the P2S-12 peptide is a naturally processed epitope of the P502S protein. Furthermore, this also demonstrates that there exists in the human T cell repertoire, high affinity T cells which are capable of recognizing this epitope. These T cells should also be capable of recognizing human tumors which express the P502S gene.

EXAMPLE 9

ELICITATION OF PROSTATE ANTIGEN-SPECIFIC CTL RESPONSES

IN HUMAN BLOOD

This Example illustrates the ability of a prostate-specific antigen to elicit a CTL response in blood of normal humans.

Autologous dendritic cells (DC) were differentiated from monocyte cultures derived from PBMC of normal donors by growth for five days in RPMI medium containing 10% human serum, 50 ng/ml GMCSF and 30 ng/ml IL-4. Following culture, DC were infected overnight with recombinant P501S-expressing vaccinia virus at an M.O.I. of 5 and matured for 8 hours by the addition of 2 micrograms/ml CD40 ligand. Virus was inactivated by UV irradiation, CD8⁺ cells were isolated by positive selection using magnetic beads, and priming cultures were initiated in 24-well plates. Following five stimulation cycles using autologous fibroblasts

retrovirally transduced to express P501S and CD80, CD8+ lines were identified that specifically produced interferon-gamma when stimulated with autologous P501S-transduced fibroblasts. The P501S-specific activity of cell line 3A-1 could be maintained following additional stimulation cycles on autologous B-LCL transduced with P501S. Line 3A-1 was shown to specifically recognize autologous B-LCL transduced to express P501S, but not EGFP-transduced autologous B-LCL, as measured by cytotoxicity assays (^{51}Cr release) and interferon-gamma production (Interferon-gamma Elispot; *see above and Lalvani et al., J. Exp. Med. 186:859-865, 1997*). The results of these assays are presented in Figures 6A and 6B.

10

EXAMPLE 10

IDENTIFICATION OF A NATURALLY PROCESSED CTL EPITOPE CONTAINED WITHIN THE
PROSTATE-SPECIFIC ANTIGEN P703P

The 9-mer peptide p5 (SEQ ID NO: 338) was derived from the P703P antigen (also referred to as P20). The p5 peptide is immunogenic in human HLA-A2 donors and is a naturally processed epitope. Antigen specific human CD8+ T cells can be primed following repeated *in vitro* stimulations with monocytes pulsed with p5 peptide. These CTL specifically recognize p5-pulsed and P703P-transduced target cells in both ELISPOT (as described above) and chromium release assays. Additionally, immunization of HLA-A2Kb transgenic mice with p5 leads to the generation of CTL lines which recognize a variety of HLA-A2Kb or HLA-A2 transduced target cells expressing P703P.

Initial studies demonstrating that p5 is a naturally processed epitope were done using HLA-A2Kb transgenic mice. HLA-A2Kb transgenic mice were immunized subcutaneously in the footpad with 100 μg of p5 peptide together with 140 μg of hepatitis B virus core peptide (a Th peptide) in Freund's incomplete adjuvant. Three weeks post immunization, spleen cells from immunized mice were stimulated *in vitro* with peptide-pulsed LPS blasts. CTL activity was assessed by chromium release assay five days after primary *in vitro* stimulation. Retrovirally transduced cells expressing the

control antigen P703P and HLA-A2Kb were used as targets. CTL lines that specifically recognized both p5-pulsed targets as well as P703P-expressing targets were identified.

Human *in vitro* priming experiments demonstrated that the p5 peptide is immunogenic in humans. Dendritic cells (DC) were differentiated from monocyte
5 cultures derived from PBMC of normal human donors by culturing for five days in RPMI medium containing 10% human serum, 50 ng/ml human GM-CSF and 30 ng/ml human IL-4. Following culture, the DC were pulsed with 1 ug/ml p5 peptide and cultured with CD8+ T cell enriched PBMC. CTL lines were restimulated on a weekly basis with p5-pulsed monocytes. Five to six weeks after initiation of the CTL cultures,
10 CTL recognition of p5-pulsed target cells was demonstrated. CTL were additionally shown to recognize human cells transduced to express P703P, demonstrating that p5 is a naturally processed epitope.

Studies identifying a further peptide epitope (referred to as peptide 4) derived from the prostate tumor-specific antigen P703P that is capable of being
15 recognized by CD4 T cells on the surface of cells in the context of HLA class II molecules were carried out as follows. The amino acid sequence for peptide 4 is provided in SEQ ID NO: 638, with the corresponding cDNA sequence being provided in SEQ ID NO: 639.

Twenty 15-mer peptides overlapping by 10 amino acids and derived
20 from the carboxy-terminal fragment of P703P were generated using standard procedures. Dendritic cells (DC) were derived from PBMC of a normal female donor using GM-CSF and IL-4 by standard protocols. CD4 T cells were generated from the same donor as the DC using MACS beads and negative selection. DC were pulsed overnight with pools of the 15-mer peptides, with each peptide at a final concentration
25 of 0.25 microgram/ml. Pulsed DC were washed and plated at 1×10^4 cells/well of 96-well V-bottom plates and purified CD4 T cells were added at 1×10^5 /well. Cultures were supplemented with 60 ng/ml IL-6 and 10 ng/ml IL-12 and incubated at 37 °C. Cultures were restimulated as above on a weekly basis using DC generated and pulsed as above as antigen presenting cells, supplemented with 5 ng/ml IL-7 and 10 u/ml IL-2.
30 Following 4 *in vitro* stimulation cycles, 96 lines (each line corresponding to one well) were tested for specific proliferation and cytokine production in response to the

stimulating pools with an irrelevant pool of peptides derived from mammaglobin being used as a control.

One line (referred to as 1-F9) was identified from pool #1 that demonstrated specific proliferation (measured by ³H proliferation assays) and cytokine production (measured by interferon-gamma ELISA assays) in response to pool #1 of P703P peptides. This line was further tested for specific recognition of the peptide pool, specific recognition of individual peptides in the pool, and in HLA mismatch analyses to identify the relevant restricting allele. Line 1-F9 was found to specifically proliferate and produce interferon-gamma in response to peptide pool #1, and also to peptide 4 (SEQ ID NO: 638). Peptide 4 corresponds to amino acids 126-140 of SEQ ID NO: 327. Peptide titration experiments were conducted to assess the sensitivity of line 1-F9 for the specific peptide. The line was found to specifically respond to peptide 4 at concentrations as low as 0.25 ng/ml, indicating that the T cells are very sensitive and therefore likely to have high affinity for the epitope.

To determine the HLA restriction of the P703P response, a panel of antigen presenting cells (APC) was generated that was partially matched with the donor used to generate the T cells. The APC were pulsed with the peptide and used in proliferation and cytokine assays together with line 1-F9. APC matched with the donor at HLA-DRB0701 and HLA-DQB02 alleles were able to present the peptide to the T cells, indicating that the P703P-specific response is restricted to one of these alleles.

Antibody blocking assays were utilized to determine if the restricting allele was HLA-DR0701 or HLA-DQ02. The anti-HLA-DR blocking antibody L243 or an irrelevant isotype matched IgG2a were added to T cells and APC cultures pulsed with the peptide RMPTVLQCVNVSVS (SEQ ID NO: 638) at 250 ng/ml. Standard interferon-gamma and proliferation assays were performed. Whereas the control antibody had no effect on the ability of the T cells to recognize peptide-pulsed APC, in both assays the anti-HLA-DR antibody completely blocked the ability of the T cells to specifically recognize peptide-pulsed APC.

To determine if the peptide epitope RMPTVLQCVNVSVS (SEQ ID NO: 638) was naturally processed, the ability of line 1-F9 to recognize APC pulsed with recombinant P703P protein was examined. For these experiments a number of

recombinant P703P sources were utilized; *E. coli*-derived P703P, Pichia-derived P703P and baculovirus-derived P703P. Irrelevant protein controls used were *E. coli*-derived L3E (a lung-specific antigen) and baculovirus-derived mammaglobin. In interferon-gamma ELISA assays, line 1-F9 was able to efficiently recognize both *E. coli* forms of P703P as well as Pichia-derived recombinant P703P, while baculovirus-derived P703P was recognized less efficiently. Subsequent Western blot analysis revealed that the *E. coli* and Pichia P703P protein preparations were intact while the baculovirus P703P preparation was approximately 75% degraded. Thus, peptide RMPTVLQCVNVS VVS (SEQ ID NO: 638) from P703P is a naturally processed peptide epitope derived from P703P and presented to T cells in the context of HLA-DRB-0701

In further studies, twenty-four 15-mer peptides overlapping by 10 amino acids and derived from the N-terminal fragment of P703P (corresponding to amino acids 27-154 of SEQ ID NO: 525) were generated by standard procedures and their ability to be recognized by CD4 cells was determined essentially as described above. DC were pulsed overnight with pools of the peptides with each peptide at a final concentration of 10 microgram/ml. A large number of individual CD4 T cell lines (65/480) demonstrated significant proliferation and cytokine release (IFN-gamma) in response to the P703P peptide pools but not to a control peptide pool. The CD4 T cell lines which demonstrated specific activity were restimulated on the appropriate pool of P703P peptides and reassayed on the individual peptides of each pool as well as a peptide dose titration of the pool of peptides in a IFN-gamma release assay and in a proliferation assay.

Sixteen immunogenic peptides were recognized by the T cells from the entire set of peptide antigens tested. The amino acid sequences of these peptides are provided in SEQ ID NO: 656-671, with the corresponding cDNA sequences being provided in SEQ ID NO: 640-655, respectively. In some cases the peptide reactivity of the T cell line could be mapped to a single peptide, however some could be mapped to more than one peptide in each pool. Those CD4 T cell lines that displayed a representative pattern of recognition from each peptide pool with a reasonable affinity for peptide were chosen for further analysis (I-1A, -6A; II-4C, -5E; III-6E, IV-4B, -3F, -9B, -10F, V-5B, -4D, and -10F). These CD4 T cell lines were restimulated on the

appropriate individual peptide and reassayed on autologous DC pulsed with a truncated form of recombinant P703P protein made in *E. coli* (a.a. 96 - 254 of SEQ ID NO: 525), full-length P703P made in the baculovirus expression system, and a fusion between influenza virus NS1 and P703P made in *E. coli*. Of the T cell lines tested, line I-1A
5 recognized specifically the truncated form of P703P (*E. coli*) but no other recombinant form of P703P. This line also recognized the peptide used to elicit the T cells. Line 2-4C recognized the truncated form of P703P (*E. coli*) and the full length form of P703P made in baculovirus, as well as peptide. The remaining T cell lines tested were either peptide-specific only (II-5E, II-6F, IV-4B, IV-3F, IV-9B, IV-10F, V-5B and V-4D) or
10 were non-responsive to any antigen tested (V-10F). These results demonstrate that the peptide sequence RPLLANDLMLIKLDE (SEQ ID NO: 671; corresponding to a.a. 110-124 of SEQ ID NO: 525) recognized by the T cell line I-1A, and the peptide sequences SVSESDTIRSISIAS (SEQ ID NO: 668; corresponding to a.a. 125-139 of SEQ ID NO: 525) and ISIASQCPTAGNSCL (SEQ ID NO: 667; corresponding to a.a. 135-149 of
15 SEQ ID NO: 525) recognized by the T cell line II-4C may be naturally processed epitopes of the P703P protein.

EXAMPLE 11

EXPRESSION OF A BREAST TUMOR-DERIVED ANTIGEN

20

IN PROSTATE

Isolation of the antigen B305D from breast tumor by differential display is described in US Patent Application No. 08/700,014, filed August 20, 1996. Several different splice forms of this antigen were isolated. The determined cDNA sequences
25 for these splice forms are provided in SEQ ID NO: 366-375, with the predicted amino acid sequences corresponding to the sequences of SEQ ID NO: 292, 298 and 301-303 being provided in SEQ ID NO: 299-306, respectively. In further studies, a splice variant of the cDNA sequence of SEQ ID NO: 366 was isolated which was found to contain an additional guanine residue at position 884 (SEQ ID NO: 530), leading to a
30 frameshift in the open reading frame. The determined DNA sequence of this ORF is

provided in SEQ ID NO: 531. This frameshift generates a protein sequence (provided in SEQ ID NO: 532) of 293 amino acids that contains the C-terminal domain common to the other isoforms of B305D but that differs in the N-terminal region.

The expression levels of B305D in a variety of tumor and normal tissues were examined by real time PCR and by Northern analysis. The results indicated that B305D is highly expressed in breast tumor, prostate tumor, normal prostate and normal testes, with expression being low or undetectable in all other tissues examined (colon tumor, lung tumor, ovary tumor, and normal bone marrow, colon, kidney, liver, lung, ovary, skin, small intestine, stomach). Using real-time PCR on a panel of prostate tumors, expression of B305D in prostate tumors was shown to increase with increasing Gleason grade, demonstrating that expression of B305D increases as prostate cancer progresses.

EXAMPLE 12

15 GENERATION OF HUMAN CTL *IN VITRO* USING WHOLE GENE PRIMING AND STIMULATION TECHNIQUES WITH THE PROSTATE-SPECIFIC ANTIGEN P501S

Using *in vitro* whole-gene priming with P501S-vaccinia infected DC (see, for example, Yee et al, *The Journal of Immunology*, 157(9):4079-86, 1996), human CTL lines were derived that specifically recognize autologous fibroblasts transduced with P501S (also known as L1-12), as determined by interferon- γ ELISPOT analysis as described above. Using a panel of HLA-mismatched B-LCL lines transduced with P501S, these CTL lines were shown to be likely restricted to HLAB class I allele. Specifically, dendritic cells (DC) were differentiated from monocyte cultures derived from PBMC of normal human donors by growing for five days in RPMI medium containing 10% human serum, 50 ng/ml human GM-CSF and 30 ng/ml human IL-4. Following culture, DC were infected overnight with recombinant P501S vaccinia virus at a multiplicity of infection (M.O.I) of five, and matured overnight by the addition of 3 μ g/ml CD40 ligand. Virus was inactivated by UV irradiation. CD8+ T cells were isolated using a magnetic bead system, and priming cultures were initiated

using standard culture techniques. Cultures were restimulated every 7-10 days using autologous primary fibroblasts retrovirally transduced with P501S and CD80. Following four stimulation cycles, CD8⁺ T cell lines were identified that specifically produced interferon- γ when stimulated with P501S and CD80-transduced autologous
5 fibroblasts. A panel of HLA-mismatched B-LCL lines transduced with P501S were generated to define the restriction allele of the response. By measuring interferon- γ in an ELISPOT assay, the P501S specific response was shown to be likely restricted by HLA B alleles. These results demonstrate that a CD8⁺ CTL response to P501S can be elicited.

10 To identify the epitope(s) recognized, cDNA encoding P501S was fragmented by various restriction digests, and sub-cloned into the retroviral expression vector pBIB-KS. Retroviral supernatants were generated by transfection of the helper packaging line Phoenix-Ampho. Supernatants were then used to transduce Jurkat/A2Kb cells for CTL screening. CTL were screened in IFN-gamma ELISPOT
15 assays against these A2Kb targets transduced with the "library" of P501S fragments. Initial positive fragments P501S/H3 and P501S/F2 were sequenced and found to encode amino acids 106-553 and amino acids 136-547, respectively, of SEQ ID NO: 113. A truncation of H3 was made to encode amino acid residues 106-351 of SEQ ID NO: 113, which was unable to stimulate the CTL, thus localizing the epitope to amino acid
20 residues 351-547. Additional fragments encoding amino acids 1-472 (Fragment A) and amino acids 1-351 (Fragment B) were also constructed. Fragment A but not Fragment B stimulated the CTL thus localizing the epitope to amino acid residues 351-472. Overlapping 20-mer and 18-mer peptides representing this region were tested by pulsing Jurkat/A2Kb cells versus CTL in an IFN-gamma assay. Only peptides P501S-369(20)
25 and P501S-369(18) stimulated the CTL. Nine-mer and 10-mer peptides representing this region were synthesized and similarly tested. Peptide P501S-370 (SEQ ID NO: 539) was the minimal 9-mer giving a strong response. Peptide P501S-376 (SEQ ID NO: 540) also gave a weak response, suggesting that it might represent a cross-reactive epitope.

In subsequent studies, the ability of primary human B cells transduced with P501S to prime MHC class I-restricted, P501S-specific, autologous CD8 T cells was examined. Primary B cells were derived from PBMC of a homozygous HLA-A2 donor by culture in CD40 ligand and IL-4, transduced at high frequency with recombinant P501S in the vector pBIB, and selected with blastocidin-S. For *in vitro* priming, purified CD8+ T cells were cultured with autologous CD40 ligand + IL-4 derived, P501S-transduced B cells in a 96-well microculture format. These CTL microcultures were re-stimulated with P501S-transduced B cells and then assayed for specificity. Following this initial screen, microcultures with significant signal above background were cloned on autologous EBV-transformed B cells (BLCL), also transduced with P501S. Using IFN-gamma ELISPOT for detection, several of these CD8 T cell clones were found to be specific for P501S, as demonstrated by reactivity to BLCL/P501S but not BLCL transduced with control antigen. It was further demonstrated that the anti-P501S CD8 T cell specificity is HLA-A2-restricted. First, antibody blocking experiments with anti-HLA-A,B,C monoclonal antibody (W6.32), anti-HLA-B,C monoclonal antibody (B1.23.2) and a control monoclonal antibody showed that only the anti-HLA-A,B,C antibody blocked recognition of P501S-expressing autologous BLCL. Secondly, the anti-P501S CTL also recognized an HLA-A2 matched, heterologous BLCL transduced with P501S, but not the corresponding EGFP transduced control BLCL.

A naturally processed, CD8, class I-restricted peptide epitope of P501S was identified as follows. Dendritic Cells (DC) were isolated by Percol gradient followed by differential adherence, and cultured for 5 days in the presence of RPMI medium containing 1% human serum, 50ng/ml GM-CSF and 30ng/ml IL-4. Following culture, DC were infected for 24 hours with P501S-expressing adenovirus at an MOI of 10 and matured for an additional 24 hours by the addition of 2ug/ml CD40 ligand. CD8 cells were enriched for by the subtraction of CD4+, CD14+ and CD16+ populations from PBMC with magnetic beads. Priming cultures containing 10,000 P501S-expressing DC and 100,000 CD8+ T cells per well were set up in 96-well V-bottom plates with RPMI containing 10% human serum, 5ng/ml IL-12 and 10ng/ml IL-6. Cultures were stimulated every 7 days using autologous fibroblasts retrovirally

transduced to express P501S and CD80, and were treated with IFN-gamma for 48-72 hours to upregulate MHC Class I expression. 10u/ml IL-2 was added at the time of stimulation and on days 2 and 5 following stimulation. Following 4 stimulation cycles, one P501S-specific CD8+ T cell line (referred to as 2A2) was identified that produced
5 IFN-gamma in response to IFN-gamma-treated P501S/CD80 expressing autologous fibroblasts, but not in response to IFN-gamma-treated P703P/CD80 expressing autologous fibroblasts in a γ -IFN Elispot assay. Line 2A2 was cloned in 96-well plates with 0.5 cell/well or 2 cells/well in the presence of 75,000 PBMC/well, 10,000 B-LCL/well, 30ng/ml OKT3 and 50u/ml IL-2. Twelve clones were isolated that showed
10 strong P501S specificity in response to transduced fibroblasts.

Fluorescence activated cell sorting (FACS) analysis was performed on P501S-specific clones using CD3-, CD4- and CD8-specific antibodies conjugated to PercP, FITC and PE respectively. Consistent with the use of CD8 enriched T cells in the priming cultures, P5401S-specific clones were determined to be CD3+, CD8+ and
15 CD4-.

To identify the relevant P501S epitope recognized by P501S specific CTL, pools of 18-20 mer or 30-mer peptides that spanned the majority of the amino acid sequence of P501S were loaded onto autologous B-LCL and tested in γ -IFN Elispot assays for the ability to stimulate two P501S-specific CTL clones, referred to as 4E5
20 and 4E7. One pool, composed of five 18-20 mer peptides that spanned amino acids 411-486 of P501S (SEQ ID NO: 113), was found to be recognized by both P501S-specific clones. To identify the specific 18-20 mer peptide recognized by the clones, each of the 18-20 mer peptides that comprised the positive pool were tested individually in γ -IFN Elispot assays for the ability to stimulate the two P501S-specific CTL clones, 4E5 and
25 4E7. Both 4E5 and 4E7 specifically recognized one 20-mer peptide (SEQ ID NO: 710; cDNA sequence provided in SEQ ID NO: 711) that spanned amino acids 453-472 of P501S. Since the minimal epitope recognized by CD8+ T cells is almost always either a 9 or 10-mer peptide sequence, 10-mer peptides that spanned the entire sequence of SEQ ID NO: 710 were synthesized that differed by 1 amino acid. Each of these 10-mer
30 peptides was tested for the ability to stimulate two P501S-specific clones, (referred to as 1D5 and 1E12). One 10-mer peptide (SEQ ID NO: 712; cDNA sequence provided in

SEQ ID NO: 713) was identified that specifically stimulated the P501S-specific clones. This epitope spans amino acids 463-472 of P501S. This sequence defines a minimal 10-mer epitope from P501S that can be naturally processed and to which CTL responses can be identified in normal PBMC. Thus, this epitope is a candidate for use as a vaccine moiety, and as a therapeutic and/or diagnostic reagent for prostate cancer.

To identify the class I restriction element for the P501S-derived sequence of SEQ ID NO: 712, HLA blocking and mismatch analyses were performed. In γ -IFN Elispot assays, the specific response of clones 4A7 and 4E5 to P501S-transduced autologous fibroblasts was blocked by pre-incubation with 25ug/ml W6/32 (pan-Class I blocking antibody) and B1.23.2 (HLA-B/C blocking antibody). These results demonstrate that the SEQ ID NO: 712-specific response is restricted to an HLA-B or HLA-C allele.

For the HLA mismatch analysis, autologous B-LCL (HLA-A1,A2,B8,B51, Cw1, Cw7) and heterologous B-LCL (HLA-A2,A3,B18,B51,Cw5,Cw14) that share the HLAB51 allele were pulsed for one hour with 20ug/ml of peptide of SEQ ID NO: 712, washed, and tested in γ -IFN Elispot assays for the ability to stimulate clones 4A7 and 4E5. Antibody blocking assays with the B1.23.2 (HLA-B/C blocking antibody) were also performed. SEQ ID NO: 712-specific response was detected using both the autologous (D326) and heterologous (D107) B-LCL, and furthermore the responses were blocked by pre-incubation with 25ug/ml of B1.23.2 HLA-B/C blocking antibody. Together these results demonstrate that the P501S-specific response to the peptide of SEQ ID NO: 712 is restricted to the HLA-B51 class I allele. Molecular cloning and sequence analysis of the HLA-B51 allele from D3326 revealed that the HLA-B51 subtype of D326 is HLA-B51011.

Based on the 10-mer P501S-derived epitope of SEQ ID NO: 712, two 9-mers with the sequences of SEQ ID NO: 714 and 715 were synthesized and tested in Elispot assays for the ability to stimulate two P501S-specific CTL clones derived from line 2A2. The 10-mer peptide of SEQ ID NO: 712, as well as the 9-mer peptide of SEQ ID NO: 715, but not the 9-mer peptide of SEQ ID NO: 714, were capable of stimulating the P501S-specific CTL to produce IFN-gamma. These results demonstrate that the peptide of SEQ ID NO: 715 is a 9-mer P501S-derived epitope recognized by P501S-

specific CTL. The DNA sequence encoding the epitope of SEQ ID NO: 715 is provided in SEQ ID NO: 716.

To identify the class I restricting allele for the P501S-derived peptide of SEQ ID NO: 712 and 715 specific response, each of the HLA B and C alleles were
5 cloned from the donor used in the *in vitro* priming experiment. Sequence analysis indicated that the relevant alleles were HLA-B8, HLA-B51, HLA-Cw01 and HLA-Cw07. Each of these alleles were subcloned into an expression vector and co-transfected together with the P501S gene into VA-13 cells. Transfected VA-13 cells were then tested for the ability to specifically stimulate the P501S-specific CTL in
10 ELISPOT assays. VA-13 cells transfected with P501S and HLA-B51 were capable of stimulating the P501S-specific CTL to secrete gamma-IFN. VA-13 cells transfected with HLA-B51 alone or P501S + the other HLA-alleles were not capable of stimulating the P501S-specific CTL. These results demonstrate that the restricting allele for the P501S-specific response is the HLAB51 allele. Sequence analysis revealed that the
15 subtype of the relevant restricting allele is HLA-B51011.

To determine if the P501S-specific CTL could recognize prostate tumor cells that express P501S, the P501S-positive lines LnCAP and CRL2422 (both expressing "moderate" amounts of P501S mRNA and protein), and PC-3 (expressing low amounts of P501S mRNA and protein), plus the P501S-negative cell line DU-145
20 were retrovirally transduced with the HLA-B51011 allele that was cloned from the donor used to generate the P501S-specific CTL. HLA-B51011- or EGFP-transduced and selected tumor cells were treated with gamma-interferon and androgen (to upregulate stimulatory functions and P501S, respectively) and used in gamma-interferon Elispot assays with the P501S-specific CTL clones 4E5 and 4E7. Untreated
25 cells were used as a control.

Both 4E5 and 4E7 efficiently and specifically recognized LnCAP and CRL2422 cells that were transduced with the HLA-B51011 allele, but not the same cell lines transduced with EGFP. Additionally, both CTL clones specifically recognized PC-3 cells transduced with HLA-B51011, but not the P501S-negative tumor cell line
30 DU-145. Treatment with gamma-interferon or androgen did not enhance the ability of CTL to recognize tumor cells. These results demonstrate that P501S-specific CTL,

generated by *in vitro* whole gene priming, specifically and efficiently recognize prostate tumor cell lines that express P501S.

A naturally processed CD4 epitope of P501S was identified as follows.

CD4 cells specific for P501S were prepared as described above. A series
5 of 16 overlapping peptides were synthesized that spanned approximately 50% of the amino terminal portion of the P501S gene (amino acids 1- 325 of SEQ ID NO: 113). For priming, peptides were combined into pools of 4 peptides, pulsed at 4 μ g/ml onto dendritic cells (DC) for 24 hours, with TNF-alpha. DC were then washed and mixed with negatively selected CD4+ T cells in 96 well U-bottom plates. Cultures were re-
10 stimulated weekly on fresh DC loaded with peptide pools. Following a total of 4 stimulation cycles, cells were rested for an additional week and tested for specificity to APC pulsed with peptide pools using γ -IFN ELISA and proliferation assays. For these assays, adherent monocytes loaded with either the relevant peptide pool at 4 μ g/ml or an irrelevant peptide at μ g/ml were used as APC. T cell lines that demonstrated either
15 specific cytokine secretion or proliferation were then tested for recognition of individual peptides that were present in the pool. T cell lines could be identified from pools A and B that recognized individual peptides from these pools.

From pool A, lines AD9 and AE10 specifically recognized peptide 1 (SEQ ID NO: 719), and line AF5 recognized peptide 39 (SEQ ID NO: 718). From pool B, line BC6 could be identified that recognized peptide 58 (SEQ ID NO: 717). Each of these lines were stimulated on the specific peptide and tested for specific recognition of the peptide in a titration assay as well as cell lysates generated by infection of HEK 293 cells with adenovirus expressing either P501S or an irrelevant antigen. For these assays, APC-adherent monocytes were pulsed with either 10, 1, or 0.1 µg/ml individual P501S peptides, and DC were pulsed overnight with a 1:5 dilution of adenovirally infected cell lysates. Lines AD9, AE10 and AF5 retained significant recognition of the relevant P501S-derived peptides even at 0.1 mg/ml. Furthermore, line AD9 demonstrated significant (8.1 fold stimulation index) specific activity for lysates from adenovirus-P501S infected cells. These results demonstrate that high affinity CD4 T cell lines can be generated toward P501S-derived epitopes, and that at least a subset of these T cells specific for the P501S derived sequence of SEQ ID NO: 719 are specific for an epitope that is naturally processed by human cells. The DNA sequences encoding the amino acid sequences of SEQ ID NO: 717-719 are provided in SEQ ID NO: 720-722, respectively.

To further characterize the P501S-specific activity of AD9, the line was cloned using anti-CD3. Three clones, referred to as 1A1, 1A9 and 1F5, were identified that were specific for the P501S-1 peptide (SEQ ID NO: 719). To determine the HLA restriction allele for the P501S-specific response, each of these clones was tested in class II antibody blocking and HLA mismatch assays using proliferation and gamma-interferon assays. In antibody blocking assays and measuring gamma-interferon production using ELISA assays, the ability of all three clones to recognize peptide pulsed APC was specifically blocked by co-incubation with either a pan-class II blocking antibody or a HLA-DR blocking antibody, but not with a HLA-DQ or an irrelevant antibody. Proliferation assays performed simultaneously with the same cells confirmed these results. These data indicate that the P501S-specific response of the clones is restricted by an HLA-DR allele. Further studies demonstrated that the restricting allele for the P501S-specific response is HLA-DRB1501.

EXAMPLE 13
IDENTIFICATION OF PROSTATE-SPECIFIC ANTIGENS
BY MICROARRAY ANALYSIS

5 This Example describes the isolation of certain prostate-specific polypeptides from a prostate tumor cDNA library.

 A human prostate tumor cDNA expression library as described above was screened using microarray analysis to identify clones that display at least a three fold over-expression in prostate tumor and/or normal prostate tissue, as compared to
10 non-prostate normal tissues (not including testis). 372 clones were identified, and 319 were successfully sequenced. Table I presents a summary of these clones, which are shown in SEQ ID NOs:385-400. Of these sequences SEQ ID NOs:386, 389, 390 and 392 correspond to novel genes, and SEQ ID NOs: 393 and 396 correspond to previously identified sequences. The others (SEQ ID NOs:385, 387, 388, 391, 394, 395 and 397-
15 400) correspond to known sequences, as shown in Table I.

Table I
Summary of Prostate Tumor Antigens

Known Genes	Previously Identified Genes	Novel Genes
T-cell gamma chain	P504S	23379 (SEQ ID NO:389)
Kallikrein	P1000C	23399 (SEQ ID NO:392)
Vector	P501S	23320 (SEQ ID NO:386)
CGI-82 protein mRNA (23319; SEQ ID NO:385)	P503S	23381 (SEQ ID NO:390)
PSA	P510S	
Ald. 6 Dehyd.	P784P	
L-iditol-2 dehydrogenase (23376; SEQ ID NO:388)	P502S	
Ets transcription factor PDEF (22672; SEQ ID NO:398)	P706P	
hTGR (22678; SEQ ID NO:399)	19142.2, bangur.seq (22621; SEQ ID NO:396)	
KIAA0295(22685; SEQ ID NO:400)	5566.1 Wang (23404; SEQ ID NO:393)	
Prostatic Acid Phosphatase(22655; SEQ ID NO:397)	P712P	
transglutaminase (22611; SEQ ID NO:395)	P778P	
HDLBP (23508; SEQ ID NO:394)		
CGI-69 Protein(23367; SEQ ID NO:387)		
KIAA0122(23383; SEQ ID NO:391)		
TEEG		

CGI-82 showed 4.06 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 43% of prostate tumors, 25% normal prostate, not detected in other normal tissues tested. L-idoitol-2 dehydrogenase showed 4.94 fold over-expression in prostate tissues as compared to
5 other normal tissues tested. It was over-expressed in 90% of prostate tumors, 100% of normal prostate, and not detected in other normal tissues tested. Ets transcription factor PDEF showed 5.55 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 47% prostate tumors, 25% normal prostate and not detected in other normal tissues tested. hTGR1 showed 9.11 fold over-expression in
10 prostate tissues as compared to other normal tissues tested. It was over-expressed in 63% of prostate tumors and is not detected in normal tissues tested including normal prostate. KIAA0295 showed 5.59 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 47% of prostate tumors, low to undetectable in normal tissues tested including normal prostate tissues. Prostatic acid
15 phosphatase showed 9.14 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 67% of prostate tumors, 50% of normal prostate, and not detected in other normal tissues tested. Transglutaminase showed 14.84 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 30% of prostate tumors, 50% of normal prostate, and is
20 not detected in other normal tissues tested. High density lipoprotein binding protein (HDLBP) showed 28.06 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 97% of prostate tumors, 75% of normal prostate, and is undetectable in all other normal tissues tested. CGI-69 showed 3.56 fold over-expression in prostate tissues as compared to other normal tissues tested. It is
25 a low abundant gene, detected in more than 90% of prostate tumors, and in 75% normal prostate tissues. The expression of this gene in normal tissues was very low. KIAA0122 showed 4.24 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 57% of prostate tumors, it was undetectable in all normal tissues tested including normal prostate tissues. 19142.2
30 bangur showed 23.25 fold over-expression in prostate tissues as compared to other

normal tissues tested. It was over-expressed in 97% of prostate tumors and 100% of normal prostate. It was undetectable in other normal tissues tested. .5566.1 Wang showed 3.31 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 97% of prostate tumors, 75% normal prostate and was also over-expressed in normal bone marrow, pancreas, and activated PBMC. Novel clone 23379 (also referred to as P553S) showed 4.86 fold over-expression in prostate tissues as compared to other normal tissues tested. It was detectable in 97% of prostate tumors and 75% normal prostate and is undetectable in all other normal tissues tested. Novel clone 23399 showed 4.09 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 27% of prostate tumors and was undetectable in all normal tissues tested including normal prostate tissues. Novel clone 23320 showed 3.15 fold over-expression in prostate tissues as compared to other normal tissues tested. It was detectable in all prostate tumors and 50% of normal prostate tissues. It was also expressed in normal colon and trachea. Other normal tissues do not express this gene at high level.

Subsequent full-length cloning studies on P553S, using standard techniques, revealed that this clone is an incomplete spliced form of P501S. The determined cDNA sequences for four splice variants of P553S are provided in SEQ ID NO: 623-626. An amino acid sequence encoded by SEQ ID NO: 626 is provided in SEQ ID NO: 627. The cDNA sequence of SEQ ID NO: 623 was found to contain two open reading frames (ORFs). The amino acid sequences encoded by these two ORFs are provided in SEQ ID NO: 628 and 629.

EXAMPLE 14

IDENTIFICATION OF PROSTATE-SPECIFIC ANTIGENS BY ELECTRONIC SUBTRACTION

This Example describes the use of an electronic subtraction technique to identify prostate-specific antigens.

Potential prostate-specific genes present in the GenBank human EST database were identified by electronic subtraction (similar to that described by Vasmatzis et al., *Proc. Natl. Acad. Sci. USA* 95:300-304, 1998). The sequences of EST clones (43,482) derived from various prostate libraries were obtained from the GenBank public human EST database. Each prostate EST sequence was used as a query sequence in a BLASTN (National Center for Biotechnology Information) search against the human EST database. All matches considered identical (length of matching sequence >100 base pairs, density of identical matches over this region > 70%) were grouped (aligned) together in a cluster. Clusters containing more than 200 ESTs were discarded since they probably represented repetitive elements or highly expressed genes such as those for ribosomal proteins. If two or more clusters shared common ESTs, those clusters were grouped together into a "supercluster," resulting in 4,345 prostate superclusters.

Records for the 479 human cDNA libraries represented in the GenBank release were downloaded to create a database of these cDNA library records. These 479 cDNA libraries were grouped into three groups: Plus (normal prostate and prostate tumor libraries, and breast cell line libraries, in which expression was desired), Minus (libraries from other normal adult tissues, in which expression was not desirable), and Other (libraries from fetal tissue, infant tissue, tissues found only in women, non-prostate tumors and cell lines other than prostate cell lines, in which expression was considered to be irrelevant). A summary of these library groups is presented in Table II.

Table II
Prostate cDNA Libraries and ESTs

Library	# of Libraries	# of ESTs
Plus	25	43,482
Normal	11	18,875
Tumor	11	21,769
Cell lines	3	2,838
Minus	166	
Other	287	

- 5 Each supercluster was analyzed in terms of the ESTs within the supercluster. The tissue source of each EST clone was noted and used to classify the superclusters into four groups: Type 1- EST clones found in the Plus group libraries only; no expression detected in Minus or Other group libraries; Type 2- EST clones derived from the Plus and Other group libraries only; no expression detected in the
- 10 Minus group; Type 3- EST clones derived from the Plus, Minus and Other group libraries, but the number of ESTs derived from the Plus group is higher than in either the Minus or Other groups; and Type 4- EST clones derived from Plus, Minus and Other group libraries, but the number derived from the Plus group is higher than the number derived from the Minus group. This analysis identified 4,345 breast clusters
- 15 (see Table III). From these clusters, 3,172 EST clones were ordered from Research Genetics, Inc., and were received as frozen glycerol stocks in 96-well plates.

Table III
Prostate Cluster Summary

Type	# of Superclusters	# of ESTs Ordered
1	688	677
2	2899	2484
3	85	11
4	673	0
Total	4345	3172

5 The EST clone inserts were PCR-amplified using amino-linked PCR primers for Synteni microarray analysis. When more than one PCR product was obtained for a particular clone, that PCR product was not used for expression analysis. In total, 2,528 clones from the electronic subtraction method were analyzed by microarray analysis to identify electronic subtraction breast clones that had high levels
10 of tumor vs. normal tissue mRNA. Such screens were performed using a Synteni (Palo Alto, CA) microarray, according to the manufacturer's instructions (and essentially as described by Schena et al., *Proc. Natl. Acad. Sci. USA* 93:10614-10619, 1996 and Heller et al., *Proc. Natl. Acad. Sci. USA* 94:2150-2155, 1997). Within these analyses, the clones were arrayed on the chip, which was then probed with fluorescent probes
15 generated from normal and tumor prostate cDNA, as well as various other normal tissues. The slides were scanned and the fluorescence intensity was measured.

 Clones with an expression ratio greater than 3 (*i.e.*, the level in prostate tumor and normal prostate mRNA was at least three times the level in other normal tissue mRNA) were identified as prostate tumor-specific sequences (Table IV). The
20 sequences of these clones are provided in SEQ ID NO: 401-453, with certain novel sequences shown in SEQ ID NO: 407, 413, 416-419, 422, 426, 427 and 450.

Table IV

Prostate-tumor Specific Clones

SEQ ID NO.	Sequence Designation	Comments
401	22545	previously identified P1000C
402	22547	previously identified P704P
403	22548	known
404	22550	known
405	22551	PSA
406	22552	prostate secretory protein 94
407	22553	novel
408	22558	previously identified P509S
409	22562	glandular kallikrein
410	22565	previously identified P1000C
411	22567	PAP
412	22568	B1006C (breast tumor antigen)
413	22570	novel
414	22571	PSA
415	22572	previously identified P706P
416	22573	novel
417	22574	novel
418	22575	novel
419	22580	novel
420	22581	PAP
421	22582	prostatic secretory protein 94
422	22583	novel
423	22584	prostatic secretory protein 94
424	22585	prostatic secretory protein 94
425	22586	known
426	22587	novel
427	22588	novel
428	22589	PAP
429	22590	known
430	22591	PSA
431	22592	known
432	22593	Previously identified P777P
433	22594	T cell receptor gamma chain
434	22595	Previously identified P705P
435	22596	Previously identified P707P
436	22847	PAP
437	22848	known
438	22849	prostatic secretory protein 57

439	22851	PAP
440	22852	PAP
441	22853	PAP
442	22854	previously identified P509S
443	22855	previously identified P705P
444	22856	previously identified P774P
445	22857	PSA
446	23601	previously identified P777P
447	23602	PSA
448	23605	PSA
449	23606	PSA
450	23612	novel
451	23614	PSA
452	23618	previously identified P1000C
453	23622	previously identified P705P

Further studies on the clone of SEQ ID NO: 407 (also referred to as P1020C) led to the isolation of an extended cDNA sequence provided in SEQ ID NO: 591. This extended cDNA sequence was found to contain an open reading frame that encodes the predicted amino acid sequence of SEQ ID NO: 592. The P1020C cDNA and amino acid sequences were found to show some similarity to the human endogenous retroviral HERV-K pol gene and protein.

EXAMPLE 15

10 FURTHER IDENTIFICATION OF PROSTATE-SPECIFIC ANTIGENS BY MICROARRAY ANALYSIS

This Example describes the isolation of additional prostate-specific polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library as described above was screened using microarray analysis to identify clones that display at least a three fold over-expression in prostate tumor and/or normal prostate tissue, as compared to non-prostate normal tissues (not including testis). 142 clones were identified and sequenced. Certain of these clones are shown in SEQ ID NO: 454-467. Of these sequences, SEQ ID NO: 459-460 represent novel genes. The others (SEQ ID NO: 454-458 and 461-467) correspond to known sequences. Comparison of the determined

cDNA sequence of SEQ ID NO: 461 with sequences in the Genbank database using the BLAST program revealed homology to the previously identified transmembrane protease serine 2 (TMPRSS2). The full-length cDNA sequence for this clone is provided in SEQ ID NO: 751, with the corresponding amino acid sequence being
5 provided in SEQ ID NO: 752. The cDNA sequence encoding the first 209 amino acids of TMPRSS2 is provided in SEQ ID NO: 753, with the first 209 amino acids being provided in SEQ ID NO: 754.

The sequence of SEQ ID NO: 462 (referred to as P835P) was found to correspond to the previously identified clone FLJ13518 (Accession AK023643; SEQ ID
10 NO: 774), which had no associated open reading frame (ORF). This clone was used to search the Geneseq DNA database and matched a clone previously identified as a G protein-coupled receptor protein (DNA Geneseq Accession A09351; amino acid Geneseq Accession Y92365), that is characterized by the presence of seven transmembrane domains. The sequences of fragments between these domains are
15 provided in SEQ ID NO: 778-785, with SEQ ID NO: 778, 780, 782 and 784 representing extracellular domains and SEQ ID NO: 779, 781, 783 and 785 representing intracellular domains. SEQ ID NO: 778-785 represent amino acids 1-28, 53-61, 83-103, 124-143, 165-201, 226-238, 263-272 and 297-381, respectively, of P835P. The full-length cDNA sequence for P835P is provided in SEQ ID NO: 773. The cDNA
20 sequence of the open reading frame for P835P, including stop codon, is provided in SEQ ID NO: 775, with the open reading frame without stop codon being provided in SEQ ID NO: 776 and the corresponding amino acid sequence being provided in SEQ ID NO: 777.

25

EXAMPLE 16

FURTHER CHARACTERIZATION OF PROSTATE-SPECIFIC ANTIGEN P710P

This Example describes the full length cloning of P710P.

The prostate cDNA library described above was screened with the P710P
30 fragment described above. One million colonies were plated on LB/Ampicillin plates.

Nylon membrane filters were used to lift these colonies, and the cDNAs picked up by these filters were then denatured and cross-linked to the filters by UV light. The P710P fragment was radiolabeled and used to hybridize with the filters. Positive cDNA clones were selected and their cDNAs recovered and sequenced by an automatic Perkin Elmer/Applied Biosystems Division Sequencer. Four sequences were obtained, and are presented in SEQ ID NO: 468-471. These sequences appear to represent different splice variants of the P710P gene. Subsequent comparison of the cDNA sequences of P710P with those in Genbank revealed homology to the DD3 gene (Genbank accession numbers AF103907 & AF103908). The cDNA sequence of DD3 is provided in SEQ ID NO: 618.

EXAMPLE 17

PROTEIN EXPRESSION OF PROSTATE-SPECIFIC ANTIGENS

This example describes the expression and purification of prostate-specific antigens in *E. coli*, baculovirus, mammalian and yeast cells.

a) Expression of P501S in *E. coli*

Expression of the full-length form of P501S was attempted by first cloning P501S without the leader sequence (amino acids 36-553 of SEQ ID NO: 113) downstream of the first 30 amino acids of the *M. tuberculosis* antigen Ra12 (SEQ ID NO: 484) in pET17b. Specifically, P501S DNA was used to perform PCR using the primers AW025 (SEQ ID NO: 485) and AW003 (SEQ ID NO: 486). AW025 is a sense cloning primer that contains a HindIII site. AW003 is an antisense cloning primer that contains an EcoRI site. DNA amplification was performed using 5 µl 10X Pfu buffer, 1 µl 20 mM dNTPs, 1 µl each of the PCR primers at 10 µM concentration, 40 µl water, 1 µl Pfu DNA polymerase (Stratagene, La Jolla, CA) and 1 µl DNA at 100 ng/µl. Denaturation at 95°C was performed for 30 sec, followed by 10 cycles of 95°C for 30 sec, 60°C for 1 min and by 72°C for 3 min. 20 cycles of 95°C for 30 sec, 65°C for 1 min and by 72°C for 3 min, and lastly by 1 cycle of 72°C for 10 min. The PCR product was

cloned to Ra12m/pET17b using HindIII and EcoRI. The sequence of the resulting fusion construct (referred to as Ra12-P501S-F) was confirmed by DNA sequencing.

The fusion construct was transformed into BL21(DE3)pLysE, pLysS and CodonPlus *E. coli* (Stratagene) and grown overnight in LB broth with kanamycin. The
5 resulting culture was induced with IPTG. Protein was transferred to PVDF membrane and blocked with 5% non-fat milk (in PBS-Tween buffer), washed three times and incubated with mouse anti-His tag antibody (Clontech) for 1 hour. The membrane was washed 3 times and probed with HRP-Protein A (Zymed) for 30 min. Finally, the membrane was washed 3 times and developed with ECL (Amersham). No expression
10 was detected by Western blot. Similarly, no expression was detected by Western blot when the Ra12-P501S-F fusion was used for expression in BL21CodonPlus by CE6 phage (Invitrogen).

An N-terminal fragment of P501S (amino acids 36-325 of SEQ ID NO: 113) was cloned down-stream of the first 30 amino acids of the *M. tuberculosis* antigen
15 Ra12 in pET17b as follows. P501S DNA was used to perform PCR using the primers AW025 (SEQ ID NO: 485) and AW027 (SEQ ID NO: 487). AW027 is an antisense cloning primer that contains an EcoRI site and a stop codon. DNA amplification was performed essentially as described above. The resulting PCR product was cloned to Ra12 in pET17b at the HindIII and EcoRI sites. The fusion construct (referred to as
20 Ra12-P501S-N) was confirmed by DNA sequencing.

The Ra12-P501S-N fusion construct was used for expression in BL21(DE3)pLysE, pLysS and CodonPlus, essentially as described above. Using
Western blot analysis, protein bands were observed at the expected molecular weight of 36 kDa. Some high molecular weight bands were also observed, probably due to
25 aggregation of the recombinant protein. No expression was detected by Western blot when the Ra12-P501S-F fusion was used for expression in BL21CodonPlus by CE6 phage.

A fusion construct comprising a C-terminal portion of P501S (amino acids 257-553 of SEQ ID NO: 113) located down-stream of the first 30 amino acids of
30 the *M. tuberculosis* antigen Ra12 (SEQ ID NO: 484) was prepared as follows. P501S

DNA was used to perform PCR using the primers AW026 (SEQ ID NO: 488) and AW003 (SEQ ID NO: 486). AW026 is a sense cloning primer that contains a HindIII site. DNA amplification was performed essentially as described above. The resulting PCR product was cloned to Ra12 in pET17b at the HindIII and EcoRI sites. The
5 sequence for the fusion construct (referred to as Ra12-P501S-C) was confirmed.

The Ra12-P501S-C fusion construct was used for expression in BL21(DE3)pLysE, pLysS and CodonPlus, as described above. A small amount of protein was detected by Western blot, with some molecular weight aggregates also being observed. Expression was also detected by Western blot when the Ra12-P501S-C
10 fusion was used for expression in BL21CodonPlus induced by CE6 phage.

A fusion construct comprising a fragment of P501S (amino acids 36-298 of SEQ ID NO: 113) located down-stream of the *M. tuberculosis* antigen Ra12 (SEQ ID NO: 705) was prepared as follows. P501S DNA was used to perform PCR using the primers AW042 (SEQ ID NO: 706) and AW053 (SEQ ID NO: 707). AW042 is a sense
15 cloning primer that contains a EcoRI site. AW053 is an antisense primer with stop and Xho I sites. DNA amplification was performed essentially as described above. The resulting PCR product was cloned to Ra12 in pET17b at the EcoRI and Xho I sites. The resulting fusion construct (referred to as Ra12-P501S-E2) was expressed in B834 (DE3) pLys S *E. coli* host cells in TB media for 2 h at room temperature. Expressed protein
20 was purified by washing the inclusion bodies and running on a Ni-NTA column. The purified protein stayed soluble in buffer containing 20 mM Tris-HCl (pH 8), 100 mM NaCl, 10 mM β -Me and 5% glycerol. The determined cDNA and amino acid sequences for the expressed fusion protein are provided in SEQ ID NO: 708 and 709, respectfully.

25 **b) Expression of P501S in Baculovirus**

The Bac-to-Bac baculovirus expression system (BRL Life Technologies, Inc.) was used to express P501S protein in insect cells. Full-length P501S (SEQ ID NO: 113) was amplified by PCR and cloned into the XbaI site of the donor plasmid pFastBacI. The recombinant bacmid and baculovirus were prepared according to the

manufacturer's instructions. The recombinant baculovirus was amplified in Sf9 cells and the high titer viral stocks were utilized to infect High Five cells (Invitrogen) to make the recombinant protein. The identity of the full-length protein was confirmed by N-terminal sequencing of the recombinant protein and by Western blot analysis (Figure 7). Specifically, 0.6 million High Five cells in 6-well plates were infected with either the unrelated control virus BV/ECD_PD (lane 2), with recombinant baculovirus for P501S at different amounts or MOIs (lanes 4-8), or were uninfected (lane 3). Cell lysates were run on SDS-PAGE under reducing conditions and analyzed by Western blot with the anti-P501S monoclonal antibody P501S-10E3-G4D3 (prepared as described below). Lane 1 is the biotinylated protein molecular weight marker (BioLabs).

The localization of recombinant P501S in the insect cells was investigated as follows. The insect cells overexpressing P501S were fractionated into fractions of nucleus, mitochondria, membrane and cytosol. Equal amounts of protein from each fraction were analyzed by Western blot with a monoclonal antibody against P501S. Due to the scheme of fractionation, both nucleus and mitochondria fractions contain some plasma membrane components. However, the membrane fraction is basically free from mitochondria and nucleus. P501S was found to be present in all fractions that contain the membrane component, suggesting that P501S may be associated with plasma membrane of the insect cells expressing the recombinant protein.

c) Expression of P501S in Mammalian Cells

Full-length P501S (553 amino acids; SEQ ID NO: 113) was cloned into various mammalian expression vectors, including pCEP4 (Invitrogen), pVR1012 (Vical, San Diego, CA) and a modified form of the retroviral vector pBMN, referred to as pBIB. Transfection of P501S/pCEP4 and P501S/pVR1012 into HEK293 fibroblasts was carried out using the Fugene transfection reagent (Boehringer Mannheim). Briefly, 2 ul of Fugene reagent was diluted into 100 ul of serum-free media and incubated at room temperature for 5-10 min. This mixture was added to 1 ug of P501S plasmid DNA, mixed briefly and incubated for 30 minutes at room temperature. The

Fugene/DNA mixture was added to cells and incubated for 24-48 hours. Expression of recombinant P501S in transfected HEK293 fibroblasts was detected by means of Western blot employing a monoclonal antibody to P501S.

Transfection of p501S/pCEP4 into CHO-K cells (American Type Culture Collection, Rockville, MD) was carried out using GenePorter transfection reagent (Gene Therapy Systems, San Diego, CA). Briefly, 15 μ l of GenePorter was diluted in 500 μ l of serum-free media and incubated at room temperature for 10 min. The GenePorter/media mixture was added to 2 μ g of plasmid DNA that was diluted in 500 μ l of serum-free media, mixed briefly and incubated for 30 min at room temperature. CHO-K cells were rinsed in PBS to remove serum proteins, and the GenePorter/DNA mix was added and incubated for 5 hours. The transfected cells were then fed an equal volume of 2x media and incubated for 24-48 hours.

FACS analysis of P501S transiently infected CHO-K cells, demonstrated surface expression of P501S. Expression was detected using rabbit polyclonal antisera raised against a P501S peptide, as described below. Flow cytometric analysis was performed using a FaCScan (Becton Dickinson), and the data were analyzed using the Cell Quest program.

d) Expression of P501S in *S. cerevisiae*

P501S was expressed in yeast, directed in membranes, using the yeast α prepro signal sequence. The natural signal sequence and first luminal domain of P501S was deleted in order to conserve the natural positioning of the expressed P501S protein.

Specifically, the α prepro signal sequence of *S. cerevisiae* linked to amino acids 55-553 of SEQ ID NO: 113 with a His tag tail was cloned into the plasmid pRIT15068 with the CUP1 promoter and transfected into *S. cerevisiae* strain Y1790. The Y1790 strain is Leu⁺ and His⁻. Expression of protein was induced by addition of either 500 μ M or 250 μ M of CuSO₄ at 30 °C in minimal medium supplemented with histidine. Cells were harvested 24 hours after induction. Extracts were prepared by growing cells to a concentration of OD₆₀₀ 5.0 in 50 mM citrate phosphate buffer (pH 4.0) plus 130 mM NaCl supplemented with protease inhibitors. Cells were disrupted

using glass beads and centrifuged for 20 min at 15,000 g. The recombinant protein was found to be 100% pellet associated.

Expression of the recombinant protein (molecular weight 63 kD) was demonstrated by Western blot analysis, using the anti-P501S monoclonal antibody 10E-D4-G3 described below. The amino acid sequence of the expressed protein is provided in SEQ ID NO: 792.

Fermentation processes for the production of the α prepro-P501S-His tag recombinant protein in *S. cerevisiae* (strain Y1790 – CUP1 inducible promoter) were evaluated as follows. One hundred μ l of a master seed containing 2.5×10^8 cells/ml of transformed *S. cerevisiae* Y1790 were spread on FSC004AA solid medium. The composition of the FSC004AA medium is as follows: glucose 10 g/l; $\text{Na}_2\text{MoO}_4 \cdot 2\text{H}_2\text{O}$ 0.0002 g/l; folic acid 0.000064 g/l; KH_2PO_4 1 g/l; $\text{MnSO}_4 \cdot \text{H}_2\text{O}$ 0.0004 g/l; Inositol 0.064 g/l; $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$ 0.5 g/l; H_3BO_3 0.0005 g/l; Pyridoxine 0.008 g/l; $\text{CaCl}_2 \cdot 2\text{H}_2\text{O}$ 0.1 g/l; KI 0.0001 g/l; Thiamine 0.008 g/l; NaCl 0.1 g/l; $\text{CoCl}_2 \cdot 6\text{H}_2\text{O}$ 0.00009 g/l; Niacin 0.000032 g/l; $\text{FeCl}_3 \cdot 6\text{H}_2\text{O}$ 0.0002 g/l; Riboflavin 0.000016 g/l; Panthotenate Ca 0.008 g/l; $\text{CuSO}_4 \cdot 5\text{H}_2\text{O}$ 0.00004 g/l; Biotin 0.000064 g/l; para-aminobenzoic acid 0.000016 g/l; $\text{ZnSO}_4 \cdot 7\text{H}_2\text{O}$ 0.0004 g/l; $(\text{NH}_4)_2\text{SO}_4$ 5 g/l; agar 18 g/l; Histidine 0.1 g/l.

Two plates were incubated for 26 h at 30 °C. These solid pre-cultures were harvested in 5 ml of liquid medium FSC007AA and 0.5 ml (or 9.3×10^7 cells) of this suspension was used to inoculate 2 liquid pre-cultures.

The composition of the FSC007AA medium is as follows: Glucose 10 g/l; $\text{Na}_2\text{MoO}_4 \cdot 2\text{H}_2\text{O}$ 0.0002 g/l; folic acid 0.000064 g/l; KH_2PO_4 1 g/l; $\text{MnSO}_4 \cdot \text{H}_2\text{O}$ 0.0004 g/l; Inositol 0.064 g/l; $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$ 0.5 g/l; H_3BO_3 0.0005 g/l; Pyridoxine 0.008 g/l; $\text{CaCl}_2 \cdot 2\text{H}_2\text{O}$ 0.1 g/l; KI 0.0001 g/l; Thiamine 0.008 g/l; NaCl 0.1 g/l; $\text{CoCl}_2 \cdot 6\text{H}_2\text{O}$ 0.00009 g/l; Niacine 0.000032 g/l; $\text{FeCl}_3 \cdot 6\text{H}_2\text{O}$ 0.0002 g/l; Riboflavin 0.000016 g/l; Panthotenate Ca 0.008 g/l; $\text{CuSO}_4 \cdot 5\text{H}_2\text{O}$ 0.00004 g/l; Biotin 0.000064 g/l; para-aminobenzoic acid 0.000016 g/l; $\text{ZnSO}_4 \cdot 7\text{H}_2\text{O}$ 0.0004 g/l; $(\text{NH}_4)_2\text{SO}_4$ 5 g/l; Histidine 0.1 g/l.

These pre-cultures were run for 20 hours in 2L flasks containing 400 ml of medium FSC007AA in order to obtain an OD of 1.8. The other characteristics of these pre-cultures are as follows: pH 2.8; glucose 2.3 g/L; ethanol 3.4 g/L.

The best timing for liquid pre-cultures for strain Y1790 was determined in preliminary experiments. Liquid pre-cultures containing 400 ml of medium and inoculated with various volumes of Master Seed (0.25, 0.5, 1 or 2 ml) were monitored in order to identify the best inoculum size and timing. Glucose, ethanol, pH, OD and
 5 cell number (determined by flow cytometry) were followed between 16 and 23 hours of culture. Glucose exhaustion and maximal biomass were obtained after 20 hour incubation with 0.5 inoculum. These conditions were adopted for transferring the pre-culture into fermentation.

In total, 800ml of pre-culture were used to inoculate a 20 L fermenter
 10 containing 5L of medium FSC002AA. Three ml of irradiated antifoam were added before inoculation. The composition of the FSC002AA medium is as follows:
 (NH₄)₂SO₄ 6.4 g/l; Na₂MoO₄·2H₂O 2.05 mg/l; folic acid 0.54 mg/l; KH₂PO₄ 8.25 g/l;
 MnSO₄·H₂O 4.1 mg/l; inositol 540 mg/l; MgSO₄·7H₂O 4.69 g/l; H₃BO₃ 5.17 mg/l;
 pyridoxine 68 mg/l; CaCl₂·2H₂O 0.92 g/l; KI 1.03 mg/l; thiamine 68 mg/l; NaCl 0.06g/l;
 15 CoCl₂·6H₂O 0.92 mg/l; Niacine 0.27 mg/l; HCl 1 ml/l; FeCl₃·6H₂O 9.92 mg/l;
 Riboflavin 0.13 mg/l; CuSO₄·5H₂O 0.41 mg/l; Glucose 0.14 g/l; Panthotenate Ca 68
 mg/l; ZnSO₄·7H₂O 4.1 mg/l; Biotin 0.54 mg/l; para-aminobenzoic acid 0.13 mg/l;
 Histidine 0.3 g/l

The carbon source (glucose) was supplemented by a continuous feeding
 20 of FFB004AA medium. The composition of the FFB004AA medium is as follows:
 glucose 350 g/l; Na₂MoO₄·2H₂O 5.15 mg/l; folic acid 1.36 mg/l; KH₂PO₄ 20.6 g/l;
 MnSO₄·H₂O 10.3 mg/l; inositol 1350 mg/l; MgSO₄·7H₂O 11.7 g/l; H₃BO₃ 12.9 mg/l;
 pyridoxine 170 mg/l; CaCl₂·2H₂O 2.35 g/l; KI 2.6 mg/l; thiamine 170 g/l; NaCl 0.15 g/l;
 CoCl₂·6H₂O 2.3 mg/l; niacine 0.67 mg/l; HCl 2.5 ml/l; FeCl₃·6H₂O 24.8 mg/l;
 25 riboflavin; 0.33 mg/l; CuSO₄·5H₂O 1.03 mg/l; biotin 1.36 mg/l; panthotenate Ca 170
 mg/l; ZnSO₄·7H₂O 10.3 mg/l; para-aminobenzoic acid: 0.33 mg/l; histidine 5.35 g/l.

The residual glucose concentration was maintained very low (□50 mg/L) in order to minimize ethanol production by fermentation. This was achieved by limiting the development of the microorganism using a limited glucose feed rate. The Standard
 30 biomass content (OD 80-90) was reached in fermentation after 44 hour growth phase.

CUP1 promoter was then induced by adding 500μM CuSO₄ in order to

produce P501S antigen. CuSO_4 addition was followed by ethanol accumulation (up to 6 g/L), and the glucose feeding rate was then reduced in order to consume the ethanol. The copper available for the microorganism was monitored by testing Cu ion concentration in the broth supernatant using a spectrophotometric copper assay (DETC method). The fermentation was then supplemented by CuSO_4 throughout the induction phase in order to maintain its concentration between 150 and 250 μM in the supernatant. The biomass reached an OD of 100 at the end of induction. Cells were harvested after 8 hours of induction.

Cell homogenate was prepared and analysed by SDS-PAGE and Western Blot using standard protocols. A major protein band with the expected molecular weight of 62KD was detected by Western blot using anti-P501S monoclonal antibodies. Western blot analysis also showed that the major 62KD band was progressively produced from 30 minutes of induction on, and reached a maximum after 3 hours. No more antigen seemed to be produced between 3 and 12 hours of induction.

The number of passages through a French Press necessary to extract all the antigen from the cells was evaluated. One, three and five passages were tested and total cell lysates, supernatants and pellets of cell lysates were analysed by Western blot. Three passages through a French Press were sufficient to completely extract the antigen. The antigen was present in the insoluble fraction.

20

e) Expression of P703P in Baculovirus

The cDNA for full-length P703P-DE5 (SEQ ID NO: 326), together with several flanking restriction sites, was obtained by digesting the plasmid pCDNA703 with restriction endonucleases Xba I and Hind III. The resulting restriction fragment (approx. 800 base pairs) was ligated into the transfer plasmid pFastBacI which was digested with the same restriction enzymes. The sequence of the insert was confirmed by DNA sequencing. The recombinant transfer plasmid pFBP703 was used to make recombinant bacmid DNA and baculovirus using the Bac-To-Bac Baculovirus expression system (BRL Life Technologies). High Five cells were infected with the recombinant virus BVP703, as described above, to obtain recombinant P703P protein.

30

e) Expression of P788P in *E. Coli*

A truncated, N-terminal portion, of P788P (residues 1-644 of SEQ ID NO: 777; referred to as P788P-N) fused with a C-terminal 6xHis Tag was expressed in *E. coli* as follows. P788P cDNA was amplified using the primers AW080 and AW081 (SEQ ID NO: 672 and 673). AW080 is a sense cloning primer with an NdeI site. AW081 is an antisense cloning primer with a XhoI site. The PCR-amplified P788P, as well as the vector pCRX1, were digested with NdeI and XhoI. Vector and insert were ligated and transformed into NovaBlue cells. Colonies were randomly screened for insert and then sequenced. P788P-N clone #6 was confirmed to be identical to the designed construct. The expression construct P788P-N #6/pCRX1 was transformed into *E. coli* BL21 CodonPlus-RIL competent cells. After induction, most of the cells grew well, achieving OD600 of greater than 2.0 after 3 hr. Coomassie stained SDS-PAGE showed an over-expressed band at about 75 kD. Western blot analysis using a 6xHisTag antibody confirmed the band was P788P-N. The determined cDNA sequence for P788P-N is provided in SEQ ID NO: 674, with the corresponding amino acid sequence being provided in SEQ ID NO: 675.

f) Expression of P510S in *E. Coli*

The P510S protein has 9 potential transmembrane domains and is predicted to be located at the plasma membrane. The C-terminal protein of this protein, as well as the predicted third extracellular domain of P510S were expressed in *E. coli* as follows.

The expression construct referred to as Ra12-P501S-C was designed to have a 6 HisTag at the N-terminal end, followed by the *M. tuberculosis* antigen Ra12 (SEQ ID NO: 676) and then the C-terminal portion of P510S (amino residues 1176-1261 of SEQ ID NO: 538). Full-length P510S was used to amplify the P510S-C fragment by PCR using the primers AW056 and AW057 (SEQ ID NO: 677 and 678, respectively). AW056 is a sense cloning primer with an EcoRI site. AW057 is an antisense primer with stop and XhoI sites. The amplified P501S fragment and Ra12/pCRX1 were digested with EcoRI and XhoI and then purified. The insert and

vector were ligated together and transformed into NovaBlue. Colonies were randomly screened for insert and sequences. For protein expression, the expression construct was transformed into *E. coli* BL21 (DE3) CodonPlus-RIL competent cells. A mini-induction screen was performed to optimize the expression conditions. After induction
5 the cells grew well, achieving OD 600 nm greater than 2.0 after 3 hours. Coomassie stain SDS-PAGE showed a highly over-expressed band at approx. 30 kD. Though this is higher than the expected molecular weight, western blot analysis was positive, showing this band to be the His tag-containing protein. The optimized culture conditions are as follows. Dilute overnight culture/daytime culture (LB + kanamycin +
10 chloramphenicol) into 2xYT (with kanamycin and chloramphenicol) at a ratio of 25 ml culture to 1 liter 2xYT. Allow to grow at 37 °C until OD600 = 0.6. Take an aliquot out as T0 sample. Add 1 mM IPTG and allow to grow at 30 °C for 3 hours. Take out a T3 sample, spin down cells and store at -80 °C. The determined cDNA and amino acid sequences for the Ra12-P510S-C construct are provided in SEQ ID NO: 679 and 682,
15 respectively.

The expression construct P510S-C was designed to have a 5' added start codon and a glycine (GGA) codon and then the P510S C terminal fragment followed by the in frame 6x histidine tag and stop codon from the pET28b vector. The cloning strategy is similar to that used for Ra12-P510S-C, except that the PCR primers employed were
20 those shown in SEQ ID NO: 685 and 686, respectively and the NcoI/XhoI cut in pET28b was used. The primer of SEQ ID NO: 685 created a 5' NcoI site and added a start codon. The antisense primer of SEQ ID NO: 686 creates a XhoI site on P510S C terminal fragment. Clones were confirmed by sequencing. For protein expression, the expression construct was transformed into *E. coli* BL21 (DE3) CodonPlus-RIL
25 competent cells. An OD600 of greater than 2.0 was obtained 30 hours after induction. Coomassie stained SDS-PAGE showed an over-expressed band at about 11 kD. Western blot analysis confirmed that the band was P510S-C, as did N-terminal protein sequencing. The optimized culture conditions are as follows: dilute overnight culture/daytime culture (LB + kanamycin + chloramphenicol) into 2x YT (+ kanamycin
30 and chloramphenicol) at a ratio of 25 mL culture to 1 liter 2x YT, and allow to grow at

37 °C until an OD 600 of about 0.5 is reached. Take out an aliquot as T0 sample. Add 1 mM IPTG and allow to grow at 30 °C for 3 hours. Spin down the cells and store at -80 °C until purification. The determined cDNA and amino acid sequences for the P510S-C construct are shown in SEQ ID NO: 680 and 683, respectively.

5 The predicted third extracellular domain of P510S (P510S-E3; residues 328-676 of SEQ ID NO: 538) was expressed in *E. coli* as follows. The P510S fragment was amplified by PCR using the primers shown in SEQ ID NO: 687 and 688. The primer of SEQ ID NO: 687 is a sense primer with an NdeI site for use in ligating into pPDM. The primer of SEQ ID NO: 688 is an antisense primer with an added XhoI site
10 for use in ligating into pPDM. The resulting fragment was cloned to pPDM at the NdeI and XhoI sites. Clones were confirmed by sequencing. For protein expression, the clone was transformed into *E. coli* BL21 (DE3) CodonPlus-RIL competent cells. After induction, an OD600 of greater than 2.0 was achieved after 3 hours. Coomassie stained SDS-PAGE showed an over-expressed band at about 39 kD, and N-terminal sequencing
15 confirmed the N-terminal to be that of P510S-E3. Optimized culture conditions are as follows: dilute overnight culture/daytime culture (LB + kanamycin + chloramphenicol) into 2x YT (kanamycin and chloramphenicol) at a ratio of 25 ml culture to 1 liter 2x YT. Allow to grow at 37 °C until OD 600 equals 0.6. Take out an aliquot as T0 sample. Add 1 mM IPTG and allow to grow at 30 °C for 3 hours. Take out a T3
20 sample, spin down the cells and store at -80 °C until purification. The determined cDNA and amino acid sequences for the P501S-E3 construct are provided in SEQ ID NO: 681 and 684, respectively.

g) Expression of P775S in *E. Coli*

 The antigen P775P contains multiple open reading frames (ORF). The
25 third ORF, encoding the protein of SEQ ID NO: 483, has the best motif score. An expression fusion construct containing the *M. tuberculosis* antigen Ra12 (SEQ ID NO: 676) and P775P-ORF3 with an N-terminal 6x HisTag was prepared as follows. P775P-ORF3 was amplified using the sense PCR primers of SEQ ID NO: 689 and the anti-sense PCR primer of SEQ ID NO: 690. The PCR amplified fragment of P775P and

Ra12/pCRX1 were digested with the restriction enzymes EcoRI and XhoI. Vector and insert were ligated and then transformed into NovaBlue cells. Colonies were randomly screened for insert and then sequenced. A clone having the desired sequence was transformed into *E. coli* BL21 (DE3) CodonPlus-RIL competent cells. Two hours after
5 induction, the cell density peaked at OD600 of approximately 1.8. Coomassie stained SDS-PAGE showed an over-expressed band at about 31 kD. Western blot using 6x HisTag antibody confirmed that the band was Ra12-P775P-ORF3. The determined cDNA and amino acid sequences for the fusion construct are provided in SEQ ID NO: 691 and 692, respectively.

10

H) EXPRESSION OF A P703P HIS TAG FUSION PROTEIN IN *E. COLI*

The cDNA for the coding region of P703P was prepared by PCR using the primers of SEQ ID NO: 693 and 694. The PCR product was digested with EcoRI restriction enzyme, gel purified and cloned into a modified pET28 vector with a His tag
15 in frame, which had been digested with Eco72I and EcoRI restriction enzymes. The correct construct was confirmed by DNA sequence analysis and then transformed into *E. coli* BL21 (DE3) pLys S expression host cells. The determined amino acid and cDNA sequences for the expressed recombinant P703P are provided in SEQ ID NO: 695 and 696, respectively.

20

I) EXPRESSION OF A P705P HIS TAG FUSION PROTEIN IN *E. COLI*

The cDNA for the coding region of P705P was prepared by PCR using the primers of SEQ ID NO: 697 and 698. The PCR product was digested with EcoRI restriction enzyme, gel purified and cloned into a modified pET28 vector with a His tag
25 in frame, which had been digested with Eco72I and EcoRI restriction enzymes. The correct construct was confirmed by DNA sequence analysis and then transformed into *E. coli* BL21 (DE3) pLys S and BL21 (DE3) CodonPlus expression host cells. The determined amino acid and cDNA sequences for the expressed recombinant P705P are provided in SEQ ID NO: 699 and 700, respectively.

30

J) EXPRESSION OF A P711P HIS TAG FUSION PROTEIN IN *E. COLI*

The cDNA for the coding region of P711P was prepared by PCR using the primers of SEQ ID NO: 701 and 702. The PCR product was digested with EcoRI restriction enzyme, gel purified and cloned into a modified pET28 vector with a His tag in frame, which had been digested with Eco72I and EcoRI restriction enzymes. The correct construct was confirmed by DNA sequence analysis and then transformed into *E. coli* BL21 (DE3) pLys S and BL21 (DE3) CodonPlus expression host cells. The determined amino acid and cDNA sequences for the expressed recombinant P711P are provided in SEQ ID NO: 703 and 704, respectively.

10

EXAMPLE 18

PREPARATION AND CHARACTERIZATION OF ANTIBODIES

AGAINST PROSTATE-SPECIFIC POLYPEPTIDES

15

a) Preparation and Characterization of Polyclonal Antibodies against P703P, P504S and P509S

Polyclonal antibodies against P703P, P504S and P509S were prepared as follows.

20

Each prostate tumor antigen expressed in an *E. coli* recombinant expression system was grown overnight in LB broth with the appropriate antibiotics at 37°C in a shaking incubator. The next morning, 10 ml of the overnight culture was added to 500 ml to 2x YT plus appropriate antibiotics in a 2L-baffled Erlenmeyer flask. When the Optical Density (at 560 nm) of the culture reached 0.4-0.6, the cells were induced with IPTG (1 mM). Four hours after induction with IPTG, the cells were harvested by centrifugation. The cells were then washed with phosphate buffered saline and centrifuged again. The supernatant was discarded and the cells were either frozen for future use or immediately processed. Twenty ml of lysis buffer was added to the cell pellets and vortexed. To break open the *E. coli* cells, this mixture was then run

25

through the French Press at a pressure of 16,000 psi. The cells were then centrifuged again and the supernatant and pellet were checked by SDS-PAGE for the partitioning of the recombinant protein. For proteins that localized to the cell pellet, the pellet was resuspended in 10 mM Tris pH 8.0, 1% CHAPS and the inclusion body pellet was washed and centrifuged again. This procedure was repeated twice more. The washed inclusion body pellet was solubilized with either 8 M urea or 6 M guanidine HCl containing 10 mM Tris pH 8.0 plus 10 mM imidazole. The solubilized protein was added to 5 ml of nickel-chelate resin (Qiagen) and incubated for 45 min to 1 hour at room temperature with continuous agitation. After incubation, the resin and protein mixture were poured through a disposable column and the flow through was collected. The column was then washed with 10-20 column volumes of the solubilization buffer. The antigen was then eluted from the column using 8M urea, 10 mM Tris pH 8.0 and 300 mM imidazole and collected in 3 ml fractions. A SDS-PAGE gel was run to determine which fractions to pool for further purification.

As a final purification step, a strong anion exchange resin such as HiPrepQ (Biorad) was equilibrated with the appropriate buffer and the pooled fractions from above were loaded onto the column. Each antigen was eluted off the column with a increasing salt gradient. Fractions were collected as the column was run and another SDS-PAGE gel was run to determine which fractions from the column to pool. The pooled fractions were dialyzed against 10 mM Tris pH 8.0. The proteins were then vialled after filtration through a 0.22 micron filter and the antigens were frozen until needed for immunization.

Four hundred micrograms of each prostate antigen was combined with 100 micrograms of muramyl dipeptide (MDP). Every four weeks rabbits were boosted with 100 micrograms mixed with an equal volume of Incomplete Freund's Adjuvant (IFA). Seven days following each boost, the animal was bled. Sera was generated by incubating the blood at 4°C for 12-4 hours followed by centrifugation.

Ninety-six well plates were coated with antigen by incubating with 50 microliters (typically 1 microgram) of recombinant protein at 4 °C for 20 hours. 250 microliters of BSA blocking buffer was added to the wells and incubated at room

temperature for 2 hours. Plates were washed 6 times with PBS/0.01% Tween. Rabbit sera was diluted in PBS. Fifty microliters of diluted sera was added to each well and incubated at room temperature for 30 min. Plates were washed as described above before 50 microliters of goat anti-rabbit horse radish peroxidase (HRP) at a 1:10000 dilution was added and incubated at room temperature for 30 min. Plates were again washed as described above and 100 microliters of TMB microwell peroxidase substrate was added to each well. Following a 15 min incubation in the dark at room temperature, the colorimetric reaction was stopped with 100 microliters of 1N H₂SO₄ and read immediately at 450 nm. All polyclonal antibodies showed immunoreactivity to the appropriate antigen.

b) Preparation and Characterization of Antibodies against P501S

A murine monoclonal antibody directed against the carboxy-terminus of the prostate-specific antigen P501S was prepared as follows.

A truncated fragment of P501S (amino acids 355-526 of SEQ ID NO: 113) was generated and cloned into the pET28b vector (Novagen) and expressed in *E. coli* as a thioredoxin fusion protein with a histidine tag. The trx-P501S fusion protein was purified by nickel chromatography, digested with thrombin to remove the trx fragment and further purified by an acid precipitation procedure followed by reverse phase HPLC.

Mice were immunized with truncated P501S protein. Serum bleeds from mice that potentially contained anti-P501S polyclonal sera were tested for P501S-specific reactivity using ELISA assays with purified P501S and trx-P501S proteins. Serum bleeds that appeared to react specifically with P501S were then screened for P501S reactivity by Western analysis. Mice that contained a P501S-specific antibody component were sacrificed and spleen cells were used to generate anti-P501S antibody producing hybridomas using standard techniques. Hybridoma supernatants were tested for P501S-specific reactivity initially by ELISA, and subsequently by FACS analysis of reactivity with P501S transduced cells. Based on these results, a monoclonal hybridoma referred to as 10E3 was chosen for further subcloning. A number of subclones were

generated, tested for specific reactivity to P501S using ELISA and typed for IgG isotype. The results of this analysis are shown below in Table V. Of the 16 subclones tested, the monoclonal antibody 10E3-G4-D3 was selected for further study.

5

Table V

Isotype analysis of murine anti-P501S monoclonal antibodies

Hybridoma clone	Isotype	Estimated [Ig] in supernatant ($\mu\text{g/ml}$)
4D11	IgG1	14.6
1G1	IgG1	0.6
4F6	IgG1	72
4H5	IgG1	13.8
4H5-E12	IgG1	10.7
4H5-EH2	IgG1	9.2
4H5-H2-A10	IgG1	10
4H5-H2-A3	IgG1	12.8
4H5-H2-A10-G6	IgG1	13.6
4H5-H2-B11	IgG1	12.3
10E3	IgG2a	3.4
10E3-D4	IgG2a	3.8
10E3-D4-G3	IgG2a	9.5
10E3-D4-G6	IgG2a	10.4
10E3-E7	IgG2a	6.5
8H12	IgG2a	0.6

The specificity of 10E3-G4-D3 for P501S was examined by FACS analysis. Specifically, cells were fixed (2% formaldehyde, 10 minutes), permeabilized (0.1% saponin, 10 minutes) and stained with 10E3-G4-D3 at 0.5 – 1 $\mu\text{g/ml}$, followed by incubation with a secondary, FITC-conjugated goat anti-mouse Ig antibody (Pharmingen, San Diego, CA). Cells were then analyzed for FITC fluorescence using an Excalibur fluorescence activated cell sorter. For FACS analysis of transduced cells, B-LCL were retrovirally transduced with P501S. For analysis of infected cells, B-LCL were infected with a vaccinia vector that expresses P501S. To demonstrate specificity in these assays, B-LCL transduced with a different antigen (P703P) and uninfected B-LCL vectors were utilized. 10E3-G4-D3 was shown to bind with P501S-transduced B-

10

15

LCL and also with P501S-infected B-LCL, but not with either uninfected cells or P703P-transduced cells.

To determine whether the epitope recognized by 10E3-G4-D3 was found on the surface or in an intracellular compartment of cells, B-LCL were transduced with P501S or HLA-B8' as a control antigen and either fixed and permeabilized as described above or directly stained with 10E3-G4-D3 and analyzed as above. Specific recognition of P501S by 10E3-G4-D3 was found to require permeabilization, suggesting that the epitope recognized by this antibody is intracellular.

The reactivity of 10E3-G4-D3 with the three prostate tumor cell lines Lncap, PC-3 and DU-145, which are known to express high, medium and very low levels of P501S, respectively, was examined by permeabilizing the cells and treating them as described above. Higher reactivity of 10E3-G4-D3 was seen with Lncap than with PC-3, which in turn showed higher reactivity than DU-145. These results are in agreement with the real time PCR and demonstrate that the antibody specifically recognizes P501S in these tumor cell lines and that the epitope recognized in prostate tumor cell lines is also intracellular.

Specificity of 10E3-G4-D3 for P501S was also demonstrated by Western blot analysis. Lysates from the prostate tumor cell lines Lncap, DU-145 and PC-3, from P501S-transiently transfected HEK293 cells, and from non-transfected HEK293 cells were generated. Western blot analysis of these lysates with 10E3-G4-D3 revealed a 46 kDa immunoreactive band in Lncap, PC-3 and P501S-transfected HEK cells, but not in DU-145 cells or non-transfected HEK293 cells. P501S mRNA expression is consistent with these results since semi-quantitative PCR analysis revealed that P501S mRNA is expressed in Lncap, to a lesser but detectable level in PC-3 and not at all in DU-145 cells. Bacterially expressed and purified recombinant P501S (referred to as P501SStr2) was recognized by 10E3-G4-D3 (24 kDa), as was full-length P501S that was transiently expressed in HEK293 cells using either the expression vector VR1012 or pCEP4. Although the predicted molecular weight of P501S is 60.5 kDa, both transfected and "native" P501S run at a slightly lower mobility due to its hydrophobic nature.

Immunohistochemical analysis was performed on prostate tumor and a panel of normal tissue sections (prostate, adrenal, breast, cervix, colon, duodenum, gall bladder, ileum, kidney, ovary, pancreas, parotid gland, skeletal muscle, spleen and testis). Tissue samples were fixed in formalin solution for 24 hours and embedded in paraffin before being sliced into 10 micron sections. Tissue sections were permeabilized and incubated with 10E3-G4-D3 antibody for 1 hr. HRP-labeled anti-mouse followed by incubation with DAB chromogen was used to visualize P501S immunoreactivity. P501S was found to be highly expressed in both normal prostate and prostate tumor tissue but was not detected in any of the other tissues tested.

To identify the epitope recognized by 10E3-G4-D3, an epitope mapping approach was pursued. A series of 13 overlapping 20-21 mers (5 amino acid overlap; SEQ ID NO: 489-501) was synthesized that spanned the fragment of P501S used to generate 10E3-G4-D3. Flat bottom 96 well microtiter plates were coated with either the peptides or the P501S fragment used to immunize mice, at 1 microgram/ml for 2 hours at 37 °C. Wells were then aspirated and blocked with phosphate buffered saline containing 1% (w/v) BSA for 2 hours at room temperature, and subsequently washed in PBS containing 0.1% Tween 20 (PBST). Purified antibody 10E3-G4-D3 was added at 2 fold dilutions (1000 ng – 16 ng) in PBST and incubated for 30 minutes at room temperature. This was followed by washing 6 times with PBST and subsequently incubating with HRP-conjugated donkey anti-mouse IgG (H+L) Affinipure F(ab') fragment (Jackson Immunoresearch, West Grove, PA) at 1:20000 for 30 minutes. Plates were then washed and incubated for 15 minutes in tetramethyl benzidine. Reactions were stopped by the addition of 1N sulfuric acid and plates were read at 450 nm using an ELISA plate reader. As shown in Fig. 8, reactivity was seen with the peptide of SEQ ID NO: 496 (corresponding to amino acids 439-459 of P501S) and with the P501S fragment but not with the remaining peptides, demonstrating that the epitope recognized by 10E3-G4-D3 is localized to amino acids 439-459 of SEQ ID NO: 113.

In order to further evaluate the tissue specificity of P501S, multi-array immunohistochemical analysis was performed on approximately 4700 different human tissues encompassing all the major normal organs as well as neoplasias derived from

these tissues. Sixty-five of these human tissue samples were of prostate origin. Tissue sections 0.6 mm in diameter were formalin-fixed and paraffin embedded. Samples were pretreated with HIER using 10 mM citrate buffer pH 6.0 and boiling for 10 min. Sections were stained with 10E3-G4-D3 and P501S immunoreactivity was visualized with HRP. All the 65 prostate tissues samples (5 normal, 55 untreated prostate tumors, 5 hormone refractory prostate tumors) were positive, showing distinct perinuclear staining. All other tissues examined were negative for P501S expression.

c) Preparation and Characterization of Antibodies against P503S

A fragment of P503S (amino acids 113-241 of SEQ ID NO: 114) was expressed and purified from bacteria essentially as described above for P501S and used to immunize both rabbits and mice. Mouse monoclonal antibodies were isolated using standard hybridoma technology as described above. Rabbit monoclonal antibodies were isolated using Selected Lymphocyte Antibody Method (SLAM) technology at Immgenics Pharmaceuticals (Vancouver, BC, Canada). Table VI, below, lists the monoclonal antibodies that were developed against P503S.

Table VI

Antibody	Species
20D4	Rabbit
JA1	Rabbit
1A4	Mouse
1C3	Mouse
1C9	Mouse
1D12	Mouse
2A11	Mouse
2H9	Mouse
4H7	Mouse
8A8	Mouse
8D10	Mouse
9C12	Mouse
6D12	Mouse

The DNA sequences encoding the complementarity determining regions (CDRs) for the rabbit monoclonal antibodies 20D4 and JA1 were determined and are provided in SEQ ID NO: 502 and 503, respectively.

5 In order to better define the epitope binding region of each of the antibodies, a series of overlapping peptides were generated that span amino acids 109-213 of SEQ ID NO: 114. These peptides were used to epitope map the anti-P503S monoclonal antibodies by ELISA as follows. The recombinant fragment of P503S that was employed as the immunogen was used as a positive control. Ninety-six well
10 microtiter plates were coated with either peptide or recombinant antigen at 20 ng/well overnight at 4 °C. Plates were aspirated and blocked with phosphate buffered saline containing 1% (w/v) BSA for 2 hours at room temperature then washed in PBS containing 0.1% Tween 20 (PBST). Purified rabbit monoclonal antibodies diluted in PBST were added to the wells and incubated for 30 min at room temperature. This was
15 followed by washing 6 times with PBST and incubation with Protein-A HRP conjugate at a 1:2000 dilution for a further 30 min. Plates were washed six times in PBST and incubated with tetramethylbenzidine (TMB) substrate for a further 15 min. The reaction was stopped by the addition of 1N sulfuric acid and plates were read at 450 nm using at ELISA plate reader. ELISA with the mouse monoclonal antibodies was performed with
20 supernatants from tissue culture run neat in the assay.

All of the antibodies bound to the recombinant P503S fragment, with the exception of the negative control SP2 supernatant. 20D4, JA1 and 1D12 bound strictly to peptide #2101 (SEQ ID NO: 504), which corresponds to amino acids 151-169 of SEQ ID NO: 114. 1C3 bound to peptide #2102 (SEQ ID NO: 505), which corresponds
25 to amino acids 165-184 of SEQ ID NO: 114. 9C12 bound to peptide #2099 (SEQ ID NO: 522), which corresponds to amino acids 120-139 of SEQ ID NO: 114. The other antibodies bind to regions that were not examined in these studies.

Subsequent to epitope mapping, the antibodies were tested by FACS analysis on a cell line that stably expressed P503S to confirm that the antibodies bind to
30 cell surface epitopes. Cells stably transfected with a control plasmid were employed as

a negative control. Cells were stained live with no fixative. 0.5 ug of anti-P503S monoclonal antibody was added and cells were incubated on ice for 30 min before being washed twice and incubated with a FITC-labelled goat anti-rabbit or mouse secondary antibody for 20 min. After being washed twice, cells were analyzed with an Excalibur
5 fluorescent activated cell sorter. The monoclonal antibodies 1C3, 1D12, 9C12, 20D4 and JA1, but not 8D3, were found to bind to a cell surface epitope of P503S.

In order to determine which tissues express P503S, immunohistochemical analysis was performed, essentially as described above, on a panel of normal tissues (prostate, adrenal, breast, cervix, colon, duodenum, gall bladder,
10 ileum, kidney, ovary, pancreas, parotid gland, skeletal muscle, spleen and testis). HRP-labeled anti-mouse or anti-rabbit antibody followed by incubation with TMB was used to visualize P503S immunoreactivity. P503S was found to be highly expressed in prostate tissue, with lower levels of expression being observed in cervix, colon, ileum and kidney, and no expression being observed in adrenal, breast, duodenum, gall
15 bladder, ovary, pancreas, parotid gland, skeletal muscle, spleen and testis.

Western blot analysis was used to characterize anti-P503S monoclonal antibody specificity. SDS-PAGE was performed on recombinant (rec) P503S expressed in and purified from bacteria and on lysates from HEK293 cells transfected with full length P503S. Protein was transferred to nitrocellulose and then Western blotted with
20 each of the anti-P503S monoclonal antibodies (20D4, JA1, 1D12, 6D12 and 9C12) at an antibody concentration of 1 ug/ml. Protein was detected using horse radish peroxidase (HRP) conjugated to either a goat anti-mouse monoclonal antibody or to protein A-sepharose. The monoclonal antibody 20D4 detected the appropriate molecular weight 14 kDa recombinant P503S (amino acids 113-241) and the 23.5 kDa
25 species in the HEK293 cell lysates transfected with full length P503S. Other anti-P503S monoclonal antibodies displayed similar specificity by Western blot.

d) Preparation and Characterization of Antibodies against P703P

Rabbits were immunized with either a truncated (P703Ptr1; SEQ ID NO: 172) or full-length mature form (P703Pfl; SEQ ID NO: 523) of recombinant P703P

protein was expressed in and purified from bacteria as described above. Affinity purified polyclonal antibody was generated using immunogen P703Pfl or P703Ptrl attached to a solid support. Rabbit monoclonal antibodies were isolated using SLAM technology at Immgenics Pharmaceuticals. Table VII below lists both the polyclonal and monoclonal antibodies that were generated against P703P.

Table VII

Antibody	Immunogen	Species/type
Aff. Purif. P703P (truncated); #2594	P703Ptrl	Rabbit polyclonal
Aff. Purif. P703P (full length); #9245	P703Pfl	Rabbit polyclonal
2D4	P703Ptrl	Rabbit monoclonal
8H2	P703Ptrl	Rabbit monoclonal
7H8	P703Ptrl	Rabbit monoclonal

The DNA sequences encoding the complementarity determining regions (CDRs) for the rabbit monoclonal antibodies 8H2, 7H8 and 2D4 were determined and are provided in SEQ ID NO: 506-508, respectively.

Epitope mapping studies were performed as described above. Monoclonal antibodies 2D4 and 7H8 were found to specifically bind to the peptides of SEQ ID NO: 509 (corresponding to amino acids 145-159 of SEQ ID NO: 172) and SEQ ID NO: 510 (corresponding to amino acids 11-25 of SEQ ID NO: 172), respectively. The polyclonal antibody 2594 was found to bind to the peptides of SEQ ID NO: 511-514, with the polyclonal antibody 9427 binding to the peptides of SEQ ID NO: 515-517.

The specificity of the anti-P703P antibodies was determined by Western blot analysis as follows. SDS-PAGE was performed on (1) bacterially expressed recombinant antigen; (2) lysates of HEK293 cells and Ltk^{-/-} cells either untransfected or transfected with a plasmid expressing full length P703P; and (3) supernatant isolated from these cell cultures. Protein was transferred to nitrocellulose and then Western blotted using the anti-P703P polyclonal antibody #2594 at an antibody concentration of 1 ug/ml. Protein was detected using horse radish peroxidase (HRP) conjugated to an anti-rabbit antibody. A 35 kDa immunoreactive band could be observed with

recombinant P703P. Recombinant P703P runs at a slightly higher molecular weight since it is epitope tagged. In lysates and supernatants from cells transfected with full length P703P, a 30 kDa band corresponding to P703P was observed. To assure specificity, lysates from HEK293 cells stably transfected with a control plasmid were
5 also tested and were negative for P703P expression. Other anti-P703P antibodies showed similar results.

Immunohistochemical studies were performed as described above, using anti-P703P monoclonal antibody. P703P was found to be expressed at high levels in normal prostate and prostate tumor tissue but was not detectable in all other tissues
10 tested (breast tumor, lung tumor and normal kidney).

e) Preparation and Characterization of Antibodies against P504S

Full-length P504S (SEQ ID NO: 108) was expressed and purified from bacteria essentially as described above for P501S and employed to raise rabbit monoclonal antibodies using Selected Lymphocyte Antibody Method (SLAM)
15 technology at Immgenics Pharmaceuticals (Vancouver, BC, Canada). The anti-P504S monoclonal antibody 13H4 was shown by Western blot to bind to both expressed recombinant P504S and to native P504S in tumor cells.

Immunohistochemical studies using 13H4 to assess P504S expression in various prostate tissues were performed as described above. A total of 104 cases,
20 including 65 cases of radical prostatectomies with prostate cancer (PC), 26 cases of prostate biopsies and 13 cases of benign prostate hyperplasia (BPH), were stained with the anti-P504S monoclonal antibody 13H4. P504S showed strongly cytoplasmic granular staining in 64/65 (98.5%) of PCs in prostatectomies and 26/26 (100%) of PCs in prostatic biopsies. P504S was stained strongly and diffusely in carcinomas (4+ in
25 91.2% of cases of PC; 3+ in 5.5%; 2+ in 2.2% and 1+ in 1.1%) and high grade prostatic intraepithelial neoplasia (4+ in all cases). The expression of P504S did not vary with Gleason score. Only 17/91 (18.7%) of cases of NP/BPH around PC and 2/13 (15.4%) of BPH cases were focally (1+, no 2+ to 4+ in all cases) and weakly positive for P504S in large glands. Expression of P504S was not found in small atrophic glands, postatrophic
30 hyperplasia, basal cell hyperplasia and transitional cell metaplasia in either biopsies or

prostatectomies. P504S was thus found to be over-expressed in all Gleason scores of prostate cancer (98.5 to 100% of sensitivity) and exhibited only focal positivities in large normal glands in 19/104 of cases (82.3% of specificity). These findings indicate that P504S may be usefully employed for the diagnosis of prostate cancer.

5

EXAMPLE 19

CHARACTERIZATION OF CELL SURFACE EXPRESSION AND
CHROMOSOME LOCALIZATION OF THE PROSTATE-SPECIFIC ANTIGEN P501S

10

This example describes studies demonstrating that the prostate-specific antigen P501S is expressed on the surface of cells, together with studies to determine the probable chromosomal location of P501S.

The protein P501S (SEQ ID NO: 113) is predicted to have 11 transmembrane domains. Based on the discovery that the epitope recognized by the anti-
15 P501S monoclonal antibody 10E3-G4-D3 (described above in Example 17) is intracellular, it was predicted that following transmembrane determinants would allow the prediction of extracellular domains of P501S. Fig. 9 is a schematic representation of the P501S protein showing the predicted location of the transmembrane domains and the intracellular epitope described in Example 17. Underlined sequence represents the
20 predicted transmembrane domains, bold sequence represents the predicted extracellular domains, and italicized sequence represents the predicted intracellular domains. Sequence that is both bold and underlined represents sequence employed to generate polyclonal rabbit serum. The location of the transmembrane domains was predicted using HHMTOP as described by Tusnady and Simon (Principles Governing Amino
25 Acid Composition of Integral Membrane Proteins: Applications to Topology Prediction, *J. Mol. Biol.* 283:489-506, 1998).

Based on Fig. 9, the P501S domain flanked by the transmembrane domains corresponding to amino acids 274-295 and 323-342 is predicted to be extracellular. The peptide of SEQ ID NO: 518 corresponds to amino acids 306-320 of
30 P501S and lies in the predicted extracellular domain. The peptide of SEQ ID NO: 519,

which is identical to the peptide of SEQ ID NO: 518 with the exception of the substitution of the histidine with an asparagine, was synthesized as described above. A Cys-Gly was added to the C-terminus of the peptide to facilitate conjugation to the carrier protein. Cleavage of the peptide from the solid support was carried out using the following cleavage mixture: trifluoroacetic acid:ethanediol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for two hours, the peptide was precipitated in cold ether. The peptide pellet was then dissolved in 10% v/v acetic acid and lyophilized prior to purification by C18 reverse phase hplc. A gradient of 5-60% acetonitrile (containing 0.05% TFA) in water (containing 0.05% TFA) was used to elute the peptide. The purity of the peptide was verified by hplc and mass spectrometry, and was determined to be >95%. The purified peptide was used to generate rabbit polyclonal antisera as described above.

Surface expression of P501S was examined by FACS analysis. Cells were stained with the polyclonal anti-P501S peptide serum at 10 µg/ml, washed, incubated with a secondary FITC-conjugated goat anti-rabbit Ig antibody (ICN), washed and analyzed for FITC fluorescence using an Excalibur fluorescence activated cell sorter. For FACS analysis of transduced cells, B-LCL were retrovirally transduced with P501S. To demonstrate specificity in these assays, B-LCL transduced with an irrelevant antigen (P703P) or nontransduced were stained in parallel. For FACS analysis of prostate tumor cell lines, Lncap, PC-3 and DU-145 were utilized. Prostate tumor cell lines were dissociated from tissue culture plates using cell dissociation medium and stained as above. All samples were treated with propidium iodide (PI) prior to FACS analysis, and data was obtained from PI-excluding (*i.e.*, intact and non-permeabilized) cells. The rabbit polyclonal serum generated against the peptide of SEQ ID NO: 519 was shown to specifically recognize the surface of cells transduced to express P501S, demonstrating that the epitope recognized by the polyclonal serum is extracellular.

To determine biochemically if P501S is expressed on the cell surface, peripheral membranes from Lncap cells were isolated and subjected to Western blot analysis. Specifically, Lncap cells were lysed using a dounce homogenizer in 5 ml of homogenization buffer (250 mM sucrose, 10 mM HEPES, 1mM EDTA, pH 8.0, 1

complete protease inhibitor tablet (Boehringer Mannheim)). Lysate samples were spun at 1000 g for 5 min at 4 °C. The supernatant was then spun at 8000g for 10 min at 4 °C. Supernatant from the 8000g spin was recovered and subjected to a 100,000g spin for 30 min at 4 °C to recover peripheral membrane. Samples were then separated by SDS-
5 PAGE and Western blotted with the mouse monoclonal antibody 10E3-G4-D3 (described above in Example 17) using conditions described above. Recombinant purified P501S, as well as HEK293 cells transfected with and over-expressing P501S were included as positive controls for P501S detection. LCL cell lysate was included as a negative control. P501S could be detected in Lncap total cell lysate, the 8000g
10 (internal membrane) fraction and also in the 100,000g (plasma membrane) fraction. These results indicate that P501S is expressed at, and localizes to, the peripheral membrane.

To demonstrate that the rabbit polyclonal antiserum generated to the peptide of SEQ ID NO: 519 specifically recognizes this peptide as well as the
15 corresponding native peptide of SEQ ID NO: 518, ELISA analyses were performed. For these analyses, flat-bottomed 96 well microtiter plates were coated with either the peptide of SEQ ID NO: 519, the longer peptide of SEQ ID NO: 520 that spans the entire predicted extracellular domain, the peptide of SEQ ID NO: 521 which represents the epitope recognized by the P501S-specific antibody 10E3-G4-D3, or a P501S fragment
20 (corresponding to amino acids 355-526 of SEQ ID NO: 113) that does not include the immunizing peptide sequence, at 1 µg/ml for 2 hours at 37 °C. Wells were aspirated, blocked with phosphate buffered saline containing 1% (w/v) BSA for 2 hours at room temperature and subsequently washed in PBS containing 0.1% Tween 20 (PBST). Purified anti-P501S polyclonal rabbit serum was added at 2 fold dilutions (1000 ng -
25 125 ng) in PBST and incubated for 30 min at room temperature. This was followed by washing 6 times with PBST and incubating with HRP-conjugated goat anti-rabbit IgG (H+L) Affinipure F(ab') fragment at 1:20000 for 30 min. Plates were then washed and incubated for 15 min in tetramethyl benzidine. Reactions were stopped by the addition of 1N sulfuric acid and plates were read at 450 nm using an ELISA plate reader. As
30 shown in Fig. 11, the anti-P501S polyclonal rabbit serum specifically recognized the

peptide of SEQ ID NO: 519 used in the immunization as well as the longer peptide of SEQ ID NO: 520, but did not recognize the irrelevant P501S-derived peptides and fragments.

In further studies, rabbits were immunized with peptides derived from the P501S sequence and predicted to be either extracellular or intracellular, as shown in Fig. 9. Polyclonal rabbit sera were isolated and polyclonal antibodies in the serum were purified, as described above. To determine specific reactivity with P501S, FACS analysis was employed, utilizing either B-LCL transduced with P501S or the irrelevant antigen P703P, of B-LCL infected with vaccinia virus-expressing P501S. For surface expression, dead and non-intact cells were excluded from the analysis as described above. For intracellular staining, cells were fixed and permeabilized as described above. Rabbit polyclonal serum generated against the peptide of SEQ ID NO: 548, which corresponds to amino acids 181-198 of P501S, was found to recognize a surface epitope of P501S. Rabbit polyclonal serum generated against the peptide SEQ ID NO: 551, which corresponds to amino acids 543-553 of P501S, was found to recognize an epitope that was either potentially extracellular or intracellular since in different experiments intact or permeabilized cells were recognized by the polyclonal sera. Based on similar deductive reasoning, the sequences of SEQ ID NO: 541-547, 549 and 550, which correspond to amino acids 109-122, 539-553, 509-520, 37-54, 342-359, 295-323, 217-274, 143-160 and 75-88, respectively, of P501S, can be considered to be potential surface epitopes of P501S recognized by antibodies.

In further studies, mouse monoclonal antibodies were raised against amino acids 296 to 322 to P501S, which are predicted to be in an extracellular domain. A/J mice were immunized with P501S/adenovirus, followed by subsequent boosts with an *E. coli* recombinant protein, referred to as P501N, that contains amino acids 296 to 322 of P501S, and with peptide 296-322 (SEQ ID NO: 755) coupled with KLH. The mice were subsequently used for splenic B cell fusions to generate anti-peptide hybridomas. The resulting 3 clones, referred to as 4F4 (IgG1,kappa), 4G5 (IgG2a,kappa) and 9B9 (IgG1,kappa), were grown for antibody production. The 4G5 mAb was purified by passing the supernatant over a Protein A-sepharose column,

followed by antibody elution using 0.2M glycine, pH 2.3. Purified antibody was neutralized by the addition of 1M Tris, pH 8, and buffer exchanged into PBS.

For ELISA analysis, 96 well plates were coated with P501S peptide 296-322 (referred to as P501-long), an irrelevant P775 peptide, P501S-N, P501TR2, P501S-long-KLH, P501S peptide 306-319 (referred to as P501-short)-KLH, or the irrelevant peptide 2073-KLH, all at a concentration of 2 ug/ml and allowed to incubate for 60 minutes at 37 °C. After coating, plates were washed 5X with PBS + 0.1% Tween and then blocked with PBS, 0.5% BSA, 0.4% Tween20 for 2 hours at room temperature. Following the addition of supernatants or purified mAb, the plates were incubated for 60 minutes at room temperature. Plates were washed as above and donkey anti-mouse IgHRP-linked secondary antibody was added and incubated for 30 minutes at room temperature, followed by a final washing as above. TMB peroxidase substrate was added and incubated 15 minutes at room temperature in the dark. The reaction was stopped by the addition of 1N H₂SO₄ and the OD was read at 450 nM. All three hybrid clones secreted mAb that recognized peptide 296-322 and the recombinant protein P501N.

For FACS analysis, HEK293 cells were transiently transfected with a P501S/VR1012 expression constructs using Fugene 6 reagent. After 2 days of culture, cells were harvested and washed, then incubated with purified 4G5 mAb for 30 minutes on ice. After several washes in PBS, 0.5% BSA, 0.01% azide, goat anti-mouse Ig-FITC was added to the cells and incubated for 30 minutes on ice. Cells were washed and resuspended in wash buffer including 1% propidium iodide and subjected to FACS analysis. The FACS analysis confirmed that amino acids 296-322 of P501S are in an extracellular domain and are cell surface expressed.

The chromosomal location of P501S was determined using the GeneBridge 4 Radiation Hybrid panel (Research Genetics). The PCR primers of SEQ ID NO: 528 and 529 were employed in PCR with DNA pools from the hybrid panel according to the manufacturer's directions. After 38 cycles of amplification, the reaction products were separated on a 1.2% agarose gel, and the results were analyzed through the Whitehead Institute/MIT Center for Genome Research web server

(<http://www-genome.wi.mit.edu/cgi-bin/contig/rhmapper.pl>) to determine the probable chromosomal location. Using this approach, P501S was mapped to the long arm of chromosome 1 at WI-9641 between q32 and q42. This region of chromosome 1 has been linked to prostate cancer susceptibility in hereditary prostate cancer (Smith *et al.* *Science* 274:1371-1374, 1996 and Berthon *et al.* *Am. J. Hum. Genet.* 62:1416-1424, 1998). These results suggest that P501S may play a role in prostate cancer malignancy.

EXAMPLE 20

REGULATION OF EXPRESSION OF THE PROSTATE-SPECIFIC ANTIGEN P501S

10

Steroid (androgen) hormone modulation is a common treatment modality in prostate cancer. The expression of a number of prostate tissue-specific antigens have previously been demonstrated to respond to androgen. The responsiveness of the prostate-specific antigen P501S to androgen treatment was examined in a tissue culture system as follows.

15

Cells from the prostate tumor cell line LNCaP were plated at 1.5×10^6 cells/T75 flask (for RNA isolation) or 3×10^5 cells/well of a 6-well plate (for FACS analysis) and grown overnight in RPMI 1640 media containing 10% charcoal-stripped fetal calf serum (BRL Life Technologies, Gaithersburg, MD). Cell culture was continued for an additional 72 hours in RPMI 1640 media containing 10% charcoal-stripped fetal calf serum, with 1 nM of the synthetic androgen Methyltrienolone (R1881; New England Nuclear) added at various time points. Cells were then harvested for RNA isolation and FACS analysis at 0, 1, 2, 4, 8, 16, 24, 28 and 72-hours post androgen addition. FACS analysis was performed using the anti-P501S antibody 10E3-G4-D3 and permeabilized cells.

20

For Northern analysis, 5-10 micrograms of total RNA was run on a formaldehyde denaturing gel, transferred to Hybond-N nylon membrane (Amersham Pharmacia Biotech, Piscataway, NJ), cross-linked and stained with methylene blue. The filter was then prehybridized with Church's Buffer (250 mM Na_2HPO_4 , 70 mM H_3PO_4 , 1 mM EDTA, 1% SDS, 1% BSA in pH 7.2) at 65 °C for 1 hour. P501S DNA was

25

30

labeled with ^{32}P using High Prime random-primed DNA labeling kit (Boehringer Mannheim). Unincorporated label was removed using MicroSpin S300-HR columns (Amersham Pharmacia Biotech). The RNA filter was then hybridized with fresh Church's Buffer containing labeled cDNA overnight, washed with 1X SCP (0.1 M NaCl, 0.03 M $\text{Na}_2\text{HPO}_4 \cdot 7\text{H}_2\text{O}$, 0.001 M Na_2EDTA), 1% sarkosyl (n-lauroylsarcosine) and exposed to X-ray film.

Using both FACS and Northern analysis, P501S message and protein levels were found to increase in response to androgen treatment.

10

EXAMPLE 20

PREPARATION OF FUSION PROTEINS OF PROSTATE-SPECIFIC ANTIGENS

The example describes the preparation of a fusion protein of the prostate-specific antigen P703P and a truncated form of the known prostate antigen PSA. The truncated form of PSA has a 21 amino acid deletion around the active serine site. The expression construct for the fusion protein also has a restriction site at 3' end, immediately prior to the termination codon, to aid in adding cDNA for additional antigens.

The full-length cDNA for PSA was obtained by RT-PCR from a pool of RNA from human prostate tumor tissues using the primers of SEQ ID NO: 607 and 608, and cloned in the vector pCR-Blunt II-TOPO. The resulting cDNA was employed as a template to make two different fragments of PSA by PCR with two sets of primers (SEQ ID NO: 609 and 610; and SEQ ID NO: 611 and 612). The PCR products having the expected size were used as templates to make truncated forms of PSA by PCR with the primers of SEQ ID NO: 611 and 613, which generated PSA (delta 208-218 in amino acids). The cDNA for the mature form of P703P with a 6X histidine tag at the 5' end, was prepared by PCR with P703P and the primers of SEQ ID NO: 614 and 615. The cDNA for the fusion of P703P with the truncated form of PSA (referred to as FOPP) was then obtained by PCR using the modified P703P cDNA and the truncated form of PSA cDNA as templates and the primers of SEQ ID NO: 614 and 615. The FOPP

cDNA was cloned into the NdeI site and XhoI site of the expression vector pCRX1, and confirmed by DNA sequencing. The determined cDNA sequence for the fusion construct FOPP is provided in SEQ ID NO: 616, with the amino acid sequence being provided in SEQ ID NO: 617.

5 The fusion FOPP was expressed as a single recombinant protein in *E. coli* as follows. The expression plasmid pCRX1FOPP was transformed into the *E. coli* strain BL21-CodonPlus RIL. The transformant was shown to express FOPP protein upon induction with 1 mM IPTG. The culture of the corresponding expression clone was inoculated into 25 ml LB broth containing 50 ug/ml kanamycin and 34 ug/ml
10 chloramphenicol, grown at 37 °C to OD600 of about 1, and stored at 4 °C overnight. The culture was diluted into 1 liter of TB LB containing 50 ug/ml kanamycin and 34 ug/ml chloramphenicol, and grown at 37 °C to OD600 of 0.4. IPTG was added to a final concentration of 1 mM, and the culture was incubated at 30 °C for 3 hours. The cells were pelleted by centrifugation at 5,000 RPM for 8 min. To purify the protein, the
15 cell pellet was suspended in 25 ml of 10 mM Tris-Cl pH 8.0, 2mM PMSF, complete protease inhibitor and 15 ug lysozyme. The cells were lysed at 4 °C for 30 minutes, sonicated several times and the lysate centrifuged for 30 minutes at 10,000 x g. The precipitate, which contained the inclusion body, was washed twice with 10 mM Tris-Cl pH 8.0 and 1% CHAPS. The inclusion body was dissolved in 40 ml of 10 mM Tris-Cl
20 pH 8.0, 100 mM sodium phosphate and 8 M urea. The solution was bound to 8 ml Ni-NTA (Qiagen) for one hour at room temperature. The mixture was poured into a 25 ml column and washed with 50 ml of 10 mM Tris-Cl pH 6.3, 100 mM sodium phosphate, 0.5% DOC and 8M urea. The bound protein was eluted with 350 mM imidazole, 10 mM Tris-Cl pH 8.0, 100 mM sodium phosphate and 8 M urea. The fractions containing
25 FOPP proteins were combined and dialyzed extensively against 10 mM Tris-Cl pH 4.6, aliquoted and stored at - 70 °C.

EXAMPLE 21

REAL-TIME PCR CHARACTERIZATION OF THE PROSTATE-SPECIFIC ANTIGEN P501S IN
PERIPHERAL BLOOD OF PROSTATE CANCER PATIENTS

- 5 Circulating epithelial cells were isolated from fresh blood of normal individuals and metastatic prostate cancer patients, mRNA isolated and cDNA prepared using real-time PCR procedures. Real-time PCR was performed with the TaqmanTM procedure using both gene specific primers and probes to determine the levels of gene expression.
- 10 Epithelial cells were enriched from blood samples using an immunomagnetic bead separation method (Dynal A.S., Oslo, Norway). Isolated cells were lysed and the magnetic beads removed. The lysate was then processed for poly A+ mRNA isolation using magnetic beads coated with Oligo(dT)25. After washing the beads in buffer, bead/poly A+ RNA samples were suspended in 10 mM Tris HCl pH 8.0
- 15 and subjected to reversed transcription. The resulting cDNA was subjected to real-time PCR using gene specific primers. Beta-actin content was also determined and used for normalization. Samples with P501S copies greater than the mean of the normal samples + 3 standard deviations were considered positive. Real time PCR on blood samples was performed using the TaqmanTM procedure but extending to 50 cycles using
- 20 forward and reverse primers and probes specific for P501S. Of the eight samples tested, 6 were positive for P501S and β -actin signal. The remaining 2 samples had no detectable β -actin or P501S. No P501S signal was observed in the four normal blood samples tested.

25

EXAMPLE 22

EXPRESSION OF THE PROSTATE-SPECIFIC ANTIGENS P703P AND P501S IN
SCID MOUSE-PASSAGED PROSTATE TUMORS

- When considering the effectiveness of antigens in the treatment of
- 30 prostate cancer, the continued presence of the antigens in tumors during androgen

ablation therapy is important. The presence of the prostate-specific antigens P703P and P501S in prostate tumor samples grown in SCID mice in the presence of testosterone was evaluated as follows.

Two prostate tumors that had metastasized to the bone were removed from patients, implanted into SCID mice and grown in the presence of testosterone. Tumors were evaluated for mRNA expression of P703P, P501S and PSA using quantitative real time PCR with the SYBR green assay method. Expression of P703P and P501S in a prostate tumor was used as a positive control and the absence in normal intestine and normal heart as negative controls. In both cases, the specific mRNA was present in late passage tumors. Since the bone metastases were grown in the presence of testosterone, this implies that the presence of these genes would not be lost during androgen ablation therapy.

EXAMPLE 23

ANTI-P503S MONOCLONAL ANTIBODY INHIBITS TUMOR GROWTH *IN VIVO*

The ability of the anti-P503S monoclonal antibody 20D4 to suppress tumor formation in mice was examined as follows.

Ten SCID mice were injected subcutaneously with HEK293 cells that expressed P503S. Five mice received 150 micrograms of 20D4 intravenously at day 0 (time of tumor cell injection), day 5 and day 9. Tumor size was measured for 50 days. Of the five animals that received no 20D4, three formed detectable tumors after about 2 weeks which continued to enlarge throughout the study. In contrast, none of the five mice that received 20D4 formed tumors. These results demonstrate that the anti-P503S Mab 20D4 displays potent anti-tumor activity *in vivo*.

EXAMPLE 24

CHARACTERIZATION OF A T CELL RECEPTOR CLONE FROM A P501S-SPECIFIC T CELL CLONE

T cells have a limited lifespan. However, cloning of T cell receptor (TCR) chains and subsequent transfer essentially enables infinite propagation of the T

cell specificity. Cloning of tumor-antigen TCR chains allows the transfer of the specificity into T cells isolated from patients that share the TCR MHC-restricting allele. Such T cells could then be expanded and used in adoptive transfer settings to introduce the tumor antigen specificity into patients carrying tumors that express the antigen. T cell receptor alpha and beta chains from a CD8 T cell clone specific for the prostate-specific antigen P501S were isolated and sequenced as follows.

Total mRNA from 2×10^6 cells from CTL clone 4E5 (described above in Example 12) was isolated using Trizol reagent and cDNA was synthesized. To determine Va and Vb sequences in this clone, a panel of Va and Vb subtype-specific primers was synthesized and used in RT-PCR reactions with cDNA generated from each of the clones. The RT-PCR reactions demonstrated that each of the clones expressed a common Vb sequence that corresponded to the Vb7 subfamily. Furthermore, using cDNA generated from the clone, the Va sequence expressed was determined to be Va6. To clone the full TCR alpha and beta chains from clone 4E5, primers were designed that spanned the initiator and terminator-coding TCR nucleotides. The primers were as follows: TCR Valpha-6 5'(sense): GGATCC---GCCGCCACC---ATGTCACCTTTCTAGCCTGCT (SEQ ID NO: 756) BamHI site Kozak TCR alpha sequence TCR alpha 3' (antisense): GTCGAC---TCAGCTGGACCACAGCCGCAG (SEQ ID NO: 757) SalI site TCR alpha constant sequence TCR Vbeta-7. 5'(sense): GGATCC---GCCGCCACC---ATGGGCTGCAGGCTGCTCT (SEQ ID NO: 758) BamHI site Kozak TCR alpha sequence TCR beta 3' (antisense): GTCGAC---TCAGAAATCCTTTCTCTTGAC (SEQ ID NO: 759) SalI site TCR beta constant sequence. Standard 35 cycle RT-PCR reactions were established using cDNA synthesized from the CTL clone and the above primers, employing the proofreading thermostable polymerase PWO (Roche, Nutley, NJ).

The resultant specific bands (approx. 850 bp for alpha and approx. 950 for beta) were ligated into the PCR blunt vector (Invitrogen) and transformed into *E. coli*. *E. coli* transformed with plasmids containing full-length alpha and beta chains were identified, and large scale preparations of the corresponding plasmids were generated. Plasmids containing full-length TCR alpha and beta chains were submitted

for sequencing. The sequencing reactions demonstrated the cloning of full-length TCR alpha and beta chains with the determined cDNA sequences for the Vb and Va chains being shown in SEQ ID NO: 760 and 761, respectively. The corresponding amino acid sequences are shown in SEQ ID NO: 762 and 763, respectively. The Va sequence was
5 shown by nucleotide sequence alignment to be 99% identical (347/348) to Va6.2, and the Vb to be 99% identical to Vb7 (336/338).

From the foregoing it will be appreciated that, although specific embodiments of the invention have been described herein for purposes of illustration,
10 various modifications may be made without deviating from the spirit and scope of the invention. Accordingly, the invention is not limited except as by the appended claims.

CLAIMS

What is Claimed:

1. An isolated polynucleotide comprising a sequence selected from the group consisting of:

(a) sequences provided in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-626, 630, 631, 634, 636, 639-655, 674, 680, 681, 711, 713, 716, 720-722, 735, 737-739, 751, 753, 764, 765, 773-776 and 786-788;

(b) complements of the sequences provided in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-626, 630, 631, 634, 636, 639-655, 674, 680, 681, 711, 713, 716, 720-722, 735, 737-739, 751, 753, 764, 765, 773-776 and 786-788;

(c) sequences consisting of at least 20 contiguous residues of a sequence provided in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-626, 630, 631, 634, 636, 639-655, 674, 680, 681, 711, 713, 716, 720-722, 735, 737-739, 751, 753, 764, 765, 773-776 and 786-788;

(d) sequences that hybridize to a sequence provided in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-626, 630, 631, 634, 636, 639-655, 674, 680, 681, 711, 713, 716, 720-722, 735, 737-739, 751, 753, 764, 765, 773-776 and 786-788 under moderately stringent conditions;

(e) sequences having at least 75% identity to a sequence of SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-

375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-626, 630, 631, 634, 636, 639-655, 674, 680, 681, 711, 713, 716, 720-722, 735, 737-739, 751, 753, 764, 765, 773-776 and 786-788;

(f) sequences having at least 90% identity to a sequence of SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-626, 630, 631, 634, 636, 639-655, 674, 680, 681, 711, 713, 716, 720-722, 735, 737-739, 751, 753, 764, 765, 773-776 and 786-788; and

(g) degenerate variants of a sequence provided in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-626, 630, 631, 634, 636, 639-655, 674, 680, 681, 711, 713, 716, 720-722, 735, 737-739, 751, 753, 764, 765, 773-776 and 786-788.

2. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of:

(a) sequences recited in SEQ ID NO: 112-114, 172, 176, 178, 327, 329, 331, 336, 339, 376-380, 383, 477-483, 496, 504, 505, 519, 520, 522, 525, 527, 532, 534, 537-551, 553-568, 573-586, 588-590, 592, 627-629, 632, 633, 635, 637, 638, 656-671, 675, 683, 684, 710, 712, 714, 715, 717-719, 723-734, 736, 740-750, 752, 754, 755, 766-772, 777-785 and 789-791;

(b) sequences having at least 70% identity to a sequence of SEQ ID NO: 112-114, 172, 176, 178, 327, 329, 331, 336, 339, 376-380, 383, 477-483, 496, 504, 505, 519, 520, 522, 525, 527, 532, 534, 537-551, 553-568, 573-586, 588-590, 592, 627-629, 632, 633, 635, 637, 638, 656-671, 675, 683, 684, 710, 712, 714, 715, 717-719, 723-734, 736, 740-750, 752, 754, 755, 766-772, 777-785 and 789-791;

(c) sequences having at least 90% identity to a sequence of SEQ ID NO: 112-114, 172, 176, 178, 327, 329, 331, 336, 339, 376-380, 383, 477-483, 496, 504, 505, 519, 520, 522, 525, 527, 532, 534, 537-551, 553-568, 573-586, 588-590, 592, 627-

629, 632, 633, 635, 637, 638, 656-671, 675, 683, 684, 710, 712, 714, 715, 717-719, 723-734, 736, 740-750, 752, 754, 755, 766-772, 777-785 and 789-791;

- (d) sequences encoded by a polynucleotide of claim 1;
- (e) sequences having at least 70% identity to a sequence encoded by a polynucleotide of claim 1; and
- (f) sequences having at least 90% identity to a sequence encoded by a polynucleotide of claim 1.

3. An expression vector comprising a polynucleotide of claim 1 operably linked to an expression control sequence.

4. A host cell transformed or transfected with an expression vector according to claim 3.

5. An isolated antibody, or antigen-binding fragment thereof, that specifically binds to a polypeptide of claim 2.

6. A method for detecting the presence of a cancer in a patient, comprising the steps of:

- (a) obtaining a biological sample from the patient;
- (b) contacting the biological sample with a binding agent that binds to a polypeptide of claim 2;
- (c) detecting in the sample an amount of polypeptide that binds to the binding agent; and
- (d) comparing the amount of polypeptide to a predetermined cut-off value and therefrom determining the presence of a cancer in the patient.

7. A fusion protein comprising at least one polypeptide according to claim 2.

8. The fusion protein of claim 7, wherein the fusion protein comprises a sequence selected from the group consisting of:

(a) sequences provided in SEQ ID NO: 682, 692, 695, 699, 703 and 709; and

(b) sequences encoded by SEQ ID NO: 679, 691, 696, 700, 704 and 708.

9. An oligonucleotide that hybridizes to a sequence recited in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-626, 630, 631, 634, 636, 639-655, 674, 680, 681, 711, 713, 716, 720-722, 735, 737-739, 751, 753, 764, 765, 773-776 or 786-788 under moderately stringent conditions.

10. A method for stimulating and/or expanding T cells specific for a tumor protein, comprising contacting T cells with at least one component selected from the group consisting of:

(a) polypeptides according to claim 2;
(b) polynucleotides according to claim 1; and
(c) antigen-presenting cells that express a polypeptide according to claim 1,

under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells.

11. An isolated T cell population, comprising T cells prepared according to the method of claim 10.

12. A composition comprising a first component selected from the group consisting of physiologically acceptable carriers and immunostimulants, and a second component selected from the group consisting of:

- (a) polypeptides according to claim 2;
- (b) polynucleotides according to claim 1;
- (c) antibodies according to claim 5;
- (d) fusion proteins according to claim 7;
- (e) T cell populations according to claim 11; and
- (f) antigen presenting cells that express a polypeptide according to claim 2.

13. A method for stimulating an immune response in a patient, comprising administering to the patient a composition of claim 12.

14. A method for the treatment of a cancer in a patient, comprising administering to the patient a composition of claim 12.

15. A method for determining the presence of a cancer in a patient, comprising the steps of:

- (a) obtaining a biological sample from the patient;
- (b) contacting the biological sample with an oligonucleotide according to claim 9;
- (c) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide; and
- (d) compare the amount of polynucleotide that hybridizes to the oligonucleotide to a predetermined cut-off value, and therefrom determining the presence of the cancer in the patient.

16. A diagnostic kit comprising at least one oligonucleotide according to claim 9.

17. A diagnostic kit comprising at least one antibody according to claim 5 and a detection reagent, wherein the detection reagent comprises a reporter group.

18. A method for inhibiting the development of a cancer in a patient, comprising the steps of:

(a) incubating CD4+ and/or CD8+ T cells isolated from a patient with at least one component selected from the group consisting of: (i) polypeptides according to claim 2; (ii) polynucleotides according to claim 1; and (iii) antigen presenting cells that express a polypeptide of claim 2, such that T cell proliferate; and

(b) administering to the patient an effective amount of the proliferated T cells,

thereby inhibiting the development of a cancer in the patient.

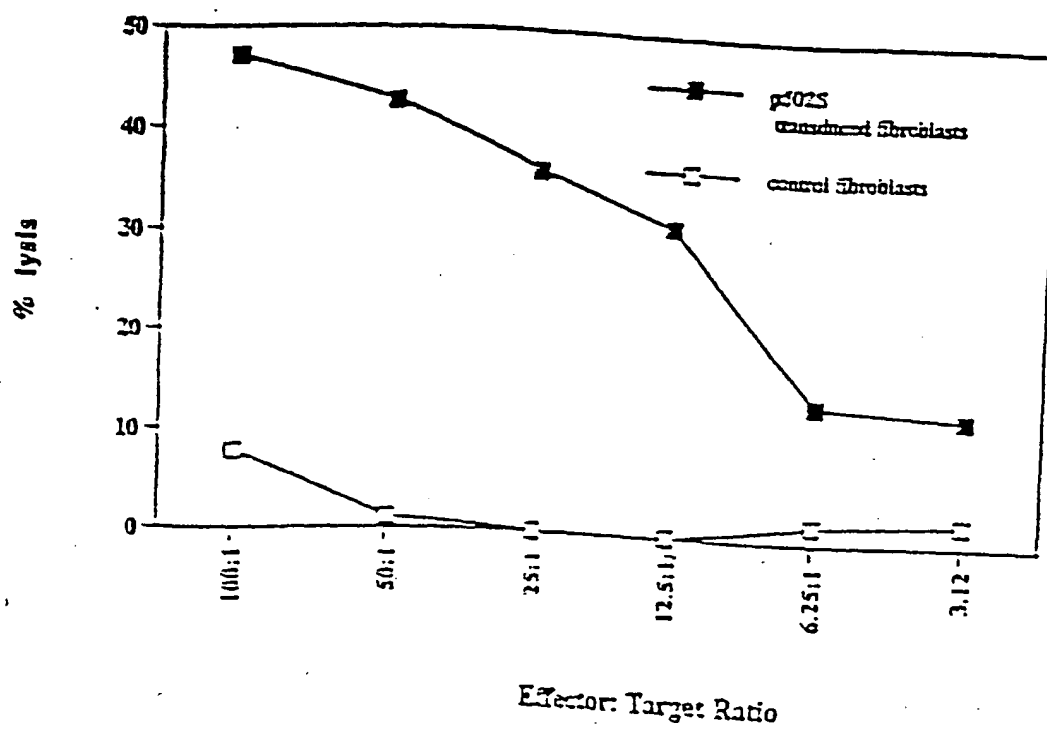


Fig. 1

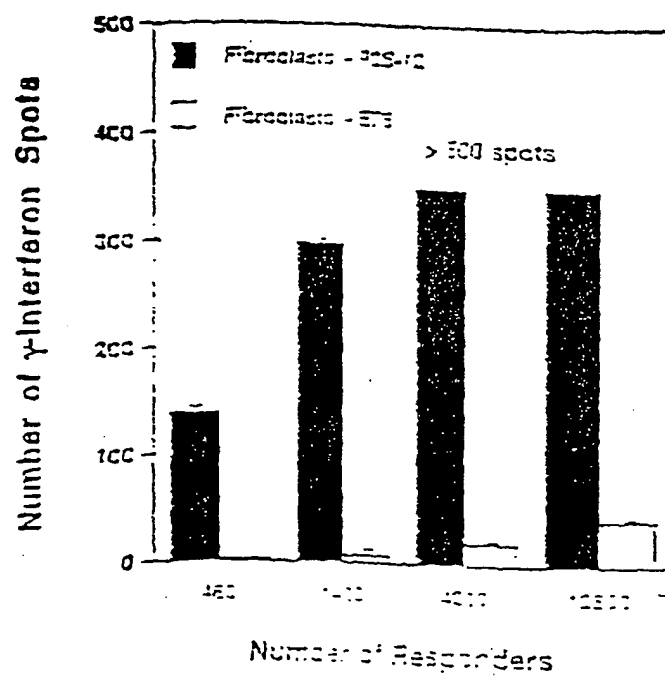


Fig. 2A

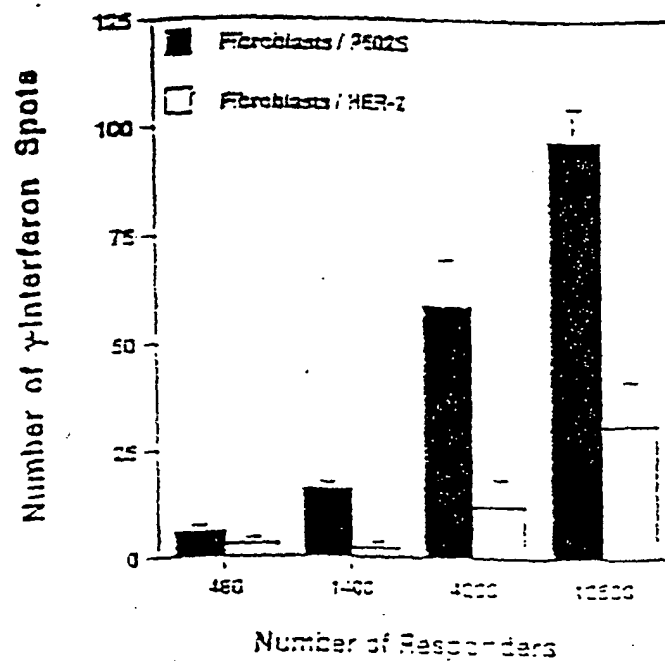


Fig. 26

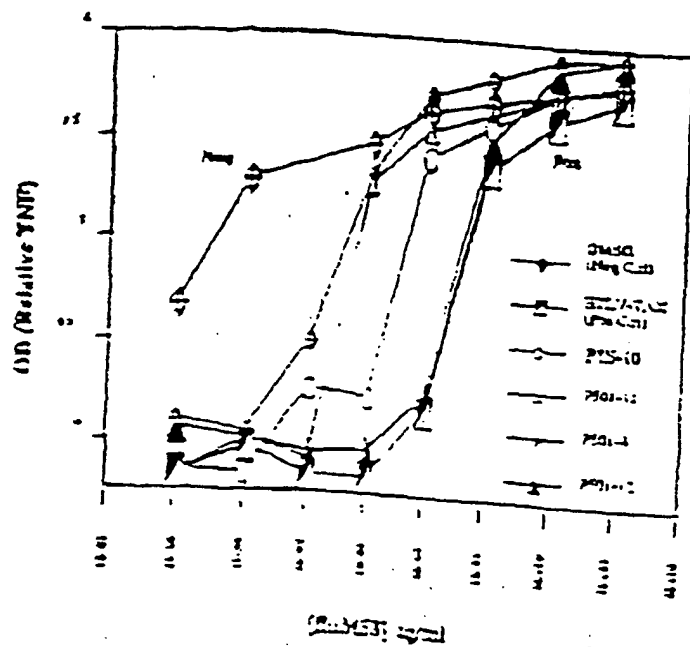


Fig. 3

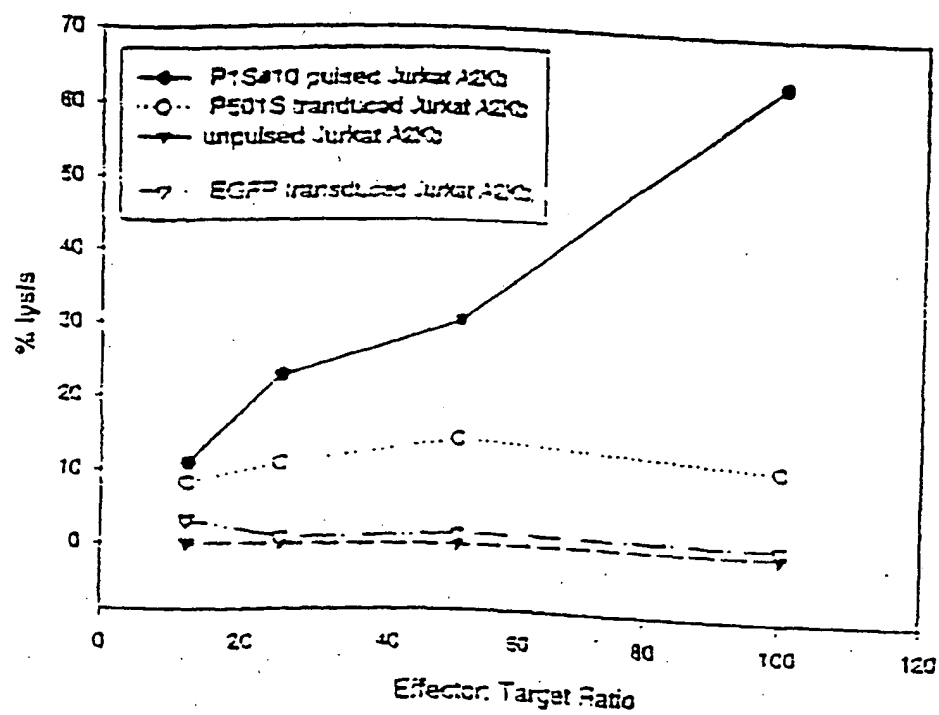


Fig. 4

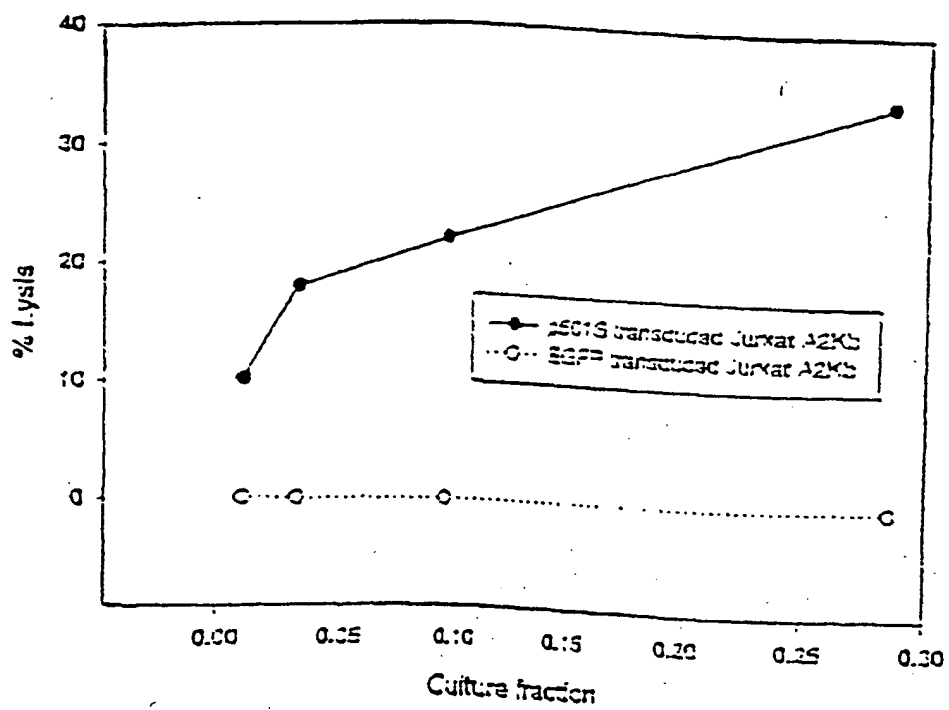


Fig. 5

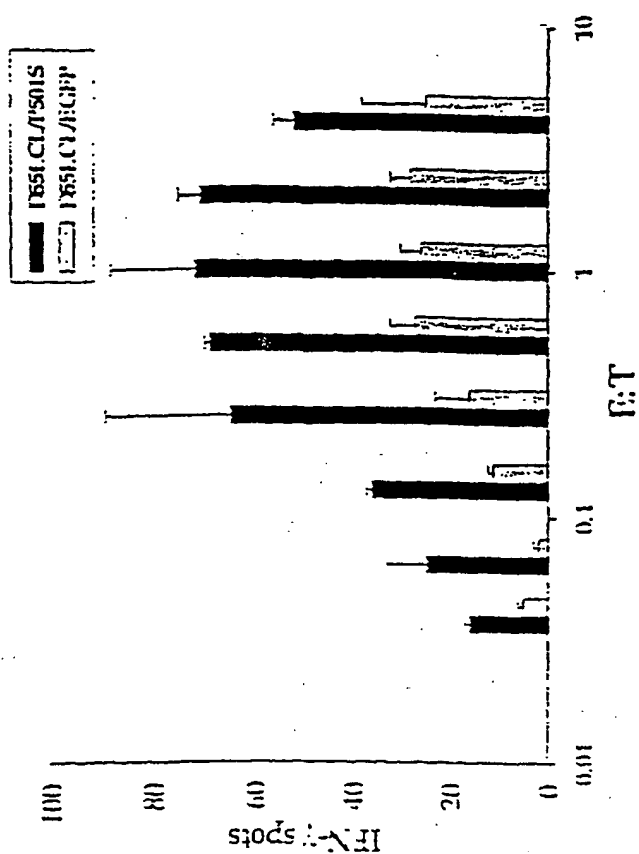


Fig. 6B

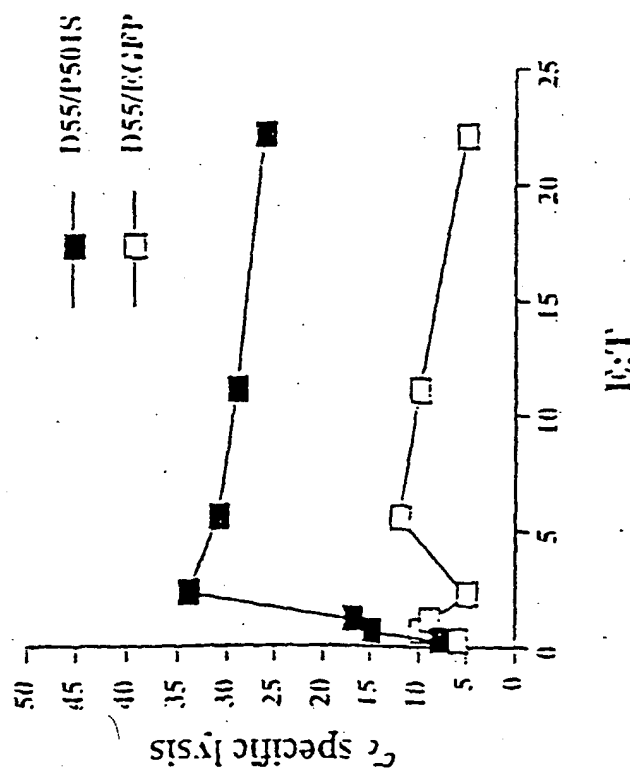
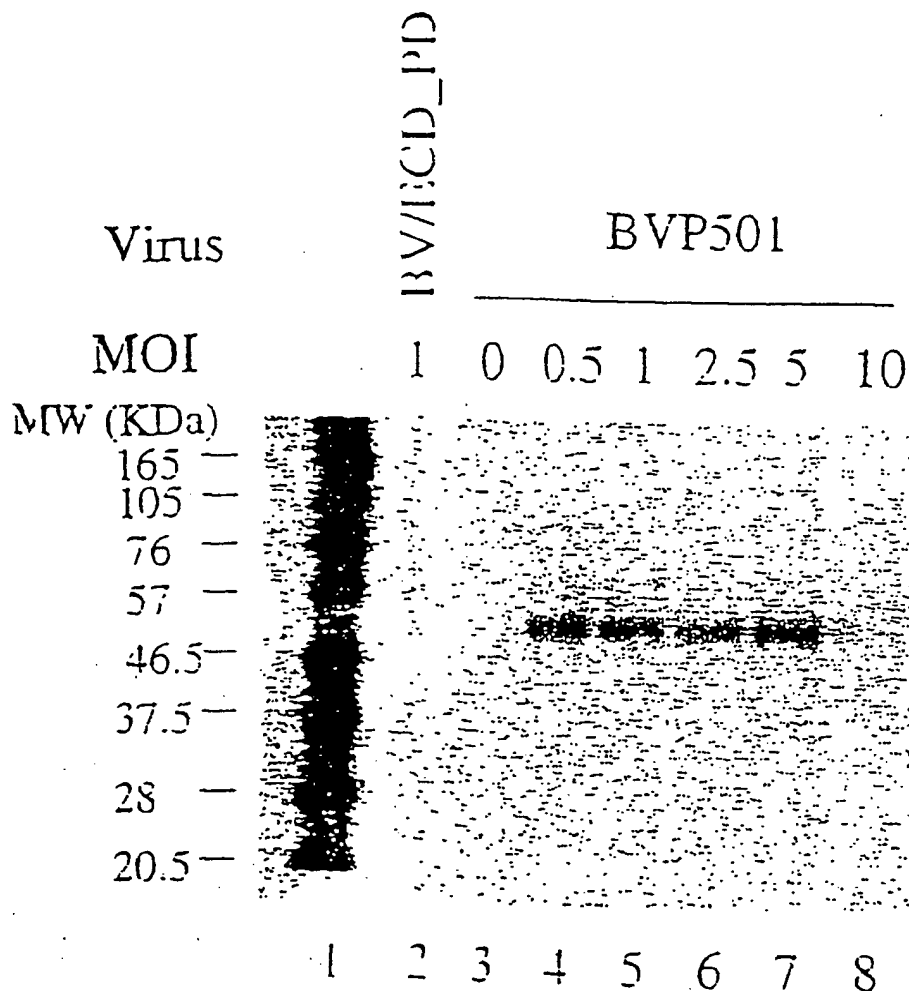


Fig. 6A

Expression of P501S by the Baculovirus Expression System



0.6 million high 5 cells in 6-well plate were infected with an unrelated control virus BV/ECD_PD (lane 2), without virus (lane 3), or with recombinant baculovirus for P501S at different MOIs (lane 4-8). Cell lysates were run on SDS-PAGE under the reducing conditions and analyzed by Western blot with a monoclonal antibody against P501S (P501S-10E3-G4D3). Lane 1 is the biotinylated protein molecular weight marker (BioLabs).

Fig. 7

Figure 1. Schematic of P501S with predicted transmembrane, cytoplasmic, and extracellular regions

MVQRLLWSSLLRRKK AQLLA.VNLLTTEGLEVCLAAGHT YVPPILLLEVGVVERKFM TNVLGIGPYVLGLYCVPLLGSAS
 DHWRGRYGRRRRP EIWALSQILLSEFLIPRAGIWL AGLLCTDDPRPLE LALLDGVCLLDFCGQVCTFPL
 FALSLLDFRDPDHCRO AYSVYAEMISLGGCTGVLLPAI DWDTSAI.AAPVLC.TQEE
 CLTGLLTLLFETCYAATLLY AEEAIGCTTEPAEGLSAPVLSPIHCTCRARIAFRNLGAILPRL
 HQLCTAMPETLRK LPVAFLCSWMAIMFTTFTYTP VGEGLLYQGVYPRAPGTTEARRHIYDEGVK
 MGLSLFLQCAISLYESLYM DRIVQREGTRAVYAS VAAFPYAAGATCLSHSVAYVTA SAA
 LTGIEIFSALQLPYTLASLY HREKQVFLPKYRGDTGGASSEDSSI.MTSFILPGKPGAPFPNGHIVGAGGSGL
 LPPPPALCGASACDVSRVVVGERTEARVVVGRG ICLDLAILDSAILLSQVAPSEF MGSIVQLSQS
 VTAYMVSAAGLCILVAIFYAT QVVFDKSDIAKYSA

Underlined sequence: Predicted transmembrane domain; **Bold sequence**: Predicted extracellular domain;
Italic sequence: Predicted intracellular domain. Sequence in bold/underlined: used to generate polyclonal rabbit serum

Localization of domains predicted using IMMTOPI (G.R. Tusnady and I. Simon (1998) Principles
 Governing Amino Acid Composition of Integral Membrane Proteins: Applications to topology Prediction. J.Mol Biol. 283,
 489-506.

Genomic Map of (5) Corixa Candidate Genes

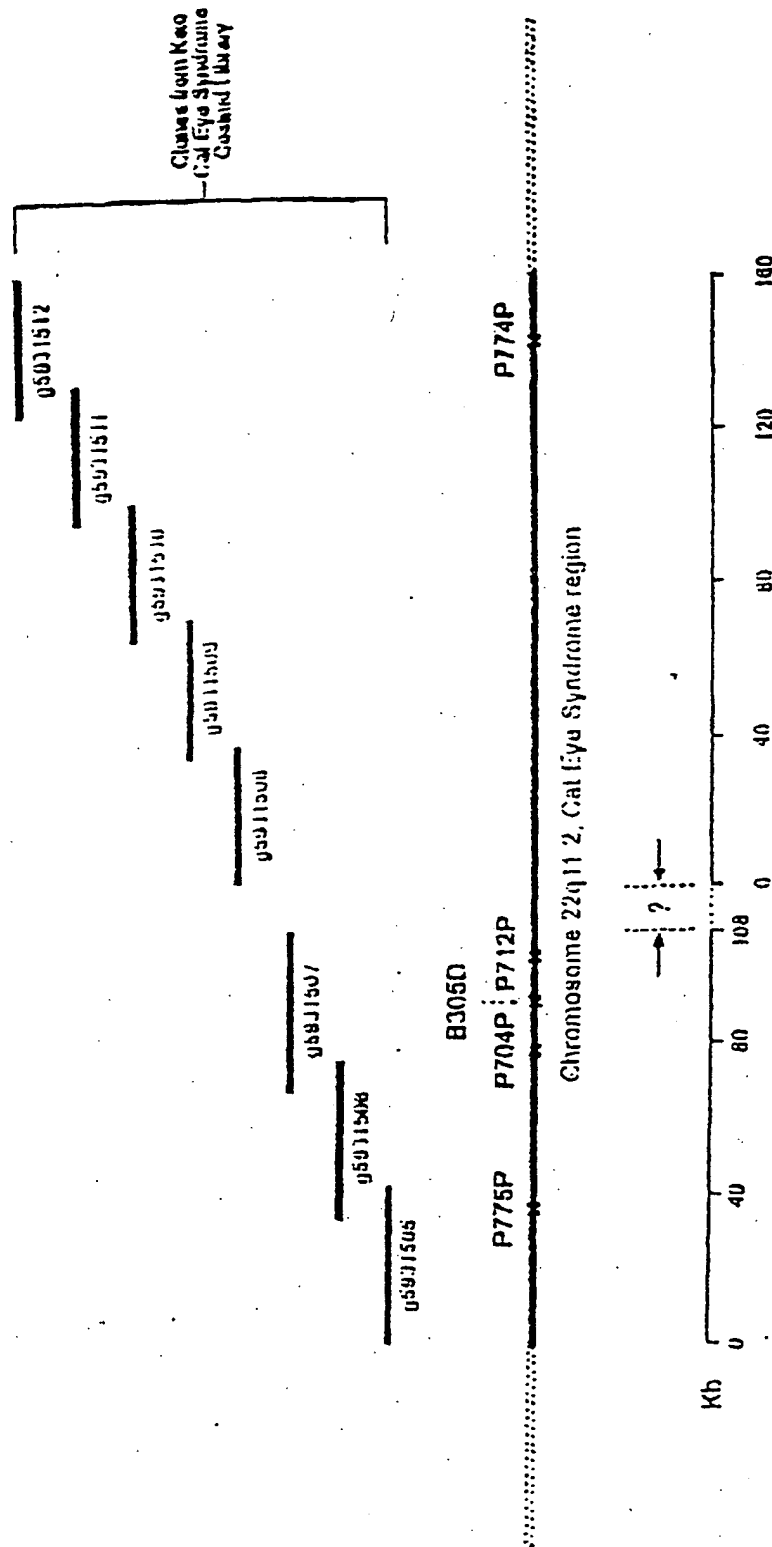


Fig. 10

FIGURE 4. Elisa assay of rabbit polyclonal antibody specificity

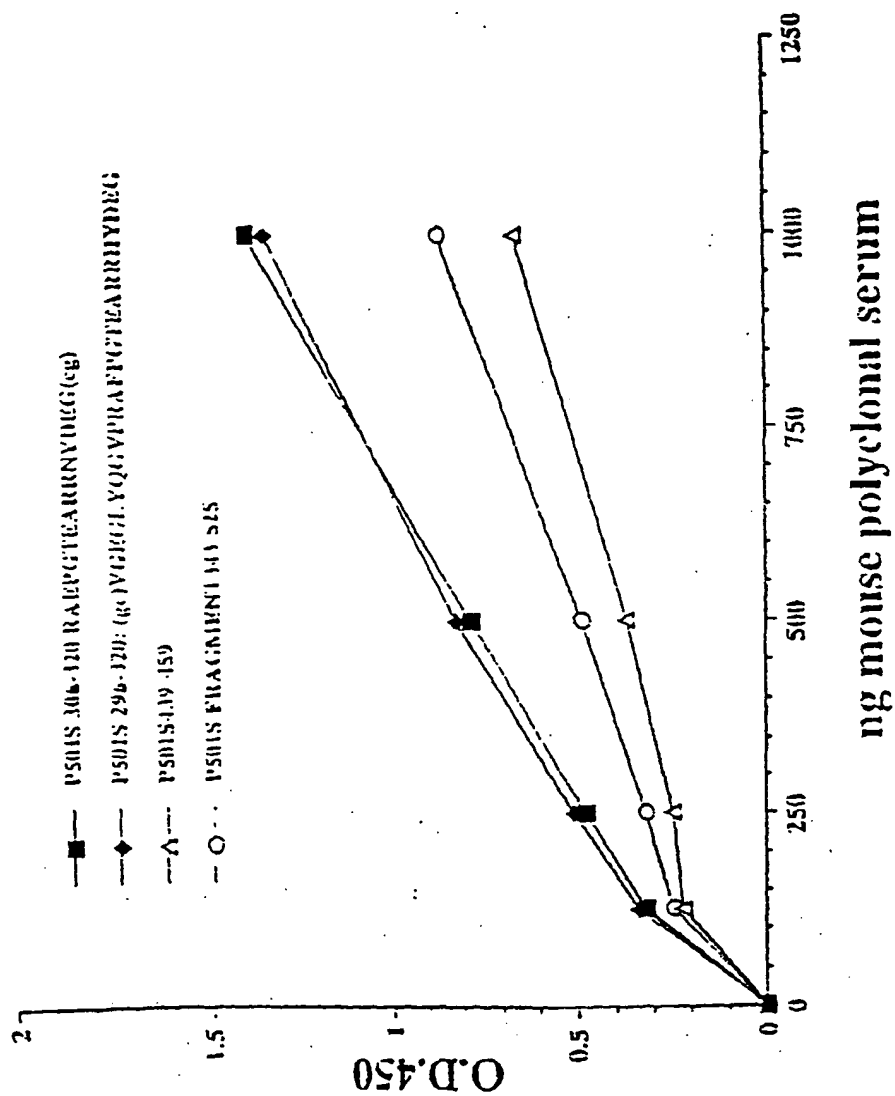


Fig. 11

SEQUENCE LISTING

<110> Corixa Corporation
 Smithkline Beechan Biologicals S.A.
 Xu, Jiangchun
 Dillon, Davin C.
 Mitcham, Jennifer L.
 Harlocker, Susan L.
 Jiang, Yuqui
 Reed, Steven G.
 Kalos, Michael D.
 Fanger, Gary R.
 Retter, Marc W.
 Stolk, John A.
 Day, Craig H.
 Skeiky, Yasir A.W.
 Wang, Aijun
 Meagher, Medeleine Joy
 Vanderbrugge, Didier
 Dewerchin, Marianne
 Dehottay, Ph.
 de Rop, Philippe

<120> COMPOSITIONS AND METHODS FOR THE THERAPY AND
 DIAGNOSIS OF PROSTATE CANCER

<130> 210121.42722PC

<140> PCT

<141> 2001-01-16

<160> 792

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 814

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(814)

<223> n = A, T, C or G

<400> 1

tttttttttt	tttttcacag	tataacagct	ctttatttct	gtgagttcta	ctaggaaatc	60
atcaaactctg	agggttgtct	ggaggacttc	aatacacctc	cccccatagt	gaatcagctt	120
ccaggggggtc	cagtccctct	ccttacttca	tccccatccc	atgccaaagg	aagaccctcc	180
ctccttggtc	cacagccttc	tctaggcttc	ccagtgcctc	caggacagag	tgggttatgt	240
tttcagctcc	atccttgctg	tgagtgtctg	gtgcgttggtg	cctccagctt	ctgctcagtg	300
cttcatggac	agtgtccagc	acatgtcact	ctccactctc	tcagtgtgga	tccactagtt	360
ctagagcggc	cgccaccgcg	gtggagctcc	agcttttggt	cccttttagtg	agggttaatt	420
gcgcgcttg	cgtaatcatg	gtcataactg	tttcctgtgt	gaaattgtta	tccgctcaca	480
attccacaca	acatacgagc	cggaagcata	aagtgtaaag	cctgggggtgc	ctaataagtg	540
anctaactca	cattaattgc	gttgcgctca	ctgncgcgtt	tccagtcnng	aaaactgtcg	600
tgccagctgc	attaatgaat	cggccaacgc	ncggggaaaa	gcgggtttg	ctttgggggc	660

tcttcgcgtt	ctcgcctcact	nantcctgcg	ctcgggtcgtt	cggtgcggg	gaacggtatc	720
actcctcaaa	gnggtatta	cggttatccn	naaatcnggg	gataccnng	aaaaanttt	780
aacaaaagg	cancaaagg	cngaaacgta	aaaa			814

<210> 2
 <211> 816
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc_feature
 <222> (1)...(816)
 <223> n = A,T,C or G

<400> 2						
acagaaatgt	tggatggtg	agcacctttc	tatacgactt	acaggacagc	agatggggaa	60
ttcatggctg	ttggagcaat	agaaccccag	ttctacgagc	tgctgatcaa	aggacttggg	120
ctaaagtctg	atgaacttcc	caatcagatg	agcatggatg	attggccaga	aatgaagaag	180
aagtttgag	atgtatttgc	aaagaagacg	aaggcagagt	ggtgtcaa	ctttgacggc	240
acagatgcct	gtgtgactcc	ggttctgact	tttgaggagg	ttgttcatca	tgatcacaa	300
aaggaacggg	gctcgtttat	caccagttag	gagcaggacg	tgagccccc	ccctgcacct	360
ctgctgttaa	acaccccagc	catcccttct	ttcaaaagg	atccactagt	tctagaagcg	420
gccgccaccg	cggtggagct	ccagcttttg	ttccctttag	tgagggttaa	ttgcgcgctt	480
ggcgtaatca	tggtcatagc	tgtttctgt	gtgaaattgt	tatccgctca	caattccccc	540
aacatacgag	ccggaacata	aagtgttaag	cctgggggtgc	ctaagtantg	agctaactcn	600
cattaattgc	gttgcgctca	ctgcccgctt	tccagtcggg	aaaactgtcg	tgccactgcn	660
ttantgaatc	ngccaccccc	cgggaaaagg	cggttgcntt	ttgggcctct	tccgctttcc	720
tcgctcattg	atcctngcnc	ccggtcttcg	gctgcggnga	acggttcaact	cctcaaaggc	780
ggtntnccgg	ttatccccaa	acnnggggata	cccnga			816

<210> 3
 <211> 773
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc_feature
 <222> (1)...(773)
 <223> n = A,T,C or G

<400> 3						
cttttgaaag	aagggtatggc	tggggtgttt	aacagcagag	gtgcagggcg	ggggctcacg	60
tcctgctcct	cactggtgat	aaacgagccc	cgttccttgt	tgtgatcatg	atgaacaacc	120
tcctcaaaaag	tcagaaccgg	agtcacacag	gcatctgtgc	cgtaaaagat	ttgacaccac	180
tctgccttcg	tcttctttgc	aaatacatct	gcaaacttct	tcttcatttc	tgccaatca	240
tccatgctca	tctgattggg	aagttcatca	gacttttagtc	canntccttt	gatcagcagc	300
tcgtagaact	ggggttctat	tgctccaaca	gccatgaatt	ccccatctgc	tgctcgttaa	360
gtcgtataga	aagggtgctcc	accatccaac	atgttctgtc	ctcgaggggg	ggcccgttac	420
ccaatcgcc	ctatantgag	tcgtattacg	cgcgctcact	ggcgcgtcgtt	ttacaacgtc	480
gtgactggga	aaacccctggg	cgttaccaac	ttaatcgctt	tgacgacat	cccccttctg	540
ccagctgggc	gtaatancca	aaaggcccgc	accgatcgcc	cttccaacag	ttgcgcacct	600
gaatgggnaa	atggggacccc	cctgtttaccg	cgcattnaac	ccccgcnggg	tttngttgtt	660
acccccacnt	nnaccgctta	cactttgcca	gcgccttanc	gcccgtccc	tttnccttt	720
cttcccttcc	tttncnccn	ctttcccccg	gggtttcccc	cntcaaacc	cna	773

<210> 4
 <211> 828
 <212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(828)

<223> n = A,T,C or G

<400> 4

cctcctgagt	cctactgacc	tgtgctttct	ggtgtggagt	ccagggctgc	taggaaaagg	60
aatgggcaga	cacaggtgta	tgccaatggt	tctgaaatgg	gtataatttc	gtcctctcct	120
tcggaacact	ggctgtctct	gaagacttct	cgctcagttt	cagtgaggac	acacacaaag	180
acgtgggtga	ccatgttggt	tgtgggggtgc	agagatggga	gggggtggggc	ccaccctgga	240
agagtggaca	gtgacacaag	gtggacactc	tctacagatc	actgaggata	agctggagcc	300
acaatgcatg	aggcacacac	acagcaagga	tgacnctgta	aacatagccc	acgctgtcct	360
gngggcactg	ggaagcctan	atnaggccgt	gagcanaaag	aaggggagga	tccactagtt	420
ctanagcggc	cgccaccgcg	gtgganctcc	ancctttgtt	cccttttagtg	aggggttaatt	480
gcgcgcttg	cntaatcatg	gtcatanctn	tttcctgtgt	gaaattgtta	tccgctcaca	540
attccacaca	acatacganc	cggaacata	aantgtaaac	ctgggggtgcc	taatgantga	600
ctaactcaca	ttaattgcgt	tgcgctcact	gcccgccttc	caatcnggaa	acctgtcttg	660
ccncttgcat	tnatgaatcn	gccaaacccc	ggggaaaagc	gtttgcgttt	tgggcgctct	720
tccgcttcct	cncctcantta	ntccctncnc	tcggtcattc	cggtgcngc	aaaccgggtc	780
accnctcca	aagggggtat	tccggtttcc	ccnaatccgg	gganance		828

<210> 5

<211> 834

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(834)

<223> n = A,T,C or G

<400> 5

ttttttttt	tttttactga	tagatggaat	ttattaagct	tttcacatgt	gatagcacat	60
agttttaatt	gcatccaaag	tactaaçaaa	aactctagca	atcaagaatg	gcagcatggt	120
attttataac	aatcaacacc	tgtggctttt	aaaatttggt	tttcataaga	taattttatac	180
tgaagtaaat	ctagccatgc	ttttaaaaaa	tgcttttaggt	cactccaagc	ttggcagtta	240
acatttgcca	taaaacaataa	taaaacaatc	acaattttaat	aaataacaaa	tacaacattg	300
taggccataa	tcatatacag	tataaggaaa	aggtggtagt	gttgagtaag	cagttattag	360
aatagaatac	cttggcctct	atgcaaatat	gtctagacac	tttgattcac	tcagccctga	420
cattcagttt	tcaaagtagg	agacagggtc	tacagtatca	ttttacagtt	tccaacacat	480
tgaaaacaag	tagaaaatga	tgagttgatt	tttattaatg	cattacatcc	tcaagagtta	540
tcaccaaccc	ctcagttata	aaaaattttc	aagttatatt	agtcataata	cttggtgtgc	600
ttattttaaa	ttagtgctaa	atggattaag	tgaagacaac	aatggtcccc	taatgtgatt	660
gatattggtc	atttttacca	gcttctaaat	ctnaactttc	aggcttttga	actggaacat	720
tgnatnacag	tgttccanag	ttncaaccta	ctggaacatt	acagtgtgct	tgattcaaaa	780
tgttattttg	ttaaaaatta	aattttaacc	tggttgaaaa	ataatttgaa	atna	834

<210> 6

<211> 818

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(818)

<223> n = A,T,C or G

<400> 6

tttttttttt	tttttttttt	aagaccctca	tcaatagatg	gagacataca	gaaatagtca	60
aaccacatct	acaaaatgcc	agtatcaggc	ggcggcttcg	aagccaaagt	gatgtttgga	120
tgtaaaagtga	aatattagtt	ggcggatgaa	gcagatagtg	aggaaagttg	agccaataat	180
gacgtgaagt	ccgtggaagc	ctgtggctac	aaaaaatgtt	gagccgtaga	tgccgtcgga	240
aatggtgaag	ggagactcga	agtactctga	ggctttagg	agggtaaaat	agagaccag	300
taaaattgta	ataagcagtg	cttgaattat	ttggtttcgg	ttgttttcta	ttagactatg	360
gtgagctcag	gtgattgata	ctcctgatgc	gagtaatacg	gatgtgttta	ggagtgggac	420
ttctagggga	tttagcgggg	tgatgcctgt	tgggggccag	tgccctccta	gttggggggg	480
aggggctagg	ctggagtgg	aaaaggctca	gaaaaatcct	gcgaagaaaa	aaacttctga	540
ggtaataaat	aggattatcc	cgtatcgaag	gccttttttg	acaggtggtg	tgtggtggcc	600
ttggtatgtg	ctttctcgtg	ttacatcgcg	ccatcattgg	tatatgggta	gtgtgttggg	660
ttantanggc	ctantatgaa	gaacttttgg	antggaatta	aatcaatngc	ttggccggaa	720
gtcattanga	nggctnaaaa	ggcctgttta	ngggtctggg	ctnggtttta	cccnaccat	780
ggaatncccc	ccccggacna	ntgnatccct	attcttaa			818

<210> 7

<211> 817

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(817)

<223> n = A,T,C or G

<400> 7

tttttttttt	tttttttttt	tggctctaga	gggggtagag	ggggtgctat	agggtaaata	60
cgggccctat	ttcaaagatt	tttaggggaa	ttaattctag	gacgatgggt	atgaaactgt	120
ggtttgctcc	acagatttca	gagcattgac	cgtagtatac	ccccggtcgt	gtagcgggta	180
aagtggtttg	gttttagacgt	ccgggaattg	catctgtttt	taagcctaata	gtggggacag	240
ctcatgagtg	caagacgtct	tgtgatgtaa	ttattatacn	aatgggggct	tcaatcggga	300
gtactactcg	attgtcaacg	tcaaggagtc	gcaggtcgcc	tggttctagg	aataatgggg	360
gaagtatgta	ggaattgaag	attaatccgc	cgtagtcggg	gttctcctag	gttcaatacc	420
attggtggcc	aattgatattg	atggtaaggg	gagggatcgt	tgaactcgtc	tgttatgtaa	480
aggatncctt	ngggatggga	aggcnatnaa	ggactangga	tnaatggcgg	gcangatatt	540
tcaaacngtc	tctanttcct	gaaacgtctg	aaatgttaat	aanaattaan	tttngttatt	600
gaatnttnng	gaaaagggct	tacaggacta	gaaaccaaata	angaaaanta	atnntaangg	660
cnttatcntn	aaaggnata	accnctccta	tnatcccacc	caatngnatt	ccccacncnn	720
acnattggat	nccccanttc	canaaaanggc	cncctcccg	tgnannccnc	cttttgttcc	780
cttnantgan	ggttattcnc	ccctngentt	atcancc			817

<210> 8

<211> 799

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(799)

<223> n = A,T,C or G

<400> 8

catttccggg	tttactttct	aaggaaagcc	gagcgggaagc	tgctaacgtg	ggaatcgggtg	60
cataaggaga	actttctgct	ggcacgcgct	agggacaagc	gggagagcga	ctccgagcgt	120
ctgaagcgca	cgtcccagaa	ggtggacttg	gcactgaaac	agctgggaca	catccgcgag	180
tacgaacage	gcctgaaagt	gctggagcgg	gaggtccagc	agtgtagccg	cgtcctgggg	240

tggttgccg	angcctganc	cgctctgcct	tgttgccccc	angtgggccc	ccacccctg	300
acctgcctg	gtccaaacac	tgagccctgc	tgggcgactt	caagganaac	ccccacang	360
ggattttgct	cctanantaa	ggctcatctg	ggcctcgccc	ccccacctg	gttgcccttg	420
tctttgangt	gagcccatg	tccatctggg	ccactgtcng	gaccaccttt	ngggagtgtt	480
ctccttacia	ccacannatg	cccggctcct	cccggaaacc	antcccancc	tgngaaggat	540
caagncctgn	atccactnnt	netanaaccg	gccnccnccg	cngtggaacc	cnccttntgt	600
tccttttctt	tnagggttaa	tnnccgcttg	gccttnccan	ngtctncnc	ntttccnnt	660
gttnaaattg	ttangcnccc	nccnntcccn	cnnnnnnan	cccgaaccnn	annttnnann	720
ncctgggggt	nccnnngat	tgacccncc	nccctntant	tgcnttnggg	nncnntgccc	780
ctttccctct	nggganncg					799

<210> 9
 <211> 801
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(801)
 <223> n = A,T,C or G

<400> 9						
acgccttgat	cctcccaggc	tgggactggt	tctgggagga	gccgggcatg	ctgtggtttg	60
taangatgac	actcccaaag	gtggtcctga	cagtggccca	gatggacatg	gggtcacct	120
caaggacaag	gccaccaggt	gcgggggccg	aagcccacat	gaccttact	ctatgagcaa	180
aatcccctgt	gggggcttct	ccttgaagtc	cgccancagg	gctcagtctt	tggacccang	240
caggtcatgg	ggttgtnngc	caactggggg	ccncaacgca	aaanggcnc	gggcctcngn	300
caccatccc	angacggggc	tacactnctg	gacctccnc	tccaccactt	tcatgcgctg	360
ttcntaccgg	cgnatntgtc	ccanctgttt	cngtgccnac	tccancttct	nggacgtggg	420
ctacatacgc	ccggantcnc	ntcccgtt	tgccctatc	cacgtncan	caacaaattt	480
cncntantg	caccnattcc	cacnttttnc	agntttccnc	nncngcttc	cttntaaaag	540
ggttganc	cggaaaatnc	cccaaagggg	gggggcccng	taccaactn	ccccctnata	600
gctgaantcc	ccatnaccnn	gnctcnatgg	ancntccnt	tttaannacn	ttctnaactt	660
gggaananc	ctcgncntn	ccccnttaa	tccnccctg	cnangnnnt	cccccnntcc	720
nccnnntng	gcntntnann	cnaaaaaggc	ccnnnanc	tctcctnn	cctcanttgc	780
ccanccctgc	aatcggccn	c				801

<210> 10
 <211> 789
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(789)
 <223> n = A,T,C or G

<400> 10						
cagtctatnt	ggccagtgtg	gcagctttcc	ctgtggctgc	cggtgccaca	tgctgtccc	60
acagtgtggc	cgtgggtgaca	gcttcagccg	ccctcaccgg	gttcaccttc	tcagccctgc	120
agatccctgc	ctacacactg	gcctccctct	accaccggga	gaagcaggtg	ttcctgcca	180
aataccgagg	ggacactgga	ggtgctagca	gtgaggacag	cctgatgacc	agcttccctg	240
caggccctaa	gcctggagct	cccttcccta	atggacacgt	gggtgctgga	ggcagtggcc	300
tgctccacc	tccaccgcg	ctctgcgggg	cctctgcctg	tgatgtctcc	gtacgtgtgg	360
tggtgggtga	gcccaccgan	gccagggtgg	ttccgggccc	gggcatctgc	ctggacctgc	420
ccatccctga	tagtgcttcc	tgtgtcccca	ngtggcccca	tccctgttta	tgggtcccat	480
tgccagctc	agccagtctg	tactgccta	tatggtgtct	gccgcaggcc	tgggtctggt	540
ccatttact	ttgctacaca	ggtantattt	gacaagaacg	anttgccaa	atactcagcg	600

ttaaaaaatt	ccagcaacat	tgggggtgga	aggcctgcct	cactgggtcc	aactccccgc	660
tcctgttaac	cccatggggc	tgccggcttg	gccgccaat	tctgttgctg	ccaaantnat	720
gtggtctctc	gctgccacct	gttgctggct	gaagtgcnta	cngcncanct	nggggggtng	780
gnggttccc						789

<210> 11
 <211> 772
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc_feature
 <222> (1)...(772)
 <223> n = A,T,C or G

<400> 11						
cccaccctac	ccaaatatta	gacaccaaca	cagaaaagct	agcaatggat	tcccttctac	60
tttgttaaat	aaataagtta	aatattttaa	tgccctgtgc	tctgtgatgg	caacagaagg	120
accaacaggc	cacatcctga	taaaaggtaa	gaggggggtg	gatcagcaaa	aagacagtgc	180
tgtgggctga	ggggacctgg	ttcttgtgtg	ttgccccca	ggactcttcc	cctacaaata	240
actttcatat	gttcaaatac	catggaggag	tgtttcatcc	tagaaactcc	catgcaagag	300
ctacattaaa	cgaagctgca	ggttaagggg	cttanagatg	ggaaaccagg	tgactgagtt	360
tattcagctc	ccaaaaaccc	ttctctaggt	gtgtctcaac	taggaggcta	gctgttaacc	420
ctgagcctgg	gtaatccacc	tgagagtgcc	cgcattcca	gtgcatggaa	cccttctggc	480
ctccctgtat	aagtccagac	tgaaaccccc	ttggaaggnc	tccagtcagg	cagccctana	540
aactggggaa	aaaagaaaaa	gacgccccan	ccccagctg	tgcanctacg	cacctcaaca	600
gcacagggtg	gcagcaaaaa	aaccacttta	ctttggcaca	aacaaaaact	ngggggggca	660
accccgccac	cccnangggg	gttaacagga	ancngggnaa	cntggaaccc	aattnaggca	720
ggcccnccac	ccnaatntt	gctgggaaat	ttttctcccc	ctaaattntt	tc	772

<210> 12
 <211> 751
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc_feature
 <222> (1)...(751)
 <223> n = A,T,C or G

<400> 12						
gcccccaattc	cagctgccac	accacccacg	gtgactgcat	tagttcggat	gtcatacaaa	60
agctgattga	agcaaccctc	tactttttgg	tcgtgagcct	tttgcttggg	gcaggtttca	120
ttggctgtgt	tggtgacgtt	gtcattgcaa	cagaatgggg	gaaaggcact	gttctctttg	180
aagtanggtg	agtcctcaaa	atccgtatag	ttgggtgaagc	cacagcactt	gagccctttc	240
atggtggtgt	tccacacttg	agtgaagtct	tcctgggaac	cataatcttt	cttgatggca	300
ggcactacca	gcaacgtcag	ggaagtgtc	agccattgtg	gtgtacacca	aggcgaccac	360
agcagctgcn	acctcagcaa	tgaagatgan	gaggangatg	aagaagaacg	tcnccagggc	420
acacttgctc	tcagtcttan	caccatanca	gccntgaaa	accaananca	aagaccacna	480
cnccggctgc	gatgaagaaa	tnaccccneg	ttgacaaact	tgcatggcac	tggganccac	540
agtggcccnna	aaaatcttca	aaaaggatgc	cccatcnatt	gaccccccaa	atgccactg	600
ccaacagggg	ctgccccacn	cncnnaacga	tgancnatt	gnacaagatc	tncntggtct	660
tnatnaacnt	gaaccctgcn	tngtggctcc	tgttcaggnc	cnnggcctga	cttctnaann	720
aangaactcn	gaagncccca	cngganannc	g			751

<210> 13
 <211> 729
 <212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(729)

<223> n = A,T,C or G

<400> 13

gagccaggcg	tccctctgcc	tgccactca	gtggcaacac	ccgggagctg	ttttgtcctt	60
tgtggancct	cagcagtncc	ctctttcaga	actcantgcc	aaganccctg	aacaggagcc	120
accatgcagt	gcttcagctt	cattaagacc	atgatgatcc	tcttcaattt	gctcatcttt	180
ctgtgtggtg	cagccctgtt	ggcagtgggc	atctgggtgt	caatcgatgg	ggcatccttt	240
ctgaagatct	tggggccact	gtcgtccagt	gccatgcagt	ttgtcaacgt	gggctacttc	300
ctcatcgag	ccggcggtgt	ggtcttagct	ctaggtttcc	tgggctgcta	tgggtgctaag	360
actgagagca	agtgtgccct	cgtgacgttc	ttcttcatcc	tcctcctcat	cttcattgct	420
gaggttgcaa	tgctgtggtc	gccttgggtg	acaccacaat	ggctgagcac	ttcctgacgt	480
tgctggtaat	gcctgccatc	aanaaaagat	tatgggttcc	caggaaanact	tcactcaagt	540
gttggaacac	caccatgaaa	gggtcaagt	gctgtggctt	cnnccaacta	tacggatttt	600
gaagantcac	ctacttcaaa	gaaaanagtg	cotttccccc	atttctgttg	caattgacaa	660
acgtcccaa	cacagccaat	tgaaaacctg	caccaacccc	aaanggtcc	ccaaccanaa	720
attnaaggg						729

<210> 14

<211> 816

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(816)

<223> n = A,T,C or G

<400> 14

tgctcttctt	caaagttggt	cttgttgcca	taacaaccac	cataggtaaa	gcgggcgcag	60
tgctcgctga	aggggttgta	gtaccagcgc	gggatgctct	ccttgccagag	tcctgtgtct	120
ggcaggtcca	cgcagtgcgc	tttgtcactg	gggaaatgga	tgcgctggag	ctcgtcaaag	180
cactcgtgtg	atttttcaca	ggcagcctcg	tccgacgcgt	cggggcagtt	gggggtgtct	240
tcacactcca	ggaaactgtc	natgcagcag	ccattgctgc	agcggaaactg	ggtgggctga	300
cangtgccag	agcacactgg	atggcgccct	tccatgnnan	gggccctgng	ggaaagtccc	360
tganccccan	anctgcctct	caaangcccc	accttgacac	ccccgacagg	ctagaatgga	420
atcttcttcc	cgaaggttag	ttnttcttgt	tgcccaancc	anccccntaa	acaaactctt	480
gcanatctgc	tccngggggg	tontantacc	ancgtgggaa	aagaacccca	ggcngcgaac	540
caancttggt	tggatncgaa	gcnataatct	notnttctgc	ttggtggaca	gcaccantna	600
ctgtnnanct	ttagnccntg	gtcctcntgg	gttgnncttg	aacctaatacn	ccnntcaact	660
gggacaaggt	aantngccnt	cctttnaatt	cccnancntn	ccccctggtt	tgggggtttt	720
cncnctecta	ccccagaaan	nccgtgttcc	cccccaacta	ggggccnaaa	ccnnttnttc	780
cacaacctn	ccccaccac	gggttcngnt	ggttng			816

<210> 15

<211> 783

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(783)

<223> n = A,T,C or G

<400> 15

ccaaggcctg	ggcaggcata	nacttgaagg	tacaacecca	ggaacccctg	gtgctgaagg	60
atgtggaaaa	cacagattgg	cgctactgc	gggtgacac	ggatgtcagg	gtagagagga	120
aagacccaaa	ccaggtggaa	ctgtggggac	tcaaggaang	cacctacctg	ttccagctga	180
cagtgactag	ctcagaccac	ccagaggaca	cgccaacgt	cacagtcaact	gtgctgtcca	240
ccaagcagac	agaagactac	tgctcgcgat	ccaacaangt	gggtcgtctg	cggggctctt	300
tcccacgctg	gtactatgac	cccacggagc	agatctgcaa	gagtttcgtt	tatggagget	360
gcttgggcaa	caagaacaac	taccttcggg	aagaagagt	cattctancc	tgtcnggggtg	420
tgcaagggtg	gcctttgana	ngcanctctg	gggtcangc	gactttcccc	cagggccct	480
ccatggaaag	gcgccatcca	ntgttctctg	gcacctgtca	gcccaccag	ttccgctgca	540
ncaatggctg	ctgcacnac	antttcctng	aattgtgaca	acacccccca	ntgcccccaa	600
ccctcccaac	aaagcttccc	tgttnaaaaa	tacnccantt	ggcttttnac	aaacnccgg	660
cncctcncntt	ttccccnntn	aacaaagggc	nctngcnttt	gaactgcccn	aaccnnggaa	720
tctnccnngg	aaaaantncc	ccccctggtt	cctnnaancc	cctcncnaa	anctncccc	780
ccc						783

<210> 16

<211> 801

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(801)

<223> n = A,T,C or G

<400> 16

gccccaatte	cagctgccac	accacccacg	gtgactgcat	tagttcggat	gtcatacaaa	60
agctgattga	agcaaccctc	tacttttttg	tcgtgagcct	tttgcttgg	gcaggtttca	120
ttggctgtgt	tggtgacgtt	gtcattgcaa	cagaatggg	gaaaggcact	gttctctttg	180
aagttagggg	agtcctcaaa	atccgtatag	ttgggtgaag	cacagcactt	gagcccttcc	240
atggtgggtg	tcacacactg	agtgaagtct	tcctgggaac	cataatcttt	cttgatggca	300
ggcactacca	gcaacgtcag	gaagtgtctc	gccattgtgg	tgtacaccaa	ggcgaccaca	360
gcagctgcaa	cctcagcaat	gaagatgagg	aggaggatga	agaagaacgt	cncgagggca	420
cacttgctct	ccgtcttagc	accatagcag	cccangaaac	caagagcaaa	gaccacaacg	480
cngctgcga	atgaaagaaa	ntaccacacgt	tgacaaaactg	catggccact	ggacgacagt	540
tgccccgaan	atcttcagaa	aagggtatgcc	ccatcgattg	aacacccana	tgcccactgc	600
cnacagggct	gcnccnccn	gaaagaatga	gccattgaag	aaggatcnc	ntggtcttaa	660
tgaactgaaa	cctgcatgg	tggccctgt	tcagggtct	tggcagtga	ttctganaaa	720
aaggaaacngc	ntnagcccc	ccaaangana	aaacaccccc	gggtgttgcc	ctgaattggc	780
ggccaaggan	ccctgccccn	g				801

<210> 17

<211> 740

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(740)

<223> n = A,T,C or G

<400> 17

gtgagagcca	ggcgtccctc	tgctgcca	ctcagtggca	acacccggga	gctgttttgt	60
cctttgtgga	gcctcagcag	ttccctcttt	cagaactcac	tgccaagagc	cctgaacagg	120
agccaccatg	cagtgttca	gcttcattaa	gacctgatg	atcctcttca	atttgctcat	180
ctttctgtgt	ggtgcagccc	tgttggcagt	gggcatctgg	gtgtcaatcg	atggggcatc	240
ctttctgaag	atcttcgggc	cactgtcgtc	cagtgccatg	cagtttgtca	acgtgggcta	300

```

cttcctcatc gcagccggcg ttgtggtctt tgctcttggg ttcctgggct gctatgggtgc 360
taagacggag agcaagtgtg ccctcgtgac gttcttcttc atcctcctcc tcattcttcat 420
tgctgaagtt gcagctgctg tggtcgcctt ggtgtacacc acaatggctg aaccattcct 480
gacgttgctg gtantgcctg ccatcaanaa agattatggg ttcccaggaa aaattcactc 540
aantntggaa caccnccatg aaaagggctc caatttctgn tggcttcccc aactataccg 600
gaattttgaa agantcnccc tacttccaaa aaaaaanant tgcctttnc cccnttctgt 660
tgcaatgaaa acntcccaan acngccaatn aaaacctgcc cnnncaaaaa ggntcncaaa 720
caaaaaaant nnaagggttn
740

```

```

<210> 18
<211> 802
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(802)
<223> n = A,T,C or G

```

```

<400> 18
ccgctgggtg cgctgggtcca gngnagccac gaagcacgtc agcatacaca gcctcaatca 60
caaggtcttc cagctgccgc acattacgca gggcaagagc ctccagcaac actgcataatg 120
ggatacactt tacttttagca gccagggtga caactgagag gtgtcgaagc ttattcttct 180
gaactctctgt tagtggagga agattccggg cttcagctaa gtagtccagc tatgtcccat 240
aagcaaacac tgtgagcagc cggaaggtag aggcaaagtc actctcagcc agctctctaa 300
cattgggcat gtccagcagt tctccaaaca cgtagacacc agnggcctcc agcacctgat 360
ggatgagtggt ggccagcgtt gccccttgg ccgacttggc taggagcaga aattgctcct 420
ggttctgccc tgtcaccttc acttcgcgac tcatcactgc actgagtgtg ggggacttgg 480
gtcaggatgt tccagagacg tggttccgcc ccctcnctta atgacaccgn ccanncaacc 540
gtcggctccc gccgantng ttcgtcgtnc ctgggtcagg gtctgctggc cncacttgc 600
aancttcgtc nggcccatgg aattcacnc accggaactn gtangatcca ctnttctat 660
aaccgngcgc caccgcnntt ggaactccac tcttnttnc tttacttgag ggttaaggtc 720
acccttncg ttacttgggt ccaaaccntn cntgtgtcg anatngtnaa tcnggncna 780
tncanccnc atangaagcc ng
802

```

```

<210> 19
<211> 731
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(731)
<223> n = A,T,C or G

```

```

<400> 19
cnaagcttcc aggtnacggg ccgcnaance tgaccnagg tancanaang cagncngcgg 60
gagcccaccg tcacngngng gngtctttat nggagggggc ggagccacat cnetggacnt 120
cntgaccca actcccncc ncnantgca gtgatgagtg cagaactgaa ggtnacgtgg 180
caggaacca gancaaannc tgctcnntc caagtccgcn nagggggcgg ggctggccac 240
gncatccnt cnagtgtgn aaagcccn cctgtctact tgtttggaga acngcnnga 300
catgccagn gttanataac nggcnagag tnannttgcc tctcccttc ggctgcgcan 360
cngtntgct tagnggacat aacctgacta cttaactgaa ccnngaate tncnccct 420
ccactaagct cagaacaaaa aacttcgaca ccactcantt gtcacctgnc tgetcaagta 480
aagtgtaccc catnccaat gntgctnga ngctctgnc tgcnttangt tcggtcctgg 540
gaagacctat caattnaagc tatgtttctg actgcctctt gctccctgna acaancnacc 600
cnnnntcca agggggggnc ggccccaat ccccccaacc ntnaattnan tttancccn 660
ccccnggcc cggccttita cnancntcn nnaacnggna aaacnnngc ttncccaac 720

```

nnaatccncc t

731

<210> 20
 <211> 754
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(754)
 <223> n = A,T,C or G

<400> 20

tttttttttt	tttttttttt	taaaaacccc	ctccattnaa	tgnaaacttc	cgaaattgtc	60
caaccccctc	ntccaaatnn	ccntttccgg	gnngggggtc	caaacccean	ttannnttgg	120
annttaaatt	aaatnttntt	tgngggnnna	ancnnaatgt	nangaaaagt	naaccanta	180
tnancttnaa	tncttgaaa	ccngtngntt	ccaaaaatnt	ttaaccctta	antccctccg	240
aaatngttna	nggaaaaccc	aantttctnt	aagggtgttt	gaaggntnaa	tnaaaanccc	300
nnccaattgt	tttngccac	gcctgaatta	attggnntcc	gntgttttcc	nttaaaanaa	360
ggnnancccc	ggttantnaa	tccccccnnc	cccaattata	ccganttttt	ttngaattgg	420
gancccnccg	gaattaacgg	ggnnnnntccc	tnttgggggg	cnggnncccc	ccccntccgg	480
ggttngggnc	aggnccnaat	tgtttaaggg	tccgaaaaat	ccctccnaga	aaaaaanctc	540
ccaggttgag	nnnggggttt	nccccccccc	cangggccct	ctcgnaaggt	tggggtttgg	600
ggggcctggg	attttntttc	ccctntttcc	tccccccccc	ccnggganag	aggttngngt	660
tttgntcnnc	ggccccnccn	aaganccttn	ccganttnan	ttaaatccnt	gcctnggcga	720
agtccttgn	aggntaaan	ggccccctnn	cggg			754

<210> 21
 <211> 755
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(755)
 <223> n = A,T,C or G

<400> 21

atcancccat	gaccccnac	nnngggaccnc	tcancgggnc	nnncnaccnc	cggccnatca	60
nngtnagnnc	actncnnttn	natcacnccc	cncnactac	gcccnanc	cnacgccta	120
nncanatncc	actganngcg	cgangtngan	ngagaaanct	nataccanag	ncaccanacn	180
ccagctgtcc	nanaangcct	nnnatacngg	nnnatccaat	ntgnancctc	cnaagtattn	240
nncnncanat	gattttcctn	anccgattac	ccntncccc	tanccctcc	cccccaacna	300
cgaaggcnct	ggncnnaagg	nngegnccnc	ccgctagntc	cccncaagt	cncnnccta	360
aactcancn	nattacncgc	ttcntgagta	tcactccccg	aatctcaccc	tactcaactc	420
aaaaanactn	gatacaaaat	aatncaagcc	tgnttatnac	actntgactg	ggtctctatt	480
ttagnngtcc	ntnaancntc	ctaatacttc	cagtctncct	tcnccaattt	ccnaanggct	540
ctttcngaca	gcatnttttg	gttcccnntt	gggttcttan	ngaattgcc	ttcntngaac	600
gggctcntct	tttccttcgg	ttancctggg	ttcnccgggc	cagttattat	ttcccntttt	660
aaattcntnc	cntttanttt	tggcnttcna	aacccccggc	cttgaaaacg	gccccctggt	720
aaaaggttgt	tttganaaaa	tttttgtttt	gttcc			755

<210> 22
 <211> 849
 <212> DNA
 <213> Homo sapien

<220>

<221> misc_feature
 <222> (1)...(849)
 <223> n = A,T,C or G

<400> 22
 tttttttttt tttttangtg tngtcgtgca ggtagaggct tactacaant gtgaanacgt 60
 acgtnggan taangcgacc cgantttctag gannccctt aaaatcanac tgtgaagatn 120
 atcctgnna cggaanggtc accggnggat nntgctaggg tgnccnctcc cannncttn 180
 cataactcng nggccctgcc caccacettc ggcgggccng ngcccgggcc cgggtcattn 240
 gnnttaaccn cactnngcna nccggtttccn nccccnng acccngggca tccggggtn 300
 tctgtcttcc cctgnagncn anaaantggg ccncggncct ctttaccctt nnacaagcca 360
 cngcenteta nccncngccc cccctccant nngggggact gccnanngt ccgtnctng 420
 nnaccccnnn gggtnccctcg gttgtcgant cnaccgnang ccanggatcc cnaaggaagg 480
 tgcgttnttg gcccctaccc ttcgctnccg nncacccttc ccgacnanga nccgctcccg 540
 cncnncgng cctcncctcg caacaccgc nctentcngt nccggnnccc ccccaccgc 600
 nccctcncnc ngncgnancn ctcnccncc gtctcannca ccaccgcgc ccgccaggcc 660
 ntcancacn ggngacnng nagnccnntc gcnccgcgn gcgncnccct cgcncngaa 720
 ctncntcngg ccantnccgc tcaancnna cnaaacgcg ctgcgcggcc cgnagcgncc 780
 nccctcncga gtccctccgn ctcccnacc angnttccn cgaggacacn nnaccccgcc 840
 nncangcgg 849

<210> 23
 <211> 872
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(872)
 <223> n = A,T,C or G

<400> 23
 gcgcaaaacta tacttcgctc gnaactcgtgc gcctcgtcnc tcttttcctc cgcaaccatg 60
 tctgacnanc ccgattnggc ngatatcnan aagntcganc agtccaaact gantaacaca 120
 cacacnncan aganaaatcc nctgccttcc anagtanacn attgaacnng agaaccange 180
 nggcgaatcg taatnaggcg tgcgcgcgcca atntgtcnc gtttatntn ccagctcnc 240
 ctncnacc ctaactcttcn nagctgtcnn acccctngtn cgnacccccc naggtcggga 300
 tcgggttttn nntgaccgng cnnccctcc cccctccat nacganccnc ccgcaccacc 360
 nanngcncgc ncccgnnct ctgcgcnc ccctgtngc ctggcncngn 420
 accgcattga ccctgcgcnn ctncnngaaa ncgnanacgt ccgggttggn annancgctg 480
 tgggnnngcg tctgcncgc gtcccttcn ncncttcca ccatcttnt tacngggtct 540
 ccncgcctc tcnncacnc cctgggagc tntcctntgc ccccttnac tccccccctt 600
 cgncgtgncc cgncccccacc ntcatttnca nacgntcttc acaannncct ggntnnctcc 660
 cnancngncn gtcancnag ggaagggngg ggnccnntg nttgacgttg ngngangtc 720
 cgaanantcc tcnccntcan cctaccct cggcggnct ctngttncc aacttancaa 780
 ntctcccccg ngngcncntc tcagcctcnc cnccccnct ctctgcantg tntctgctc 840
 tnaccnntac gantnttcgn cncctcttt cc 872

<210> 24
 <211> 815
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(815)
 <223> n = A,T,C or G

<400> 24

gcatgcaagc	ttgagtattc	tatagngtca	cctaaatanc	ttggcntaat	catggtcnta	60
nctgncttcc	tgtgtcaa	gtatacna	tanatatgaa	tctnatntga	caaganngt	120
tcntncatta	gtaacaantg	tnntgtccat	cctgtcngan	canattccca	tnnattncgn	180
cgcattcn	gcncantatn	taatngggaa	ntcnntnnn	ncaccnncat	ctatcntncc	240
gcncctgac	tggagagat	ggatnanttc	tnntntgacc	nacatgttca	tcttggattn	300
aanancccc	cgcngnccac	cggttngnng	cnagccnntc	ccaagacctc	ctgtggaggt	360
aacctgcgtc	aganncatca	aacntgggaa	acccgcnncc	angtnnaagt	ngnnncanan	420
gatcccggtc	aggnttnacc	atcccttcnc	agcgccccct	ttngtgcctt	anagnnagc	480
gtgtccnanc	cnetcaacat	ganacgcgcc	agnccanccg	caattnggca	caatgtcgnc	540
gaaccccccta	gggggantna	tncaaanccc	caggattgtc	cncncangaa	atcccnanc	600
ccnccctac	ccncttttg	gacngtgacc	aantcccgga	gtncagtc	ggccngnctc	660
ccccaccggt	nccntgggg	gggtgaanct	cngnntcanc	cngncgaggn	ntcgnaagga	720
accggncctn	ggncgaanng	ancnntcnga	agngccnct	cgtataacc	cccctcncca	780
ncenacngnt	agntcccccc	cngggtncgg	aangg			815

<210> 25

<211> 775

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(775)

<223> n = A,T,C or G

<400> 25

ccgagatgtc	tgcgtccgtg	gccttagctg	tgctcgcgct	actctctctt	tctggcctgg	60
aggctatcca	gcgtactcca	aagattcagg	tttactcacg	tcatccagca	gagaatggaa	120
agtcaaattt	cctgaattgc	tatgtgtctg	ggtttcatcc	atccgacatt	gaanttact	180
tactgaagaa	tgganagaga	attgaaaaag	tggagcattc	agacttgtct	ttcagcaagg	240
actgggtctt	ctatctcntg	tactacactg	aattcacccc	cactgaaaaa	gatgagtatg	300
cctgccgtgt	gaaccatgtg	actttgtcac	agcccaagat	agttaagtgg	gatcgagaca	360
tgtaaagcagn	cnnatggaa	gtttgaagat	gccgcatttg	gattggatga	attccaaatt	420
ctgcttgctt	gcntttta	antgatatgc	ntatacaccc	taccctttat	gncccaaat	480
tgtaggggtt	acatnantgt	tcnontngga	catgatcttc	ctttataant	ccnccnttcg	540
aattgcccgt	cncccngttn	ngaattgttc	cnaaaccacg	gttggetccc	ccaggtcncc	600
tcttacggaa	gggectgggc	cncctttncaa	gggtggggga	accnaaaatt	tcncttntgc	660
ccncccncca	cnnctcttng	nncncanttt	ggaacccttc	cnattccctt	tggectcnna	720
ncctttncta	anaaaacttn	aaancgtngc	naaanntttn	acttcccccc	ttacc	775

<210> 26

<211> 820

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(820)

<223> n = A,T,C or G

<400> 26

anattantac	agtgtaatct	tttcccagag	gtgtgtanag	ggaacggggc	ctagaggcat	60
cccanagata	ncttatanca	acagtgtctt	gaccaagagc	tgctgggcac	atttcctgca	120
gaaaagggtg	cgggtcccat	cactcctcct	ctcccatagc	catcccagag	gggtgagtag	180
ccatcangcc	ttcggtggga	gggagtcang	gaaacaacan	accacagagc	anacagacca	240
ntgatgacca	tgggcgggag	cgagcctctt	ccctgnaccg	gggtggcana	nganagccta	300
nctgaggggt	cacactataa	acgttaacga	ccnagatnan	cacctgtctc	aagtgcaccc	360

ttcctacctg	acnaccagng	accnnnaact	gengcctggg	gacagcncctg	ggancagcta	420
acnnagcact	cacctgcccc	cccatggcgg	tnegntccc	tggtcctgnc	aagggaagct	480
ccctgttgga	attncgggga	naccaaggga	nccccctcct	ccanctgtga	aggaaaaann	540
gatggaattt	tncccttccg	gccnntcccc	tcttccttta	cacgccccct	nntactcnc	600
tccctctntt	ntcctgncnc	acttttnacc	ccnnnatttc	ccttnattga	tcggannctn	660
ganattccac	tnnccgctnc	cntcnatcng	naanacnaaa	nactntctna	cccnggggat	720
gggnncctcg	ntcactcctc	ctttttcnct	accnccnntt	ctttgcctct	ccttngatca	780
tccaacntc	gntggccntn	ccccccnnn	tccttnccc			820

<210> 27

<211> 818

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(818)

<223> n = A,T,C or G

<400> 27

tctgggtgat	ggcctcttcc	tcctcagggg	cctctgactg	ctctgggcca	aagaatctct	60
tgtttcttct	ccgagcccca	ggcagcgggt	attcagccct	gccaacctg	attctgatga	120
ctgcggatgc	tgtgacggac	ccaaggggca	aatagggtcc	caggggccag	ggaggggcgc	180
ctgctgagca	cttcgcgccc	tcacctgcc	cagccctgc	catgagctct	gggctgggtc	240
tccgcctcca	gggttctgct	cttccangca	ngccancaag	tggcgctggg	ccacactggc	300
ttcttctgct	ccctccctg	gctctganc	tctgtcttcc	tgctctgtgc	angcnccttg	360
gatctcagtt	tccctcncct	anngaactct	gtttctgann	tcttcantta	actntgantt	420
tatnacnann	tggnctgtnc	tgtcnnactt	taatgggccc	gaccggctaa	tcctccctc	480
ntcccttcc	anttcnnnna	accngcttnc	cntctctccc	ccntancccg	ccnggggaanc	540
ctcctttgcc	ctnaccang	gccnnnaccg	ccctnnctn	ggggggcnnng	gtnnctncnc	600
ctgntnnccc	cncctcncnt	tnectcgtcc	cnnccnccgn	nngcannttc	ncngtcccn	660
tnnctcttcc	ngntctgnaa	ngntcncntn	tnnnnngncn	ngntnntncn	tcctctcnc	720
cnnntgnang	tnnttnnnnc	ncngnncccc	nnnnccnnnn	nggnnnntnn	tctncncngc	780
ccnncccccc	ngnattaagg	cctccnntct	ccggccnc			818

<210> 28

<211> 731

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(731)

<223> n = A,T,C or G

<400> 28

aggaagggcg	gagggatatt	gtangggatt	gagggatagg	agnataangg	gggaggtgtg	60
tccaacatg	anggtgnngt	tctcttttga	angaggggtg	ngtttttann	ccnggtgggt	120
gattnaaccc	cattgtatgg	agmnnaaggn	tttnagggat	ttttcggtct	ttatcagtat	180
ntanattcct	gtnaatcgga	aaatnatntt	tcnnccggaa	aatnttgcct	ccatccgnaa	240
attntcccg	ggtagtgc	nttngggggn	cngccangtt	tcccaggtct	ctanaatcgt	300
actaaagntt	naagtgggan	tncaaataaa	aacctnncc	agagnatccn	taccgcactg	360
tnnnntncc	tcgcccctng	actctgcnn	agcccaatac	ccnnngnngat	gtcncccngn	420
nnngcgncc	tgaaannnn	tcngngctnn	gancatcang	gggtttcgca	tcaaaagcnn	480
cgtttccat	naaggcactt	tngcctcatc	caaccnctng	ccctcnncca	tttngccgtc	540
nggttcncct	acgtntntng	cncctnnntn	ganattttnc	cgcctngggg	naancctcct	600
gnaatgggta	gggncttntc	ttttnacnnc	gnggtntact	aatcnnctnc	acgcntnctt	660
tctcnacccc	ccccctttt	caatcccanc	ggcnaatggg	gtctccccnn	cgangggggg	720

nnncccannc c

731

<210> 29
 <211> 822
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(822)
 <223> n = A,T,C or G

<400> 29
 actagtccag tgtggtggaa ttccattgtg ttggggncnc ttctatgant antnttagat 60
 cgctcanacc tcacancctc ccnacnangc ctataangaa nannaataga nctgtncnnt 120
 atntntacnc tcatanncct cnnnaccacac tccctcttaa cccntactgt gcctatngcn 180
 tnnctantct ntgccgcctn cnanccaccn gtggggccnac cncnngnatt ctcnatctcc 240
 tcnccatntn gcctananta ngtncatacc ctatacctac nccaatgcta nnnctaancn 300
 tccatnantt annntaacta ccaactgaent ngactttcnc atnanctcct aatttgaatc 360
 tactctgact cccacngcct annnattagc ancntcccc nacnatntct caaccaaatc 420
 ntcaacaacc tatctanctg ttcnccaacc nttncctccg atccccnnac aacccccctc 480
 ccaaataccc nccacctgac ncctaaccn caccatcccg gcaagccnan ggnccatttan 540
 ccactggaat cacnatngga naaaaaaac ccnaactctc tancncnat ctccctaana 600
 aatnctcctn naatttactn ncantnccat caancccaen tgaaacnnaa cccctgtttt 660
 tanatccctt ctttcgaaaa ccnacccttt annncccaac ctttngggcc ccccnctnc 720
 ccnaatgaag gncnccaat cnangaaacg nccntgaaaa ancnaggcna anannntccg 780
 canatcctat cccttanttn ggggnccctt nccnngggcc cc 822

<210> 30
 <211> 787
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(787)
 <223> n = A,T,C or G

<400> 30
 cgggcgcctg ctctggcaca tgcctcctga atggcatcaa aagtgatgga ctgcccattg 60
 ctagagaaga ccttctctcc tactgtcatt atggagccct gcagactgag ggctcccctt 120
 gtctgcagga tttgatgtct gaagtcgttg agtgtggctt ggagctcctc atctacatna 180
 gctggaagcc ctggagggcc tctctcgcca gcctccccct tctctccacg ctctccangg 240
 acaccagggg ctccaggcag cccattattc ccagnangac atggtgtttc tccacgcgga 300
 cccatggggc ctgnaaggcc agggctcctt ttgacaccat ctctccgctc ctgctggca 360
 ggccgtggga tccactantt ctanaacggg cgccaccncc gtgggagctc cagcttttgt 420
 tccnttaat gaaggttaat tgcncgcttg gcgtaatcat nggtcanaac tntttcctgt 480
 gtgaaattgt ttntccccct ncnattccnc ncnacatacn aaccgggaan cataaagtgt 540
 taaagccttg gggtnccctn nngaataaac tnaactcaat taattgcgtt ggctcatggc 600
 ccgctttccn ttcnggaaaa ctgtcntccc ctgcnttntt gaatcgcca ccccccnggg 660
 aaaagcgggt tgcnttttng ggggntcctt ccncttcccc cctcnctaan cctnccgct 720
 cggtcgttnc nggtngcggg gaanggggat nnnctcccnc naagggggng agnnngntat 780
 ccccaaa 787

<210> 31
 <211> 799
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(799)
 <223> n = A,T,C or G

<400> 31
 tttttttttt tttttttggc gatgctactg ttttaattgca ggaggtgggg gtgtgtgtac 60
 catgtaccag ggctattaga agcaagaagg aaggaggagg ggagagcgc cctgctgagc 120
 aacaaaggac tcctgcagcc ttctctgtct gtctcttggc gcaggcacat ggggaggcct 180
 cccgcagggt gggggccacc agtccagggt tgggagcact acanggggtg ggagtgggtg 240
 gtggctggtg cnaatggcct gncacanatc cctacgattc ttgacacctg gatttcacca 300
 ggggaccttc tgttctccca nggnaacttc nttnatctcn aaagaacaca actgtttctt 360
 cngcanttct ggctgttcat ggaaagcaca ggtgtccnat ttnggctggg acttggtaca 420
 tatggttccg gcccacctct cccntcnaaa aagtaattca ccccccccn cctctnttg 480
 cctgggccct taantaccca cccggaact canttantta ttcactctng gntgggcttg 540
 ntnatnccn cctgaangcg ccaagttgaa aggccacgcc gtneccnctc cccatagnan 600
 nttttnnct canctaagtc cccccnggc aacnatccaa tcccccccn tgggggcccc 660
 agcccanggc ccccgctcgc ggnnnccngn cncgnantcc ccaggtctc ccantcngnc 720
 ccnnngcncc cccgcacgca gaacanaagg ntngagccnc cgcannnnnn nggtnnac 780
 ctgcccccc ccnnccngg 799

<210> 32
 <211> 789
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(789)
 <223> n = A,T,C or G

<400> 32
 tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 60
 ttttncnag ggcaggttta ttgacaacct cncgggacac aancaggctg gggacaggac 120
 ggcaacaggc tccggcggcg gcgcgggcg ccctacctgc ggtaccaaatt ntgcagcctc 180
 cgctcccgcct tgatnttcct ctgcagctgc aggatgccnt aaaacagggc ctccggcctn 240
 ggtggggcacc ctgggatttn aatttccacg ggcacaatgc ggtcgcancc cctcaccacc 300
 nattaggaat agtggtnnta cccnccnccg ttggcncact ccccntggaa accactntc 360
 gcggctccgg catctggtct taaaccttgc aaacnctggg gccctctttt tggttantnt 420
 nccngccaca atcatnactc agactggcnc gggctggccc caaaaaancn ccccaaaacc 480
 ggnccatgtc tttnccgggt tgctgcnatn tncatcacct cccgggcnca ncaggncaac 540
 ccaaaagtgc ttgngggccn caaaaaanct cccgggggnc ccagtttcaa caaagtcac 600
 ccccttgccc cccaaatcct ccccccgnt nctgggttg ggaacccacg cctctnnctt 660
 tggngggcaa gntggntccc ccttcgggccc cccggtgggc ccnctctaa ngaaaaacnc 720
 ntccnnnca ccatccccc nngnnacgnc tancaangna tccctttttt tanaaacggg 780
 cccccnccg 789

<210> 33
 <211> 793
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(793)
 <223> n = A,T,C or G

<400> 33

gacagaacat	gttggatggt	ggagcacctt	tctatacgac	ttacaggaca	gcagatgggg	60
aattcatggc	tgttggagca	atanaacccc	agttctacga	gctgctgac	aaaggacttg	120
gactaaagtc	tgatgaactt	cccaatcaga	tgagcatgga	tgattggcca	gaaatgaana	180
agaagtttgc	agatgtatth	gcaaagaaga	cgaaggcaga	gtgggtgtcaa	atctttgacg	240
gcacagatgc	ctgtgtgact	ccggttctga	cttttgagga	ggttgttcat	catgatcaca	300
acaangaacg	gggtcgttt	atcaccantg	aggagcagga	cgtgagcccc	cgccctgcac	360
ctctgctgtt	aaacacccca	gccatccctt	ctttcaaaag	ggatccacta	cttctagagc	420
ggncgccacc	gcggtggagc	tccagctttt	gttcccttta	gtgagggtta	attgcgcgct	480
tggcgtaatc	atgggtcatan	ctgtttcctg	tgtgaaattg	ttatccgctc	acaattccac	540
acaacatacg	anccggaagc	atnaaatttt	aaagcctggn	ggtngcctaa	tgantgaact	600
nactcacatt	aattggcttt	gcgctcactg	cccgttttcc	agtccggaaa	acctgtcctt	660
gccagctgcc	nttaatgaat	cnggccaccc	cccggggaaa	aggcngtttg	cttnttgggg	720
cgccttccc	gctttctcgc	ttcctgaant	ccttcccccc	ggtctttcgg	cttgccgcn	780
acgtatcna	cct					793

<210> 34

<211> 756

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(756)

<223> n = A,T,C or G

<400> 34

gccgcgaccg	gcatgtacga	gcaactcaag	ggcgagtgga	accgtaaaag	ccccaatctt	60
ancaagtgcg	gggaanagct	gggtcgactc	aagctagttc	ttctggagct	caacttcttg	120
ccaaccacag	ggaccaagct	gaccaaacag	cagctaattc	tggcccgtga	catactggag	180
atcggggccc	aattggagcat	cctacgcaan	gacatccctt	ccttcgagcg	ctacatggcc	240
cagctcaaat	gctactactt	tgattacaan	gagcagctcc	ccgagtcagc	ctatatgcac	300
cagctcttgg	gcctcaacct	cctcttcttg	ctgtcccaga	accgggtggc	tgantnccac	360
acgganttgg	ancggctgcc	tgccaanga	catacanacc	aatgtctaca	tcnaccacca	420
gtgtcctgga	gcaatactga	tgganggcag	ctaccncaaa	gtnttcctgg	ccnagggtaa	480
catccccgcg	cgagagctac	accttcttca	ttgacatcct	gctcgacact	atcagggatg	540
aaaatcgcn	ggttgctcca	gaaaggctnc	aanaanatcc	ttttcnctga	aggcccgcg	600
atncnctagt	nctagaatcg	gcccgccatc	gcggtgganc	ctccaacctt	tcgttncctt	660
ttactgaggg	tttattgccg	cccttggcgt	tatcatggtc	acncngttn	cctgtgttga	720
aattnttaac	ccccacaaat	tccacgccna	catting			756

<210> 35

<211> 834

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(834)

<223> n = A,T,C or G

<400> 35

gggatctct	anactnacct	gnatgcattg	ttgtcgggtg	ggtcgctgtc	gatgaanatg	60
aacaggatct	tgcccttgaa	gctctcggct	gctgtnttta	agttgctcag	tctgccgtca	120
tagtcagaca	cncctctggg	caaaaaacan	caggatntga	gtcttgattt	cacctccaat	180
aatcttongg	gctgtctgct	cggtgaactc	gatgacnang	ggcagctggg	tgtgtntgat	240
aaantccanc	angttctcct	tggtagacct	cccttcaaag	ttgttccggc	cttcatcaaa	300
cttctnnaan	angannancc	canctttgtc	gagctggnat	ttgganaaca	cgtcactgtt	360

```

ggaaactgat cccaaatggt atgtcatcca tgcctctgct tgcctgcaaa aaacttgctt 420
ggcncaaata cgactcccn tccttgaaag aagccnatca cccccctc cctggactcc 480
nncaangact ctnccgctnc ccntccnng cagggttggg ggcanccgg gccntgcgc 540
ttcttcagcc agttcacnat ntcatcagc cctctgcca gctgtntat tccttggggg 600
ggaanccgct tctcccttcc tgaannaact ttgaccgtng gaatagccgc gcntcncnt 660
acntnctggg cggggttcaa antccctccn ttgncntcn cctcgggcca ttctggattt 720
nccnaacttt ttccttcccc cccccnccg ngtttgntt tttcatnggg ccccaactct 780
gctnttgcc antccctgg gggcntntan cccccctnt ggtccntng gcc 834

```

```

<210> 36
<211> 814
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(814)
<223> n = A,T,C or G

```

```

<400> 36
cgngcgttt ccngccgcgc ccggtttcca tgacnaaggc tcccttcang ttaaatacnn 60
cctagnaaac attaatgggt tgctctacta atacatcata cnaaccagta agcctgccc 120
naacgccaac tcaggccatt cctaccaaag gaagaaaggc tggctctctc accccctgta 180
ggaaaggcct gccttgtaag acaccacaat ncggctgaat ctnaagtctt gtgttttact 240
aatggaaaaa aaaaataaac aanaggtttt gttctcatgg ctgccaccg cagcctggca 300
ctaaaacanc ccagcgtca cttctgcttg ganaaatatt ctttgcctt ttggacatca 360
ggcttgatgg tatcactgcc acntttccac ccagctgggc ncccttccc catntttgtc 420
antganctgg aaggcctgaa ncttagtctc caaaagtctc ngcccacaag accggccacc 480
aggggagtc ntttncagtg gatctgccc anantaccn tatcatcnnt gaataaaaag 540
gcccctgaac ganatgttc cancancctt taagacccat aatcctngaa ccatgggtgcc 600
cttcggctct gctcnaaag gaatgttct gggctccant cctcctttg ttntttact 660
tgtnttgac cntgtctn atnaccaan tganatccc ngaagcacc tncctctggc 720
atgtgantt cntaaattct ctgcctacn nctgaaagca cnattccctn ggcnccnaan 780
ggngaactca agaaggtctn ngaaaaacca cncn 814

```

```

<210> 37
<211> 760
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(760)
<223> n = A,T,C or G

```

```

<400> 37
gcatgctgct cttcctcaaa gttgttcttg ttgccataac aaccaccata ggtaaagcgg 60
gcgcagtgtt cgctgaagg gttgtagtac cagcgcgga tgctctcctt gcagagtctt 120
gtgtctggca ggtccacgca atgcccttg tcaactggga aatggatgcg ctggagctcg 180
tcnaanccac tcgtgtattt ttcacangca gcctcctccg aagctccgg gcagtgggg 240
gtgtcgtcac actccactaa actgtcgatn cancagccca ttgctgcagc ggaactgggt 300
gggctgacag gtgacgaac acactggatn ggcctttcca tggaaaggcc tgggggaaat 360
cncctnancc caaactgcct ctcaaaggcc accttgaca ccccgacagg ctagaaatgc 420
actcttcttc ccaaaggtag ttgttcttg tgcccaagca ncctccanca aaccaaaanc 480
ttgcaaaatc tgctccgtgg gggctatnnn taccanggtt ggggaaanaa acccgcnng 540
ganccnctt gtttgaatgc naaggnaata atcctcctgt cttgcttggg tggaanagca 600
caattgaact gtaacnttg ggccngtgc cncnnggtg gtctgaaact aatcaccgtc 660
actggaaaaa ggtangtgcc ttccttgaat tcccaaant cccctngntt tgggtnttt 720

```

ctcctctncc ctaaaaatcg tnttcccccc cntanggcg

760

<210> 38
 <211> 724
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc_feature
 <222> (1)...(724)
 <223> n = A,T,C or G

<400> 38
 tttttttttt tttttttttt tttttttttt tttttaaaaa cccctcccat tgaatgaaaa 60
 cttcnaaat tgtccaaccc cctcnnecaa atnnccattt ccgggggggg gttccaaacc 120
 caaattaatt ttgganttta aattaaatnt tnatngggg aanaanccaa atgtnaagaa 180
 aatttaaccc attatnaact taaatnccn gaaaccntg gnttccaaaa atttttaacc 240
 cttaaatccc tccgaaattg ntaanggaaa accaaattcn cctaaggctn tttgaagggt 300
 ngatttaaac ccccttnant tnttttnacc cnnngctnaa ntattngnt tccggtgttt 360
 tcctnttaan cntnggtaac tcccgntaat gaannnccct aanccaatta aaccgaattt 420
 tttttgaatt ggaaattccn ngggaattna ccgggggttt tccnttttg gggccatncc 480
 cccnctttcg gggtttgggn taggttgaa tttttnnang ncccaaaaaa ncccccaana 540
 aaaaaactcc caagnnttaa ttngaattnc ccccttccca ggccttttg gaaaggnggg 600
 tttntggggg ccngggantt cnttccccn ttncncccc ccccccnggt aaanggttat 660
 ngnntttggt ttttgggcc cttnanggac cttccggatn gaaattaaat ccccggnncg 720
 gccg 724

<210> 39
 <211> 751
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc_feature
 <222> (1)...(751)
 <223> n = A,T,C or G

<400> 39
 tttttttttt tttttctttg ctcacattta atttttattt tgattttttt taatgctgca 60
 caacacaata tttatttcat ttgtttcttt tatttcattt tatttgttg ctgctgctgt 120
 tttatttatt tttactgaaa gtgagaggga acttttggtg ccttttttcc tttttctgta 180
 ggccgcctta agcttttctaa atttggaaca tctaagcaag ctgaanggaa aagggggttt 240
 cgcaaaatca ctcgggggaa nggaaagggt gctttgttaa tcatgcccta tgggtgggtga 300
 ttaactgctt gtacaattac ntttcacttt taattaattg tgctnaange ttttaattana 360
 cttggggggt cctccccan accaaccn ctgacaaaaa gtgccngccc tcaaatnatg 420
 tcccggcnnt cnttgaaaca cacngcngaa ngttctcatt ntccccncnc caggtnaaaa 480
 tgaagggtta ccatntttta cncacctcc acntggcnnn gcctgaatcc tcnaaaancn 540
 ccctcaancn aattnctnng ccccggtcnc gcntnngtcc cncccgggct ccgggaantn 600
 cacccccnga anncnntnnc naacnaaatt ccgaaaatat tcccnntcnc tcaattcccc 660
 cnnagactnt cctcnncnan cncaattttc ttttntcac gaacncggnnc cnnaaatgn 720
 nnnncnctc cncnngtcn naatcnccan c 751

<210> 40
 <211> 753
 <212> DNA
 <213> Homo sapien

<220>

<221> misc_feature
 <222> (1)...(753)
 <223> n = A,T,C or G

<400> 40
 gtgggtatttt ctgtaagatc aggtgttcct ccctcgtagg tttagaggaa acaccctcat 60
 agatgaaaac cccccgaga cagcagcaact gcaactgcca agcagccggg gtaggagggg 120
 cgccctatgc acagctgggc ccttgagaca gcagggttc gatgtcaggc tcgatgtcaa 180
 tggctctgaa gcggcggtg tacctgcgta ggggcacacc gtcagggcc accaggaact 240
 tctcaaagtt ccaggcaacn tcgttgcgac acaccggaga ccagggtatn agcttgggg 300
 cggtcataa cgcgggtggc tcgtcgctgg gagctggcag ggcctccgc aggaaggcna 360
 ataaaagggt gcggcccgca ccgttcant cgcacttctc naanaccatg angttgggct 420
 cnaaccacc accannccgg acttccttga nggaattccc aaatctcttc gntctggggc 480
 ttctnctgat gccctanctg gttgcccn gn atgccaanca nccccaancc ccggggctct 540
 aaanaccn cctcctcctt tcatctgggt tntntcccc ggacctgggt tcctctcaag 600
 ggancaccn tctcnaccn tactcacnt ncccccnt gnnaccanc cttctanngn 660
 ttccncccg nccctctggc cntcaaanan gcttnacna cctgggtctg ccttcccccc 720
 tncctatct gnaccnncn tttgtctcan tnt 753

<210> 41
 <211> 341
 <212> DNA
 <213> Homo sapien

<400> 41
 actatatcca tcacaacaga catgcttcat cccatagact tcttgacata gcttcaaag 60
 agtgaacca tcttgattt atatacatat atgttctcag tattttggga gcctttccac 120
 ttctttaaac cttgttcatt atgaacactg aaaataggaa tttgtgaaga gttaaaaagt 180
 tatagcttgt ttacgtagta agtttttgaa gtctacattc aatccagaca cttagttgag 240
 tgttaaactg tgatttttaa aaaatatcat ttgagaatat tctttcagag gtattttcat 300
 ttttactttt tgattaattg tgttttataat attagggtag t 341

<210> 42
 <211> 101
 <212> DNA
 <213> Homo sapien

<400> 42
 acttactgaa tttagttctg tgccttctc tatttagtgt tgtatcataa atactttgat 60
 gtttcaaaca ttctaaataa ataattttca gtggcttcat a 101

<210> 43
 <211> 305
 <212> DNA
 <213> Homo sapien

<400> 43
 acatctttgt tacagtctaa gatgtgttct taaatcacca ttccttctg gtcctcacc 60
 tccagggtg tctcactg taattagagc tattgaggag tctttacagc aaattaagat 120
 tcagatgcct tgctaagtct agagttctag agttatgtt cagaaagtct aagaaaccca 180
 cctcttgaga ggtcagtaaa gaggacttaa tatttcatat ctacaaaatg accacaggat 240
 tggatacaga acgagagtta tcttgataa ctcagagctg agtacctgcc cgggggccc 300
 tcgaa 305

<210> 44
 <211> 852
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(852)
 <223> n = A,T,C or G

<400> 44
 acataaatat cagagaaaag tagtctttga aatatttacg tccaggagtt ctttgtttct 60
 gattatttgg tgtgtgtttt gggttgtgtc caaagtattg gcagcttcag ttttcatttt 120
 ctctccatcc tcgggcattc ttcccaaatt tatataccag tcttcgtcca tccacacgct 180
 ccagaatttc tctttttag tagtatctca tagctcggct gagcttttca taggtcatgc 240
 tgctgttggc cttcttttta ccccatagct gagccactgc ctctgatttc aagaacctga 300
 agacgccctc agatcgggtc tcccatttta ttaatcctgg gttcttgtct gggttcaaga 360
 ggatgtcgcg gatgaattcc cataagttag tccctctcgg gttgtgcttt ttggtgtggc 420
 acttggcagg ggggtcttgc tcctttttca tctcaggtag ctctgcaaca ggaaggtgac 480
 tgggtggttg catggagatc tgagcccggc agaaagtatt gctgtccaac aaatctactg 540
 tgctaccata gttggtgtca tataaatagt tctngtcttt ccagggtgtc atgatggaag 600
 gctcagtttg ttcagtcttg acaatgacat tgtgtgtgga ctggaacagg tcactactgc 660
 actggccggt ccacttcaga tgctgcaagt tgctgtagag gagntgccc gccgtccctg 720
 ccgccgggt gaactcctgc aaactcatgc tgcaaagggt ctgccggtg atgtcgaact 780
 cntggaaagg gatacaattg gcatccagct ggttgggtgc caggaggtga tggagccact 840
 cccacacctg gt 852

<210> 45
 <211> 234
 <212> DNA
 <213> Homo sapien

<400> 45
 acaacagacc cttgctcgtc aacgacctca tgcctcatca gttggacgaa tccgtgtccg 60
 agtctgacac catccggagc atcagcattg cttcgcagtg ccctaccgcg gggaaactctt 120
 gcctcgtttc tggtcggggt ctgctggcga acggcagaat gcctaccgtg ctgcagtgcg 180
 tgaacgtgtc ggtggtgtct gaggaggtct gcagtaagct ctatgacctg ctgt 234

<210> 46
 <211> 590
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(590)
 <223> n = A,T,C or G

<400> 46
 actttttatt taaatgttta taaggcagat ctatgagaat gatagaaaac atggtgtgta 60
 atttgatagc aatatttttg agattacaga gtttttagtaa ttaccaatta cacagttaaa 120
 aagaagataa tatattccaa gcanatacaa aatatctaata gaaagatcaa ggcaggaaaa 180
 tgantataac taattgacaa tggaaaatca attttaatgt gaattgcaca ttatccttta 240
 aaagctttca aaanaaanaa ttattgcagt ctanttaatt caaacagtgt taaatggat 300
 caggataaan aactgaagg canaaaagaat taattttcac ttcagttaac ncacccan 360
 ttacaatggc ttaaatgcan ggaaaaagca gtggaagtag ggaagtantc aaggtctttc 420
 tggctctctaa tctgccttac tctttgggtg tggctttgat cctctggaga cagctgccag 480
 ggctcctgtt atatccacaa tcccagcagc aagatgaagg gatgaaaag gacacatgct 540
 gccttccttt gaggagactt catctcactg gccaacactc agtcacatgt 590

<210> 47
 <211> 774

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(774)

<223> n = A,T,C or G

<400> 47

acaagggggc	ataatgaagg	agtggggana	gattttaaag	aaggaaaaaa	aacgaggccc	60
tgaacagaat	tttcctgnac	aacggggctt	caaaataatt	ttcttgggga	ggttcaagac	120
gcttcactgc	ttgaaactta	aatggatgtg	ggacanaatt	ttctgtaatg	accctgaggg	180
cattacagac	gggactctgg	gaggaaggat	aaacagaaag	gggacaaagg	ctaataccaa	240
aacatcaaag	aaaggaaggt	ggcgtcatat	ctcccagcct	acacagttct	ccagggctct	300
cctcatccct	ggaggacgac	agtggaggaa	caactgacca	tgtccccagg	ctcctgtgtg	360
ctggctcctg	gtcttcagcc	cccagctctg	gaagcccacc	ctctgtgat	cctgcgtggc	420
ccacactcct	tgaacacaca	tcccaggtt	atattcctgg	acatggctga	acctcctatt	480
cctacttccg	agatgccttg	ctccctgcag	cctgtcaaaa	tcccactcac	cctccaaacc	540
acggcatggg	aagcctttct	gacttgcttg	attactccag	catcttgga	caatccctga	600
ttcccactc	cttagaggca	agatagggtg	gttaagagta	gggctggacc	acttgagacc	660
aggctgctgg	cttcaaattn	tggctcattt	acgagctatg	ggaccttggg	caagtnatct	720
tcacttctat	gggcntcatt	ttgttctacc	tgcaaaatgg	gggataataa	tagt	774

<210> 48

<211> 124

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(124)

<223> n = A,T,C or G

<400> 48

canaaattga	aattttataa	aaaggcattt	ttctcttata	tccataaaat	gatataattt	60
ttgcaantat	anaaatgtgt	cataaattat	aatgttcctt	aattacagct	caacgcaact	120
tggt						124

<210> 49

<211> 147

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(147)

<223> n = A,T,C or G

<400> 49

gcgatgcta	ctattttatt	gcaggaggtg	ggggtgtttt	tattattctc	tcaacagctt	60
tgtggctaca	ggtggtgtct	gactgcatna	aaaanttttt	tacgggtgat	tgcaaaaatt	120
ttagggcacc	catatcccaa	gcantgt				147

<210> 50

<211> 107

<212> DNA

<213> Homo sapien

<400> 50
acattaaatt aataaaagga ctgttggggt tctgctaaaa cacatggctt gatataattgc 60
atggtttgag gttaggagga gttaggcata tgttttggga gaggggt 107

<210> 51
<211> 204
<212> DNA
<213> Homo sapien

<400> 51
gtcctaggaa gtctagggga cacacgactc tgggggtcacg gggccgacac acttgcacgg 60
cgggaaggaa aggcagagaa gtgacaccgt cagggggaaa tgacagaaag gaaaatcaag 120
gccttgcaag gtccagaaag ggactcaggg cttccaccac agccctgccc cacttggcca 180
cctccctttt gggaccagca atgt 204

<210> 52
<211> 491
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(491)
<223> n = A,T,C or G

<400> 52
acaaagataa catttatctt ataacaaaaa tttgatagtt ttaaaggtta gtatttgtta 60
gggtattttc caaaagacta aagagataac tcaggtaaaa agttagaaat gtataaaaca 120
ccatcagaca ggttttttaa aaacaacata ttacaaaatt agacaatcat ccttaaaaaa 180
aaaacttctt gtatcaattt cttttgttca aaatgactga ctttaantatt tttaaattatt 240
tcanaaacac ttcctcaaaa attttcaana tggtagcttt canatgtnc ctcagtccca 300
atgttgetca gataaataaa tctcgtgaga acttaccacc caccacaagc tttctggggc 360
atgcaacagt gtcttttctt tnccttttct tttttttttt ttacaggcac agaaactcat 420
caattttatt tggataacaa aggttctcca aattatattg aaaaataaat ccaagttaat 480
atcactcttg t 491

<210> 53
<211> 484
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(484)
<223> n = A,T,C or G

<400> 53
acataattta gcagggctaa ttaccataag atgctattta ttaanaggtn tatgatctga 60
gtattaacag ttgctgaagt ttgggtatttt tatgcagcat tttctttttg ctttgataac 120
actacagaac cottaaggac actgaaaatt agtaagtaaa gttcagaaac attagctgct 180
caatcaaate tctacataac actatagtaa ttaaaacgtt aaaaaaaagt gttgaaatct 240
gcactagtat anaccgctcc tgtcaggata anactgcttt ggaacagaaa gggaaaaanc 300
agctttgant ttctttgtgc tgatangagg aaaggctgaa ttaccttggt gcctctccct 360
aatgattggc aggtcnggta aatnccaaaa catattccaa ctcaacactt cttttccncg 420
tancttgant ctgtgtattc caggancagg cggatggaat gggccagccc ncggatgttc 480
cant 484

<210> 54

<211> 151
 <212> DNA
 <213> Homo sapien

<400> 54
 actaaacctc gtgcttgtga actccataca gaaaacggtg ccatccctga aacgggtgg 60
 ccactgggta tactgctgac aaccgcaaca aaaaaaacac aaatccttgg cactggctag 120
 tctatgtcct ctcaagtgcc tttttgtttg t 151

<210> 55
 <211> 91
 <212> DNA
 <213> Homo sapien

<400> 55
 acctggcttg tctccgggtg gttcccggtg cccccacgg tccccagaac ggacactttc 60
 gccctccagt ggatactga gccaaagtgg t 91

<210> 56
 <211> 133
 <212> DNA
 <213> Homo sapien

<400> 56
 ggcggtatgt cggttggttat atacaaatat gtcattttat gtaagggact tgagtatact 60
 tggatttttg gtatctgtgg gttgggggga cgggtccagga accaataccc catggatacc 120
 aagggacaac tgt 133

<210> 57
 <211> 147
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)... (147)
 <223> n = A,T,C or G

<400> 57
 actctggaga acctgagccg ctgtccgcc tctgggatga ggtgatgcan gcngtggcgc 60
 gactgggagc tgagcccttc cttttgcgcc tgcctcagag gattgttgcc gacntgcana 120
 tctcantggg ctggatncat gcagggt 147

<210> 58
 <211> 198
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)... (198)
 <223> n = A,T,C or G

<400> 58
 acagggatat aggtttnaag ttattgtnat tgtaaaatac attgaatttt ctgtatactc 60
 tgattacata cttttatcct ttaaaaaaga tgtaaatctt aatttttatg ccatctatta 120
 atttaccat gagttacctt gtaaatgaga agtcatgata gcactgaatt ttaactagtt 180
 ttgacttcta agtttggt 198

<210> 59
 <211> 330
 <212> DNA
 <213> Homo sapien

<400> 59
 acaacaaatg ggttgtgagg aagtcttatac agcaaaactg gtgatggcta ctgaaaagat 60
 ccattgaaaa ttatcattaa tgattttaaa tgacaagtta tcaaaaactc actcaatttt 120
 cacctgtgct agcttgctaa aatgggagtt aactctagag caaatatagt atcttctgaa 180
 tacagtcaat aaatgacaaa gccagggcct acaggtggtt tccagacttt ccagaccag 240
 cagaaggaat ctattttatc acatggatct ccgtctgtgc tcaaaatacc taatgatatt 300
 ttctgtcttt attggacttc ttgaagagt 330

<210> 60
 <211> 175
 <212> DNA
 <213> Homo sapien

<400> 60
 accgtgggtg ccttctacat tcctgacggc tccttcacca acatctggtt ctacttcggc 60
 gtcgtgggct ccttcctctt catcctcacc cagctgggtg tgcctatcga ctttgccgac 120
 tcctggaacc agcgggtggc gggcaaggcc gaggagtgcg attcccgtgc ctggt 175

<210> 61
 <211> 154
 <212> DNA
 <213> Homo sapien

<400> 61
 accccacttt tcctcctgtg agcagtctgg acttctcact gctacatgat gaggggtgagt 60
 ggttgttgc cttcaacagt atcctccctt ttcgggatct gctgagccgg acagcagtgc 120
 tggactgcac agccccgggg ctccacattg ctgt 154

<210> 62
 <211> 30
 <212> DNA
 <213> Homo sapien

<400> 62
 cgctcgagcc ctatagttag tcgtattaga 30

<210> 63
 <211> 89
 <212> DNA
 <213> Homo sapien

<400> 63
 acaagtcatt tcagcaccct ttgctcttca aaactgacca tcttttatat ttaatgcttc 60
 ctgtatgaat aaaaatggtt atgtcaagt 89

<210> 64
 <211> 97
 <212> DNA
 <213> Homo sapien

<400> 64
 accggagtaa ctgagtcggg acgctgaatc tgaatccacc aataaataaa ggttctgcag 60

aatcagtgc tccaggattg gtccttgat ctggggg

97.

<210> 65
 <211> 377
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc_feature
 <222> (1) ... (377)
 <223> n = A,T,C or G

<400> 65
 acaacaanaa ntcccttctt taggccactg atggaaacct ggaacccctt tttgatggca 60
 gcatggcgct ctaggccttg acacagcggc tgggggtttg gctntcccaa accgcacacc 120
 ccaaccctgg tctaccaca nttctggcta tgggctgtct ctgccactga acatcagggt 180
 tcggtcataa natgaaatcc caanggggac agaggtcagt agaggaaagt caatgagaaa 240
 ggtgctgttt gctcagccag aaaacagctg cctggcattc gccgctgaac tatgaacccg 300
 tgggggtgaa ctacccccc gaggaatcat gcctgggcga tgcaanggtg ccaacaggag 360
 gggcgggagg agcatgt 377

<210> 66
 <211> 305
 <212> DNA
 <213> Homo sapien

<400> 66
 acgcctttcc ctcagaattc agggaagaga ctgtgcctg ccttctccg ttgttgcgtg 60
 agaaccctg tgccccttcc caccatatcc accctcgctc catctttgaa ctcaaacacg 120
 aggaactaac tgcaccctgg tctctctccc agtccccagt tcacctoca tccctcacct 180
 tcctccactc taagggatat caacactgcc cagcacaggg gccctgaatt tatgtggttt 240
 ttatatattt ttttaataaga tgcactttat gtcatttttt aataaagtct gaagaattac 300
 tgttt 305

<210> 67
 <211> 385
 <212> DNA
 <213> Homo sapien

<400> 67
 actacacaca ctccacttgc ctttgtgaga cactttgtcc cagcacttta ggaatgctga 60
 ggtcggacca gccacatctc atgtgcaaga ttgccagca gacatcagggt ctgagagttc 120
 cccttttaaa aaaggggact tgcttaaaaa agaagtctag ccacgattgt gtagagcagc 180
 tgtgctgtgc tggagattca cttttgagag agttctcctc tgagacctga tctttagagg 240
 ctgggcagtc ttgcacatga gatggggctg gtctgatctc agcactcctt agtctgcttg 300
 cctctcccag ggccccagcc tggccacacc tgcttacagg gcactctcag atgccatac 360
 catagtttct gtgctagtgg accgt 385

<210> 68
 <211> 73
 <212> DNA
 <213> Homo sapien

<400> 68
 acttaaccag atatattttt accccagatg gggatattct ttgtaaaaaa tgaaaataaa 60
 gtttttttaa tgg 73

<210> 69

<211> 536
 <212> DNA
 <213> Homo sapien
 <220>
 <221> misc_feature
 <222> (1)...(536)
 <223> n = A,T,C or G

<400> 69
 actagtccag tgtggtggaa ttccattgtg ttgggggctc tcaccctcct ctctgcagc 60
 tccagctttg tgctctgcct ctgaggagac catggcccag catctgagta ccctgctgct 120
 cctgctggcc accctagctg tggccctggc ctggagcccc aaggaggagg ataggataat 180
 cccgggtggc atctataacg cagacctcaa tgatgagtgg gtacagcgtg cccttcactt 240
 cgccatcagc gagtataaca aggccaccaa agatgactac tacagacgtc cgctgcgggt 300
 actaagagcc aggcaacaga ccgttggggg ggtgaattac ttcttcgacg tagaggtggg 360
 ccgaaccata tgtaccaagt cccagcccaa cttaggacacc tgtgccttcc atgaacagcc 420
 agaactgcag aagaaacagt tgtgtctctt cgagatctac gaagttccct ggggagaaca 480
 gaangtccct ggggtgaaatc caggtgtcaa gaaatcctan ggatctgttg ccaggc 536

<210> 70
 <211> 477
 <212> DNA
 <213> Homo sapien

<400> 70
 atgacccta acaggggccc tctcagccct cctaattgacc tccggcctag coattgtgatt 60
 tcacttccac tccataacgc tccatcactt aggcctacta accaaccacac taaccatata 120
 ccaatgatgg cgcgatgtaa cagagaaaag cacataccaa ggccaccaca caccacctgt 180
 ccaaaaaggc cttcgatacg ggataatcct atttattacc tcagaagttt ttttcttcgc 240
 agggattttt ctgagccttt taccactcca gcctagcccc taccceccaa ctaggagggc 300
 actggcccc aacaggcctc accccgctaa atcccctaga agtcccactc ctaaacacat 360
 ccgtattact cgcacagga gtatcaatca cctgagctca ccatagtcta atagaaaaca 420
 accgaaacca aattattcaa agcactgctt attacaattt tactgggtct ctatttt 477

<210> 71
 <211> 533
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(533)
 <223> n = A,T,C or G

<400> 71
 agagctatag gtacagtgtg atctcagctt tgcaaacaca ttttctacat agatagtact 60
 aggtattaat agatatgtaa agaaagaaat cacaccatta ataattgtaa gattggttta 120
 tgtattttta gtggtatttt tggcaccctt atatattgtt tccaaacttt cagcagtgat 180
 attattttca taacttaaaa agtgagtttg aaaaagaaaa tctccagcaa gcatctcatt 240
 taaataaagg tttgtcatct ttaaaaatac agcaatatgt gactttttta aaaagctgtc 300
 aaataggtgt gaccctacta ataattatta gaaatacatt taaaaacatc gagtacctca 360
 agtcagtttg ccttgaaaaa tatcaaatat aactcttaga gaaatgtaca taaaagaatg 420
 cttcgtaatt ttggagtang aggttccctc ctcaattttg tttttttaaa aagtacatgg 480
 taaaaaaaaa aattcacaac agtatataag gctgtaaaat gaagaattct gcc 533

<210> 72
 <211> 511

<212> DNA
 <213> Homo sapien
 <220>
 <221> misc_feature
 <222> (1)...(511)
 <223> n = A,T,C or G

<400> 72
 tattacggaa aaacacacca cataattcaa ctancaaaga anactgcttc agggcgtgta 60
 aaatgaaagg cttccaggca gttatctgat taaagaacac taaaagaggg acaaggctaa 120
 aagccgcagg atgtctacac tatancaggc gctatctggg ttggctggag gagctgtgga 180
 aaacatggan agattgggtgc tgganacgc cgtggctatt cctcattgtt attacanagt 240
 gaggttctct gtgtgcccac tggtttgaaa accgttctnc aataatgata gaatagtaca 300
 cacatgagaa ctgaaatggc ccaaaccag aaagaaagcc caactagatc ctcagaanac 360
 gcttctaggg acaataaccg atgaagaaaa gatggcctcc ttgtgcccc gtctgttatg 420
 atttctctcc attgcagcna naaaccggtt cttctaagca aacncagggtg atgatggcna 480
 aaatacaccc cctcttgaag naccnggagg a 511

<210> 73
 <211> 499
 <212> DNA
 <213> Homo sapien
 <220>
 <221> misc_feature
 <222> (1)...(499)
 <223> n = A,T,C or G

<400> 73
 cagtgccagc actggtgccca gtaccagtac caataacagt gccagtgccca gtgccagcac 60
 cagtgggtggc ttcagtgtctg gtgccagcct gaccgccact ctcacatttg ggctcttcgc 120
 tggccttggg ggagctgggt ccagcaccag tggcagctct ggtgcctgtg gtttctccta 180
 caagtgagat ttagatatt gttaatcctg ccagtcttct tcttcaagcc aggggtgcac 240
 ctcagaaacc tactcaacac agcaactctag gcagccacta tcaatcaatt gaagttagaca 300
 ctctgcatta aatctatttg ccatttctga aaaaaaaaaa aaaaaaaggg cggccgctcg 360
 antctagagg gcccggttaa acccgctgat cagcctcgac tgtgccttct anttgccagc 420
 catctgttgt ttgccctcc cccgntgcct tccttgacc tggaaagtgc cactcccact 480
 gtcccttctc aantaaat 499

<210> 74
 <211> 537
 <212> DNA
 <213> Homo sapien
 <220>
 <221> misc_feature
 <222> (1)...(537)
 <223> n = A,T,C or G

<400> 74
 tttcatagga gaacacactg aggagatact tgaagaattt ggattcagcc gcgaagagat 60
 ttatcagctt aactcagata aaatcattga aagtaataag gtaaaagcta gtctctaact 120
 tccaggccca cggtcaagt gaatttgaat actgcattta cagtgtagag taacacataa 180
 cattgtatgc atggaaacat ggaggaacag tattacagtg tcctaccact ctaatcaaga 240
 aaagaattac agactctgat tctacagtga tgattgaatt ctaaaaatgg taatcattag 300
 ggcttttgat ttataanact ttgggtactt atactaaatt atggtagtta tactgccttc 360
 cagtttgctt gatataattt ttgatattaa gattcttgac ttatattttg aatgggttct 420

actgaaaaan gaatgatata ttcttgaaga catcgatata catttattta cactcttgat 480
tctacaatgt agaaaatgaa ggaaatgccc caaattgtat ggtgataaaa gtcccgt 537

<210> 75
<211> 467
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(467)
<223> n = A,T,C or G

<400> 75
caaanacaat tgttcaaaaag atgcaaataga tacactactg ctgcagctca caaacacctc 60
tgcatattac acgtacctcc tcctgctcct caagtagtgt ggtctatttt gccatcatca 120
cctgctgtct gcttagaaga acggctttct gctgcaangg agagaaatca taacagacgg 180
tggcacaagg aggccatctt ttccatcatcg gttattgtcc ctagaagcgt cttctgagga 240
tctagtggg ctttctttct gggtttgggc catttcantt ctcattgtgtg tactattcta 300
tcattattgt ataacgggtt tcaaaccngt gggcacncag agaacctcac tctgtaataa 360
caatgaggaa tagccacggg gatctccagc accaaatctc tccatgtnt tccagagctc 420
ctccagccaa cccaaatagc cgctgctatn gtgtagaaca tccctgn 467

<210> 76
<211> 400
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(400)
<223> n = A,T,C or G

<400> 76
aagctgacag cattcggggc gagatgtctc gctccgtggc cttagctgtg ctgcgctac 60
tctctctttc tggcctggag gctatccagc gtactccaaa gattcagggt tactcacgtc 120
atccagcaga gaattgaaaag tcaaatttcc tgaattgcta tgtgtctggg tttcatccat 180
ccgacattga agttgactta ctgaagaatg gagagagaat tgaaaaagt gagcattcag 240
acttgtcttt cagcaaggac tgggtctttct atctcttgta ctacactgaa ttcaccccca 300
ctgaaaaaga tgagtatgcc tgccgtgtga accatgtgac tttgtcacag cccaagatng 360
ttnagtggga tcganacatg taagcagcan catgggaggt 400

<210> 77
<211> 248
<212> DNA
<213> Homo sapien

<400> 77
ctggagtgcc ttggtgtttc aagcccctgc aggaagcaga atgcaccttc tgaggcacct 60
ccagctgccc cggcggggga tgcgaggctc ggagcacctc tgcccggctg tgattgtctg 120
caggcactgt tcattctcagc ttttctgtcc ctttctccc ggcaagcgt tctgtgaaa 180
gttcatatct ggagcctgat gtcttaacga ataaaggtcc catgctccac ccgaaaaaaa 240
aaaaaaaa 248

<210> 78
<211> 201
<212> DNA
<213> Homo sapien

<400> 78
 actagtccag tgtggtggaa ttccattgtg ttgggcccac cacaatggct acctttaaca 60
 tcaccagac cccgccctgc ccggtcccca cgctgctgct aacgacagta tgatgcttac 120
 tctgtactc ggaaactatt tttatgtaat taatgtatgc tttcttggtt ataatgcct 180
 gatttaaaaa aaaaaaaaaa a 201

<210> 79
 <211> 552
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(552)
 <223> n = A,T,C or G

<400> 79
 tccttttggt aggtttttga gacaacccta gacctaaact gtgtcacaga ctctgaatg 60
 tttaggcagt gctagtaatt tcctcgtaat gattctgtta ttactttcct attctttatt 120
 cctctttcct ctgaagatta atgaagttga aaattgaggt ggataaatac aaaaaggtag 180
 tgtgatagta taagtatcta agtgcagatg aaagtgtgtt atatatatcc attcaaaatt 240
 atgcaagtta gtaattactc aggtttaact aaattacttt aatatgctgt tgaacctact 300
 ctgttccttg gctagaaaaa attataaaca ggactttggt agtttgggaa gccaaattga 360
 taatattcta tgttctaaaa gttgggctat acataaanta tnaagaaata tggaatttta 420
 ttcccaggaa tatgggggtc atttatgaat antaccggg anagaagttt tgantnaaac 480
 cngttttggt taatacgta atatgtcctn aatnaacaag gcntgactta tttccaaaaa 540
 aaaaaaaaaa aa 552

<210> 80
 <211> 476
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(476)
 <223> n = A,T,C or G

<400> 80
 acagggattt gagatgctaa ggccccagag atcgtttgat ccaaccctct tattttcaga 60
 ggggaaaaatg gggcctagaa gttacagagc atctagctgg tgcgctggca cccctggcct 120
 cacacagact cccgagtagc tgggactaca ggcacacagt cactgaagca ggccctgttt 180
 gcaattcacg ttgccacctc caacttaaac attcttcata tgtgatgtcc ttagtcacta 240
 aggttaaact ttcccacca gaaaaggcaa cttagataaa atcttagagt actttcatac 300
 tcttctaagt cctcttcag cctcactttg agtcctcctt gggggttgat aggaantntc 360
 tcttggttt ctcaataaaa tctctatcca tctcatgttt aatttggtac gcntaaaaat 420
 gctgaaaaaa ttaaatgtt ctggtttcnc tttaaaaaa aaaaaaaaaa aaaaaa 476

<210> 81
 <211> 232
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(232)
 <223> n = A,T,C or G

<400> 81
 tttttttttg tatgcntcn ctgtgngtt attgttgctg ccacctgga ggagcccagt 60
 ttcttctgta tctttctttt ctgggggatc ttcttgctc tgccctcca ttccagcct 120
 ctcatccca tcttgactt ttgctagggt tggaggcgt ttcttggtag cccctcagag 180
 actcagtcag cgggaataag tcttaggggt ggggggtgtg gcaagccggc ct 232

<210> 82
 <211> 383
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(383)
 <223> n = A,T,C or G

<400> 82
 aggcgggagc agaagctaaa gccaaagccc aagaagagtg gcagtgccag cactggtgcc 60
 agtaccagta ccaataacat gccagtgccg gtgccagcac cagtgggtggc ttcagtgtctg 120
 gtgccagcct gaccgccact ctacatttg ggctcttcgc tggccttggt ggagctgggtg 180
 ccagcaccag tggcagctct ggtgcctgtg gtttctcta caagtgagat tttagatatt 240
 gttaatcctg ccagctcttc tcttcaagcc aggtgcatc ctcaaaaacc tactcaacac 300
 agcactctng cgagccacta tcaatcaatt gaagttgaca ctctgcatta aatctatttg 360
 ccatttcaaa aaaaaaaaaa aaa 383

<210> 83
 <211> 494
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(494)
 <223> n = A,T,C or G

<400> 83
 accgaattgg gaccgtggc ttataagcga tcatgtctc cagtattacc tcaacgagca 60
 gggagatcga gtctatacgc tgaagaaatt tgaccgatg ggacaacaga cctgtctcagc 120
 ccactctgct cggttctccc cagatgacaa atactctcga caccgaatca ccatcaagaa 180
 acgcttcaag gtgctcatga cccagcaacc gcgccctgtc ctctgagggt ccttaaactg 240
 atgtcttttc tgccacctgt taccctcgg agactccgta accaaactct tcggactgtg 300
 agccctgatg cttttttgcc agccatactc tttggentcc agtctctcgt ggcgattgat 360
 tatgcttggtg tgaggcaatc atggtggcat caccatnaa gggaacacat ttganttttt 420
 tttcncatat tttaaattac naccagaata nttcagaata aatgaattga aaaactctta 480
 aaaaaaaaaa aaaa 494

<210> 84
 <211> 380
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(380)
 <223> n = A,T,C or G

<400> 84

```

gctggtagcc tatggcgtgg ccacggangg gtcctgagg cacgggacag tgacttccca    60
agtatcctgc gccgcgtctt ctaccgtccc tacctgcaga tcttcgggca gattccccag    120
gaggacatgg acgtggccct catggagcac agcaactgct cgtcggagcc cggcttctgg    180
gcacaccctc ctggggccca ggccggcacc tgcgtctccc agtatgcaa ctggctggtg    240
gtgctgctcc tcgtcatctt cctgctcgtg gccaacatcc tgctggtcac ttgctcattg    300
ccatgttcag ttacacattc ggcaaagtac agggcaacag cnatctctac tgggaaggcc    360
agcgtnccg cctcatccg                                     380

```

```

<210> 85
<211> 481
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(481)
<223> n = A,T,C or G

```

```

<400> 85
gagttagctc ctccacaacc ttgatgaggt cgtctgcagt ggctctcgc ttcataccgc    60
tnccatcgtc atactgtagg ttggccacca cctcctgcat cttggggcgg ctaatatcca    120
ggaaactctc aatcaagtca ccgtcnatna aacctgtggc tggttctgtc ttccgctcgg    180
tgtgaaagga tctccagaag gagtgtctga tcttcccac acttttgatg actttattga    240
gtcgattctg catgtccagc aggaggttgt accagctctc tgacagttag gtcaccagcc    300
ctatcatgcc nttgaacgtg ccgaagaaca ccgagccttg tgtggggggg gnagtctcac    360
ccagattctg cattaccaga nagccgtggc aaaaganatt gacaactcgc ccaggngaa    420
aaagaacacc tcctggaagt gctngccgct cctcgteent tggtggnngc gcntnccttt    480
t                                     481

```

```

<210> 86
<211> 472
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(472)
<223> n = A,T,C or G

```

```

<400> 86
aacatcttcc tgtataatgc tgtgtaatat cgatccgatn ttgtctgctg agaattcatt    60
acttgaaaaa gcaacttnaa gcctggacac tggattaaaa attcacaata tgcaaacatt    120
taaacagtggt gtcaatctgc tcccttactt tgtcatcacc agtctgggaa taagggtatg    180
ccctattcac acctgttaaa agggcgctaa gcatttttga ttcaacatct ttttttttga    240
cacaagtcgg aaaaaagcaa aagtaaacag ttnttaattt gttagccaat tcaactttctt    300
catgggacag agccatttga tttaaaaagc aaattgcata atattgagct ttgggagctg    360
atatntgagc ggaagantag cttttctact tcaccagaca caactccttt catattggga    420
tgtnnacnaa agttatgtct cttacagatg ggatgctttt gtggcaattc tg          472

```

```

<210> 87
<211> 413
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(413)
<223> n = A,T,C or G

```

<400> 87
 agaaaccagt atctctnaaa acaacctctc ataccttggtg gacctaatTT tgtgtgcgtg 60
 tgtgtgtgcg cgcataattat atagacaggc acatcttttt tacttttgta aaagcttatg 120
 cctcttttgg atctatatct gtgaaagttt taatgatctg ccataatgtc ttggggacct 180
 ttgtcttctg tgtaaattgg actagagaaa acacctatnt tatgagtcaa tctagttngt 240
 ttatttcgac atgaaggaaa ttccagatn acaactctna caaactctcc cttgactagg 300
 ggggacaaaag aaaagcanaa ctgaacatna gaaacaattn cctggtgaga aattncataa 360
 acagaaattg ggtngtatat tgaaananng catcattnaa acgttttttt ttt 413

<210> 88
 <211> 448
 <212> DNA
 <213> Homo sapien
 <220>
 <221> misc_feature
 <222> (1)...(448)
 <223> n = A,T,C or G

<400> 88
 cgcagcgggt cctctctatc tagctccagc ctctcgctg cccactccc cgcgtcccgc 60
 gtcctagccn accatggccg ggcccctgcg cgcctcgctg ctctctgtgg ccctcctggc 120
 cgtggccctg gccgtgagcc ccgcggcccg ctccagtcct ggcaagccgc cgcgcctggt 180
 gggaggccca tggaccccgc gtggaagaag aagggtgctg gcgtgcactg gactttgccg 240
 tcgcnanta caacaaaccc gcaacnactt ttaccnagcn cgcgtgcag gttgtgccgc 300
 cccaancaaa ttgttactng gggtaantaa ttcttggaag ttgaacctgg gccaaacnng 360
 ttaccagaa ccnagccaat tngaacaatt nccccctcat aacagcccct tttaaaaagg 420
 gaancantcc tgnctctttc caaatTTT 448

<210> 89
 <211> 463
 <212> DNA
 <213> Homo sapien
 <220>
 <221> misc_feature
 <222> (1)...(463)
 <223> n = A,T,C or G

<400> 89
 gaattttgtg cactggccac tgtgatggaa ccattgggcc aggatgcttt gagtttatca 60
 gtagtgattc tgccaaagtt ggtgttgtaa catgagtatg taaaatgtca aaaaattagc 120
 agaggtctag gtctgcatat cagcagacag tttgtccgtg tattttgtag ccttgaagtt 180
 ctcaagtaca agttnnttct gatgcgaagt tctnattcca gtgttttagt cctttgcac 240
 tttnatgtn agacttgcct ctntnaaatt gcttttgnt tctgcaggta ctatctgtgg 300
 tttacaaaa tagaannact tctctgcttn gaanatttga atatcttaca tctnaaaatn 360
 aattctctcc ccatannaaa acccangccc ttggganaat ttgaaaaang gntccttcnn 420
 aattcnana anttcagtn tcatacaaca naacngganc ccc 463

<210> 90
 <211> 400
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(400)

<223> n = A,T,C or G

<400> 90

agggattgaa	ggtctntnt	actgtcggac	tgttcancca	ccaactctac	aagttgctgt	60
cttcactca	ctgtctgtaa	gcntnttaac	ccagactgta	tcttcataaa	tagaaccaaat	120
tcttcaccag	tcacatcttc	taggaccttt	tggattcag	ttagtataag	ctcttccact	180
tcctttgtta	agacttcate	tggtaaagtc	ttagttttg	tagaaaggaa	tttaattgct	240
cgttctctaa	caatgtcctc	tccttgaagt	atttggtga	acaaccacc	tnaagtcct	300
ttgtgcatcc	attttaaata	tacttaatag	ggcattggtn	cactaggtta	aattctgcaa	360
gagtcactctg	tctgcaaaag	ttgcgttagt	atatctgcca			400

<210> 91

<211> 480

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(480)

<223> n = A,T,C or G

<400> 91

gagctcggat	ccaataatct	ttgtctgagg	gcagcacaca	tatncagtgc	catggnaact	60
ggtctacccc	acatgggagc	agcatgccgt	agntatataa	ggtcattccc	tgagtcagac	120
atgcctcttt	gactaccgtg	tgccagtgtc	ggtgattctc	acacacctcc	nnccgctctt	180
tgtgaaaaaa	ctggcacttg	nctggaacta	gcaagacatc	acttaccaat	tcacccacga	240
gacacttgaa	aggtgtaaca	aagcgactct	tgcattgtct	tttgtccctc	cggcaccagt	300
tgtcaatact	aacccgctgg	tttgccctcca	tcacatttgt	gatctgtage	tctggatata	360
tctcctgaca	gtactgaaga	acttcttctt	ttgtttcaaa	agcaactctt	ggtgcctgtt	420
ngatcagggt	cccatttccc	agtcogaatg	ttcacatggc	atatnttact	tcccacaaaa	480

<210> 92

<211> 477

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(477)

<223> n = A,T,C or G

<400> 92

atacagccca	natcccacca	cgaagatgcg	cttgttgact	gagaacctga	tgcggtcact	60
ggtcccgtg	tagcccagc	gactctccac	ctgctggaag	cggttgatgc	tgcactcctt	120
cccacgcagg	cagcagcggg	gccggtcaat	gaactccact	cgtggcttgg	ggttgacggt	180
taantgcagg	aagaggctga	ccacctcgcg	gtccaccagg	atgcccagct	gtgcgggacc	240
tgcagcgaaa	ctcctcgatg	gtcatgagcg	ggaagcgaat	gangcccagg	gccttgccca	300
gaaccttcg	cctgttctct	ggcgtcacct	gcagctgctg	ccgctnacac	tcggcctcgg	360
accagcggac	aaacggcggt	gaacagccgc	acctcacgga	tgcccantgt	gtcgcgctcc	420
aggaacggcn	ccagcgtgtc	caggtcaatg	tcggtgaanc	ctccgcgggt	aatggcg	477

<210> 93

<211> 377

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(377)

<223> n = A,T,C or G

<400> 93

gaacggctgg	accttgccctc	gcattgtgct	gctggcagga	ataccttggc	aagcagctcc	60
agtccgagca	gccccagacc	gctgccgccc	gaagctaagc	ctgcctctgg	ccttccccctc	120
cgcctcaatg	cagaaccant	agtgggagca	ctgtgttttag	agttaagagt	gaacactgtn	180
tgattttact	tgggaatttc	ctctgttata	tagcttttcc	caatgctaata	ttccaaacaa	240
caacaacaaa	ataacatgtt	tgctgttna	gttgataaaa	agtangtgat	tctgtatnta	300
aagaaaatat	tactgttaca	tatactgctt	gcaanttctg	tatttattgg	tnctctggaa	360
ataaatatat	tattaaa					377

<210> 94

<211> 495

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(495)

<223> n = A,T,C or G

<400> 94

ccctttgagg	ggttagggtc	cagttcccag	tggaagaaac	aggccaggag	aantgcgtgc	60
cgagctgang	cagatttccc	acagtgaccc	cagagccctg	ggctatagtc	tctgacccct	120
ccaaggaaag	accaccttct	ggggacatgg	gctggagggc	aggacctaga	ggcaccaagg	180
gaaggcccca	ttccggggct	gttccccgag	gaggaaggga	aggggctctg	tgtgccccc	240
acgaggaana	ggccctgant	cctgggatca	nacacccctt	cacgtgtatc	cccacacaaa	300
tgcaagctca	ccaagggtccc	ctctcagtc	cttccctaca	ccctgaacgg	ncactggccc	360
acacccaccc	agancancca	cccgccatgg	ggaatgtntc	caaggaatcg	cngggcaacg	420
tggactctng	tccennaagg	gggcagaatc	tccaatagan	gganngaacc	cttgctnana	480
aaaaaaaaana	aaaaa					495

<210> 95

<211> 472

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(472)

<223> n = A,T,C or G

<400> 95

ggttacttgg	tttcattgcc	accacttagt	ggatgtcatt	tagaaccatt	ttgtctgctc	60
cctctggaag	ccttgccgag	agcggacttt	gtaattgttg	gagaataact	gctgaatttt	120
tagctgtttt	gagttgattc	gcaccactgc	accacaactc	aatatgaaaa	ctatttnact	180
tatttattat	cttgtgaaaa	gtatacaatg	aaaattttgt	tcatactgta	tttatcaagt	240
atgatgaaaa	gcaatagata	tatattcttt	tattatgttn	aattatgatt	gccattatta	300
atcggaacaa	tgtggagtgt	atgttctttt	cacagtaata	tatgcctttt	gtaacttcac	360
ttggttattt	tattgtaaat	gaattacaaa	attcttaatt	taagaaaatg	gtangttata	420
tttanttcan	taatttcttt	ccttgtttac	gttaattttg	aaaagaatgc	at	472

<210> 96

<211> 476

<212> DNA

<213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(476)
 <223> n = A,T,C or G

<400> 96
 ctgaagcatt tcttcaaact tntctacttt tgtcattgat acctgtagta agttgacaat 60
 gtggtgaaat ttcaaaatta tatgtaactt ctactagtct tactttctcc cccaagtctt 120
 ttttaactca tgattttttac acacacaatc cagaacttat tatatagcct ctaagtcttt 180
 attcttcaca gtagatgatg aaagagtcct ccagtgtctt gngcanaatg ttctagnat 240
 agctggatac atacngtggg agttctataa actcatacct cagtgggact naaccaaaat 300
 tgtgttagtc tcaattccta ccacactgag ggagcctccc aaatcactat attcttatct 360
 gcaggtactc ctccagaaaa acngacaggg caggcttgca tgaaaaagtn acatctgcgt 420
 tacaagtct atcttctca nangtctgtn aaggaacaat ttaatcttct agcttt 476

<210> 97
 <211> 479
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(479)
 <223> n = A,T,C or G

<400> 97
 actctttcta atgctgatat gatcttgagt ataagaatgc atatgtcact agaattggata 60
 aaataatgct gcaaaacttaa tgttcttatg caaaatggaa cgctaatagaa acacagctta 120
 caatcgcaaa tcaaaaactca caagtgtctca tctgtttag atttagtgta ataagactta 180
 gattgtgctc cttecgatat gattgtttct canatcttgg gcaatnttcc ttagtcaaatt 240
 caggctacta gaattctgtt attggatatn tgagagcatg aaatttttaa naatacactt 300
 gtgattatna aattaatcac aaatttcact tatacctgct atcagcagct agaaaaacat 360
 ntnnttttta natcaaagta ttttgtgttt ggaantgttn aaatgaaatc tgaatgtggg 420
 ttcnatctta ttttttcccn gacnactant tnccttttta ggnctattc tganccatc 479

<210> 98
 <211> 461
 <212> DNA
 <213> Homo sapien

<400> 98
 agtgacttgt cctccaacaa aacccttga tcaagtttgt ggcaactgaca atcagaccta 60
 tgctagtctc tgtcatctat tgcctactaa atgcagactg gaggggacca aaaaggggca 120
 tcaactccag ctggattatt ttggagcctg caaatctatt cctacttgta cggactttga 180
 agtgattcag tttcctctac ggatgagaga ctggctcaag aatatactca tgcagcttta 240
 tgaagccact ctgaacacgc tggttatcta gatgagaaca gagaaataaa gtcagaaaat 300
 ttacctggag aaaagaggct ttggctgggg accatcccat tgaaccttct cttaaggact 360
 ttaagaaaaa ctaccacatg ttgtgtatcc tgggtccggc cgtttatgaa ctgaccaccc 420
 tttggaataa tcttgacgct cctgaacttg ctctctgcyg a 461

<210> 99
 <211> 171
 <212> DNA
 <213> Homo sapien

<400> 99
 gtggccgcgc gcaggtgttt cctcgtaccg cagggccccc tcccttcccc aggcgtccct 60
 cggcgctct gcgggcccga ggaggagcgg ctggcggtg gggggagtgt gaccacacct 120

cggtgagaaa agccttctct agcgatctga gaggcgtgcc ttgggggtac c 171

<210> 100
 <211> 269
 <212> DNA
 <213> Homo sapien

<400> 100
 cggccgcaag tgcaactcca gctggggccg tgccgacgaa gattctgcc a gcagttggtc 60
 cgactgcgac gacggcggcg gcgacagtcg caggtgcagc gcgggcgcct ggggtcttgc 120
 aaggctgagc tgacgccgca gaggtcgtgt cacgtccac gaccttgacg ccgtcgggga 180
 cagccggaac agagcccgtt gaagcgggag gcctcgggga gccctcggg aagggcggcc 240
 cgagagatac gcaggtgcag gtggccgccc 269

<210> 101
 <211> 405
 <212> DNA
 <213> Homo sapien

<400> 101
 tttttttttt ttttgaatc tactgagcgc acagcaggtc agcaacaagt ttattttgca 60
 gctagcaagg taacagggtg gggcatggtt acatgttcag gtcaacttcc ttgtcgtgg 120
 ttgattggtt tgtctttatg ggggcggggt ggggtagggg aaacgaagca aataacatgg 180
 agtgggtgca ccctccctgt agaacctggt tacaagctt ggggcagttc acctggtctg 240
 tgaccgtcat tttcttgaca tcaatgttat tagaagtcag gatattcttt agagagtcca 300
 ctgttctgga gggagattag ggtttcttgc caaatccaac aaaatccact gaaaaagttg 360
 gatgatcagt acgaataccg aggcattatc tcatatcggg ggcca 405

<210> 102
 <211> 470
 <212> DNA
 <213> Homo sapien

<400> 102
 tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 60
 ggcacttaat ccatttttat ttcaaatgt ctacaaattt aatccattta tacggtattt 120
 tcaaatctta aattattcaa attagccaaa tccttaccaa ataataccca aaaatcaaaa 180
 atatacttct ttacgcaaac ttgttacata aattaaaaaa atatatacgg ctggtgtttt 240
 caaagtacaa ttatcttaac actgcaaaac ttttaaggaa ctaaaataaa aaaaaacact 300
 ccgcaaagg taaagggaac aacaaattct tttacaacac cattataaaa atcatatctc 360
 aaatcttagg ggaatatata cttcacacgg gatcttaact tttactcact ttgtttattt 420
 ttttaaacca ttgtttgggc ccaacacaat ggaatcccc ctggactagt 470

<210> 103
 <211> 581
 <212> DNA
 <213> Homo sapien

<400> 103
 tttttttttt ttttttttga cccccctctt ataaaaaaca agttaccatt ttattttact 60
 tacacatatt tattttataa ttggtattag atattcaaaa ggcagctttt aaaatcaaac 120
 taaatggaaa ctgccttaga tacataattc ttaggaatta gcttaaaatc tgcctaaagt 180
 gaaaatcttc tctagctctt ttgactgtaa atttttgact cttgtaaaac atccaaattc 240
 atttttcttg tcttttaaat tatctaactt ttccattttt tccctattcc aagtcaattt 300
 gcttctctag cctcatttcc tagctcttat ctactattag taagtggcct ttttcctaaa 360
 agggaaaaca ggaagagaaa tggcacacaa aacaacatt ttatattcat atttctacct 420
 acgttaataa aatagcattt tgtgaagcca gctcaaaaga aggcttagat ccttttatgt 480
 ccattttagt cactaaacga tatcaaagt ccagaatgca aaaggtttgt gaacatttat 540

tcaaaagcta atataagata tttcacatac tcactctttct g

581

<210> 104
<211> 578
<212> DNA
<213> Homo sapien

<400> 104

tttttttttt	tttttttttt	tttttctctt	cttttttttt	gaaatgagga	tcgagttttt	60
cactctctag	atagggcatg	aagaaaaactc	atctttccag	ctttaaaata	acaatcaaat	120
ctcttatgct	atatcatatt	ttaagttaaa	ctaagagtc	actggcttat	cttctcctga	180
aggaaatctg	ttcattcttc	tcattcatat	agttatatca	agtactacct	tgcatattga	240
gagggttttc	ttctctattt	acacatatat	ttccatgtga	atttgtatca	aacctttatt	300
ttcatgcaaa	ctagaaaaata	atgtttcttt	tgcataagag	aagagaacaa	tatagcatta	360
caaaactgct	caaattgttt	gttaagtatt	ccattataat	tagttggcag	gagctaatac	420
aaatcacatt	tacgacagca	ataataaaac	tgaagtacca	gttaaatatc	caaaataatt	480
aaaggaacat	ttttagcctg	ggtataatta	gctaattcac	tttacaagca	tttattagaa	540
tgaattcaca	tgttattatt	cctagcccaa	cacaatgg			578

<210> 105
<211> 538
<212> DNA
<213> Homo sapien

<400> 105

tttttttttt	tttttcagta	ataatcagaa	caatatttat	ttttatattt	aaaattcata	60
gaaaagtgcc	ttacatttaa	taaaagtgtg	tttctcaaag	tgatcagagg	aattagatat	120
gtcttgaaca	ccaatattaa	tttgaggaaa	atacaccaaa	atacattaag	taaattattt	180
aagatcatag	agcttgtaag	tgaaaagata	aaatttgacc	tcagaaactc	tgagcattaa	240
aaatccacta	ttagcaata	aattactatg	gacttcttgc	tttaattttg	tgatgaatat	300
ggggtgtcac	tggtaaacca	acacattctg	aaggatacat	tacttagtga	tagattctta	360
tgtactttgc	taatacgtgg	atatgagttg	acaagtttct	ctttcttcaa	tcttttaagg	420
ggcgagaaat	gaggaagaaa	agaaaaggat	tacgcatact	gttctttcta	tggaaggatt	480
agatatgttt	cctttgccaa	tattaaaaaa	ataataatgt	ttactactag	tgaaaccc	538

<210> 106
<211> 473
<212> DNA
<213> Homo sapien

<400> 106

tttttttttt	tttttttagtc	aagtttctat	ttttattata	attaaagtct	tggtcatttc	60
atttattagc	tctgcaactt	acatatttaa	attaaagaaa	cgtttttagac	aactgtacaa	120
tttataaatg	taagggtgcca	ttattgagta	atatattcct	ccaagagtgg	atgtgtccct	180
tctcccacca	actaatgaac	agcaacatta	gtttaatttt	attagtagat	atacactgct	240
gcaaacgcta	attctcttct	ccatccccat	gtgatattgt	gtatatgtgt	gagttggtag	300
aatgcatcac	aatctacaat	caacagcaag	atgaagctag	gctgggcttt	cggtgaaaat	360
agactgtgtc	tgtctgaatc	aaatgatctg	acctatcctc	ggtggcaaga	actcttcgaa	420
ccgcttcctc	aaaggcgctg	ccacatttgc	ggctctttgc	acttgtttca	aaa	473

<210> 107
<211> 1621
<212> DNA
<213> Homo sapien

<400> 107

cgccatggca	ctgcagggca	tctcggtcat	ggagctgtcc	ggcctggccc	cgggcccgtt	60
ctgtgctatg	gtcctggctg	acttcggggc	gcgtgtggtg	cgcgtggacc	ggcccggctc	120

```

ccgctacgac gtgagccgct tgggccgggg caagcgctcg ctagtgctgg acctgaagca 180
gccgcgggga gccgccgtgc tgcggcgctc gtgcaagcgg tcggatgtgc tgctggagcc 240
cttccgccgc ggtgtcatgg agaaactcca gctgggcccc gagattctgc agcgggaaaa 300
tccaaggctt atttatgcca ggctgagtgg atttggccag tcaggaagct tctgccggtt 360
agctggccac gatatcaact atttggcttt gtcagtggtt ctctcaaaaa ttggcagaag 420
tggtgagaat ccgatgccc cgctgaatct cctggctgac tttgctggtg gtggccttat 480
gtgtgcactg ggcattataa tggctctttt tgaccgcaca cgcaactgaca agggtcaggt 540
cattgatgca aatatggtgg aaggaacagc atatttaagt tcttttctgt ggaaaactca 600
gaaatcgagt ctgtgggaag cacctcgagg acagaacatg ttggatggtg gagcaccttt 660
ctatacgact tacaggacag cagatgggga attcatggct gttggagcaa tagaacccca 720
gttctacgag ctgctgatca aaggacttgg actaaagtct gatgaacttc ccaatcagat 780
gagcatggat gattggccag aaatgaagaa gaagtttgca gatgtatttg caaagaagac 840
gaaggcagag tgggtgcaaa tctttgacgg cacagatgcc tgtgtgactc cggttctgac 900
ttttgaggag gttgttcac atgacacaa caaggaacgg ggctcgttta tcaccagtga 960
ggagcaggac gtgagccccc gccctgcacc tctgctgtta aacaccccag ccaccccttc 1020
tttcaaaagg gatcctttca taggagaaca cactgaggag atacttgaag aatttggatt 1080
cagccgcgaa gagatttata agcttaactc agataaaatc attgaaagta ataaggtaaa 1140
agctagtctc taacttcag gccacggct caagtgaatt tgaatactgc atttacagt 1200
tagagtaaca cataacattg tatgcatgga aacatggagg aacagtatta cagtgtccta 1260
ccactctaata caagaaaaga attacagact ctgattctac agtgatgatt gaattctaaa 1320
aatggttatc attagggtt ttgatttata aaactttggg tacttatact aaattatggt 1380
agttattctg ccttcagtt tgcttgatat atttgttgat attaaagattc ttgacttata 1440
ttttgaatgg gttctagtga aaaaggaatg atatattctt gaagacatcg atatacattt 1500
atttactc ttgattctac aatgtagaaa atgaggaaat gccacaaatt gtatggtgat 1560
aaaagtcacg tgaacaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1620
a

```

<210> 108

<211> 382

<212> PRT

<213> Homo sapien

<400> 108

```

Met Ala Leu Gln Gly Ile Ser Val Met Glu Leu Ser Gly Leu Ala Pro
1      5      10      15
Gly Pro Phe Cys Ala Met Val Leu Ala Asp Phe Gly Ala Arg Val Val
20     25     30
Arg Val Asp Arg Pro Gly Ser Arg Tyr Asp Val Ser Arg Leu Gly Arg
35     40     45
Gly Lys Arg Ser Leu Val Leu Asp Leu Lys Gln Pro Arg Gly Ala Ala
50     55     60
Val Leu Arg Arg Leu Cys Lys Arg Ser Asp Val Leu Leu Glu Pro Phe
65     70     75     80
Arg Arg Gly Val Met Glu Lys Leu Gln Leu Gly Pro Glu Ile Leu Gln
85     90     95
Arg Glu Asn Pro Arg Leu Ile Tyr Ala Arg Leu Ser Gly Phe Gly Gln
100    105    110
Ser Gly Ser Phe Cys Arg Leu Ala Gly His Asp Ile Asn Tyr Leu Ala
115    120    125
Leu Ser Gly Val Leu Ser Lys Ile Gly Arg Ser Gly Glu Asn Pro Tyr
130    135    140
Ala Pro Leu Asn Leu Leu Ala Asp Phe Ala Gly Gly Gly Leu Met Cys
145    150    155    160
Ala Leu Gly Ile Ile Met Ala Leu Phe Asp Arg Thr Arg Thr Asp Lys
165    170    175
Gly Gln Val Ile Asp Ala Asn Met Val Glu Gly Thr Ala Tyr Leu Ser
180    185    190
Ser Phe Leu Trp Lys Thr Gln Lys Ser Ser Leu Trp Glu Ala Pro Arg

```

195	200	205
Gly Gln Asn Met Leu Asp	Gly Gly Ala Pro Phe	Tyr Thr Thr Tyr Arg
210	215	220
Thr Ala Asp Gly Glu Phe	Met Ala Val Gly Ala	Ile Glu Pro Gln Phe
225	230	235
Tyr Glu Leu Leu Ile Lys	Gly Leu Gly Leu Lys	Ser Asp Glu Leu Pro
245	250	255
Asn Gln Met Ser Met Asp	Asp Trp Pro Glu Met	Lys Lys Lys Phe Ala
260	265	270
Asp Val Phe Ala Lys Lys	Thr Lys Ala Glu Trp	Cys Gln Ile Phe Asp
275	280	285
Gly Thr Asp Ala Cys Val	Thr Pro Val Leu Thr	Phe Glu Glu Val Val
290	295	300
His His Asp His Asn Lys	Glu Arg Gly Ser Phe	Ile Thr Ser Glu Glu
305	310	315
Gln Asp Val Ser Pro Arg	Pro Ala Pro Leu Leu	Leu Asn Thr Pro Ala
325	330	335
Ile Pro Ser Phe Lys Arg	Asp Pro Phe Ile Gly	Glu His Thr Glu Glu
340	345	350
Ile Leu Glu Glu Phe Gly	Phe Ser Arg Glu Glu	Ile Tyr Gln Leu Asn
355	360	365
Ser Asp Lys Ile Ile Glu	Ser Asn Lys Val Lys	Ala Ser Leu
370	375	380

<210> 109
 <211> 1524
 <212> DNA
 <213> Homo sapien

<400> 109

ggcacgaggg	tgccgaggg	cctgagcggg	ggcggggggca	gcctcgccag	cgggggcccc	60
gggcctggcc	atgcctcact	gagccagcgc	ctgcgcctct	acctcgccga	cagctggaac	120
cagtgcgacc	tagtggctct	cacctgcttc	ctcctgggcg	tgggctgccc	gctgaccccg	180
ggtttgtagc	acctggggccg	cactgtcctc	tgcatcgact	tcatggtttt	cacggtgcgg	240
ctgttcacaa	tcttcacggg	caacaaacag	ctggggccca	agatcgatcat	cgtgagcaag	300
atgatgaagg	acgtgttctt	cttctctctc	ttcctcgccg	tgtggctggg	agcctatggc	360
gtggccacgg	aggggctcct	gaggccacgg	gacagtgcct	tcccaagtat	cctgcgcccgc	420
gtcttctacc	gtccctacct	gcagatcttc	gggcagattc	cccaggagga	catggacgtg	480
gcccctcatg	agcacagcaa	ctgctcgctg	gagcccggct	tctgggcaca	ccctcctggg	540
gcccagggcg	gcacctgcgt	ctcccagtat	gccaactggc	tggtgggtgct	gctcctcgtc	600
atcttctctg	tcgtggccaa	catectgctg	gtcaacttgc	tcattgccat	gttcagttac	660
acattcggca	aagtacaggg	caacagcgat	ctctactgga	aggcgcagcg	ttaccgcctc	720
atccgggaat	tccactctcg	gcccgcgctg	gcccgcctct	ttatcgatcat	ctcccacttg	780
cgctcctctg	tcaggcaatt	gtgcaggcga	ccccggagcc	cccagccgtc	ctccccggcc	840
ctcgagcatt	tccgggttta	cctttctaag	gaagccgagc	ggaagctgct	aacgtgggaa	900
tcggtgcata	aggagaactt	tctgctggca	cgcgctaggg	acaagcggga	gagcgactcc	960
gagcgtctga	agcgacagtc	ccagaagggtg	gacttggcac	tgaaacagct	gggacacatc	1020
cgcgagtacg	aacagcgccct	gaaagtgcgt	gagcggggag	tccagcagtg	tagcccgctc	1080
ctgggggtgg	tggccgaggg	cctgagccgc	tctgccttgc	tgcccccagg	tgggcccgca	1140
ccccctgacc	tgccctgggtc	caaagactga	gcccgtgtgg	cggacttcaa	ggagaagccc	1200
ccacagggga	ttttgtcctc	agagtaaggc	tcatctgggc	ctcgccccc	gcacctgggtg	1260
gccttgtcct	tgaggtgagc	cccatgtcca	tctggggcac	tgtcaggacc	acctttggga	1320
gtgtcatcct	tacaaaccac	agcatgcccg	gctcctccca	gaaccagtcc	cagcctggga	1380
ggatcaaggc	ctggatcccc	ggccgttatc	catctggagg	ctgcagggtc	cttggggtaa	1440
caggggaccac	agacccctca	ccactcacag	attcctcaca	ctggggaaat	aaagccattt	1500
cagaggaataa	aaaaaaaaaa	aaaa				1524

<210> 110

<211> 3410
 <212> DNA
 <213> Homo sapien

<400> 110

gggaaccagc	ctgcacgcgc	tggtccggg	tgacagccgc	gcgcctcggc	caggatctga	60
gtgatgagac	gtgtcccccac	tgaggtgccc	cacagcagca	ggtgttgagc	atgggctgag	120
aagctggacc	ggcaccaaag	ggctggcaga	aatgggcgcc	tggtgatctc	ctaggcagtt	180
ggcggcagca	aggaggagag	gccgcagctt	ctggagcaga	gccgagacga	agcagttctg	240
gagtgcctga	acggccccct	gagccctacc	cgcctggccc	actatggtcc	agaggctgtg	300
ggtgagccgc	ctgctgcggc	accggaaagc	ccagctcttg	ctggtcaacc	tgctaacctt	360
tgccctggag	gtgtgttttg	ccgcaggcat	cacctatgtg	ccgcctctgc	tgctggaagt	420
gggggtagag	gagaagttca	tgaccatggt	gctgggcatt	ggtccagtgc	tgggcctggt	480
ctgtgtcccg	ctcctaggct	cagccagtga	ccactggcgt	ggacgctatg	gccgccgccg	540
gcccttcate	tgggcactgt	ccttgggcat	cctgctgagc	ctctttctca	tcccaagggc	600
cggctggcta	gcagggtctgc	tgtgcccggg	tcccaggccc	ctggagctgg	cactgctcat	660
cctgggcgtg	gggctgctgg	acttctgtgg	ccaggtgtgc	ttcactccac	tggaggccct	720
gctctctgac	ctcttcgggg	accgggacca	ctgtcgccag	gcctactctg	tctatgcctt	780
catgatcagt	cttgggggct	gcctgggcta	cctcctgcct	gccattgact	gggacaccag	840
tgccctggcc	ccctacctgg	gcacccagga	ggagtgcctc	tttggcctgc	tcacctcat	900
cttcctcacc	tgcgtagcag	ccacactgct	ggtggctgag	gaggcagcgc	tgggccccac	960
cggagccagca	gaagggctgt	cggccccctc	cttgtcgccc	cactgctgtc	catgccgggc	1020
ccgcttggtt	ttccggaacc	tgggcgccct	gcttccccgg	ctgcaccagc	tgtgctgccg	1080
catgccccgc	accctgcgcc	ggctcttcgt	ggctgagctg	tgcagctgga	tggcactcat	1140
gaccttcacg	ctgttttaca	cggatttcgt	gggcgagggg	ctgtaccagg	gcgtgccag	1200
agctgagccg	ggcaccgagg	cccggagaca	ctatgatgaa	ggcgctcgga	tgggcagcct	1260
ggggctgttc	ctgcagtgcg	ccatctccct	ggtcttctct	ctggtcatgg	accggctggt	1320
gcagcgattc	ggcactcgag	cagtctatct	ggccagtgtg	gcagctttcc	ctgtggctgc	1380
cgggtgccaca	tgccgtgtcc	acagtgtggc	ctgtgtgaca	gcttcagccg	ccctcaccgg	1440
gttcaccttc	tcagccctgc	agatcctgcc	ctacacactg	gcctccctct	accaccggga	1500
gaagcaggtg	ttcctgccc	aataccgagg	ggacactgga	ggtgctagca	gtgaggacag	1560
cctgatgacc	agcttcctgc	caggccctaa	gcctggagct	ccctcccta	atggacacgt	1620
gggtgctgga	ggcagtggcc	tgctcccacc	tccacccgcg	ctctgcgggg	cctctgcctg	1680
tgatgtctcc	gtacgtgtgg	tggtgggtga	gcccaccgag	gccagggtgg	ttccggggcc	1740
gggcatctgc	ctggacctcg	ccatcctgga	tagtgccctc	ctgctgtccc	aggtggcccc	1800
atccctgttt	ctcgtgtcca	ttgtccagct	cagccagtct	gtcactgcct	atatggtgtc	1860
tgccgcaggc	ctgggtctgg	tcgccattta	ctttgtctca	caggtagtat	ttgacaagag	1920
cgacttggcc	aaatactcag	cgtagaaaac	ttccagcaca	ttgggtgga	gggcctgcct	1980
cactgggtcc	cagctccccg	ctcctgttag	ccccatgggg	ctgccgggct	ggccgccagt	2040
ttctgttgct	gccaagtaa	tgtggctctc	tgctgccacc	ctgtgctgct	gaggtgcgta	2100
gctgcacagc	tgggggctgg	ggcgtccctc	tcctctctcc	ccagtctcta	gggctgcctg	2160
actggaggcc	ttccaagggg	gtttcagttc	ggacttatac	agggaggcca	gaagggtcc	2220
atgcactgga	atgcggggac	tctgcagggt	gattaccag	gctcagggtt	aacagctagc	2280
ctcctagtgt	agacacacct	agagaagggt	ttttgggagc	tgaataaact	cagtcacctg	2340
gtttcccatc	tctaagcccc	ttaacctgca	gcttcgttta	atgtagctct	tgcattgggag	2400
ttctaggat	gaaacactcc	tccatgggat	ttgaacatat	gacttatttg	taggggaaga	2460
gtcctgaggg	gcaacacaca	agaaccaggt	cccctcagcc	cacagcactg	tctttttgct	2520
gatccacccc	cctcttacct	tttatcagga	tgtggcctgt	tggtccttct	gttgccatca	2580
cagagacaca	ggcatttaaa	tatttaactt	attttttaaa	caaagtagaa	gggaatccat	2640
tgctagcttt	tctgtgttg	tgtctaata	ttgggtaggg	tgggggatcc	ccaacaatca	2700
ggtccccctga	gatagctgg	cattgggctg	atcattgcca	gaatcttctt	ctcctggggg	2760
ctggcccccc	aaaatgccta	accaggacc	ttggaaattc	tactcatccc	aaatgataat	2820
tccaaatgct	gttacccaag	gttaggggtg	tgaaggagg	tagagggtgg	ggcttcagggt	2880
ctcaacggct	tccctaacca	cccctcttct	cttgcccag	cctggttccc	cccacttcca	2940
ctccccctcta	ctctctctag	gactgggctg	atgaaggcac	tgcccaaaat	ttccccctacc	3000
cccaactttc	ccctaccccc	aactttcccc	accagctcca	caaccctggt	tggagctact	3060
gcaggaccag	aagcacaaag	tgcggtttcc	caagcctttg	tccatctcag	ccccagaggt	3120
atatctgtgc	ttggggaatc	tcacacagaa	actcaggagc	accccctgcc	tgagctaagg	3180

gaggtcttat	ctctcagggg	gggtttaagt	gccgtttgca	ataatgtcgt	cttatattatt	3240
tagcgggggtg	aatatatttat	actgtaagtg	agcaatcaga	gtataatgtt	tatggtgaca	3300
aaattaaagg	ctttcttata	tgtttaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	3360
aaaaaaaaara	aaaaaaaaaa	aaaaaaaaaa	aaaaaaataa	aaaaaaaaaa		3410

<210> 111
 <211> 1289
 <212> DNA
 <213> Homo sapien

<400> 111

agccaggcgt	ccctctgcct	gcccactcag	tggcaacacc	cgggagctgt	tttgtccttt	60
gtggagcctc	agcagttccc	tctttcagaa	ctcactgcca	agagccctga	acaggagcca	120
ccatgcagtg	cttcagcttc	attaagacca	tgatgatcct	cttcaatttg	ctcatctttc	180
tgtgtggtgc	agccctgttg	gcagtgggca	tctgggtgtc	aatcgatggg	gcaccccttc	240
tgaagatctt	cgggccactg	tcgtccagtg	ccatgcagtt	tgtcaacgtg	ggctacttcc	300
tcatcgcagc	cggcgtttgt	gtctttgtct	ttggtttcct	gggctgctat	ggtgctaaga	360
ctgagagcaa	gtgtgccctc	gtgacgttct	tcttcctcct	cctcctcctc	ttcattgctg	420
aggttgagc	tgctgtggtc	gccttgggtg	acaccacaat	ggctgagcac	ttcctgacgt	480
tgctggtagt	gcctgccatc	aagaaagatt	atggttccca	ggaagacttc	actcaagtgt	540
ggaacaccac	catgaaagg	ctcaagtgtc	gtggcttcac	caactatacg	gattttgagg	600
actcacccta	cttcaagag	aacagtgcct	ttccccatt	ctgttgcaat	gacaacgtca	660
ccaacacagc	caatgaaacc	tgcaccaagc	aaaaggctca	cgaccaaaaa	gtagagggtt	720
gcttcaatca	gcttttgtat	gacatccgaa	ctaattgcagt	caccgtgggt	ggtgtggcag	780
ctggaattgg	gggcctcgag	ctggctgcc	tgattgtgtc	catgtatctg	tactgcaatc	840
tacaataagt	ccacttctgc	ctctgccact	actgctgcc	catgggaact	gtgaaggagg	900
accctggcaa	gcagcagtga	ttgggggagg	ggacaggatc	taacaatgtc	acttgggcca	960
gaatggacct	gccctttctg	ctccagactt	ggggctagat	agggaccact	ccttttagcg	1020
atgctcgact	ttccttccat	tgggtgggtg	atgggtgggg	ggcattccag	agcctctaag	1080
gtagccagtt	ctgttgccca	ttccccagct	ctattaaacc	cttgatatgc	cccctaggcc	1140
tagtggtgat	cccagtgctc	tactggggga	tgagagaaag	gcattttata	gcctgggcat	1200
aagtgaatc	agcagagcct	ctgggtggat	gtgtagaagg	cacttcaaaa	tgcataaacc	1260
tgttacaatg	ttaaaaaaaa	aaaaaaaaaa				1289

<210> 112
 <211> 315
 <212> PRT
 <213> Homo sapien

<400> 112

Met	Val	Phe	Thr	Val	Arg	Leu	Leu	His	Ile	Phe	Thr	Val	Asn	Lys	Gln
1				5				10					15		
Leu	Gly	Pro	Lys	Ile	Val	Ile	Val	Ser	Lys	Met	Met	Lys	Asp	Val	Phe
			20					25					30		
Phe	Phe	Leu	Phe	Phe	Leu	Gly	Val	Trp	Leu	Val	Ala	Tyr	Gly	Val	Ala
			35				40					45			
Thr	Glu	Gly	Leu	Leu	Arg	Pro	Arg	Asp	Ser	Asp	Phe	Pro	Ser	Ile	Leu
			50			55					60				
Arg	Arg	Val	Phe	Tyr	Arg	Pro	Tyr	Leu	Gln	Ile	Phe	Gly	Gln	Ile	Pro
					70				75					80	
Gln	Glu	Asp	Met	Asp	Val	Ala	Leu	Met	Glu	His	Ser	Asn	Cys	Ser	Ser
			85					90						95	
Glu	Pro	Gly	Phe	Trp	Ala	His	Pro	Pro	Gly	Ala	Gln	Ala	Gly	Thr	Cys
			100				105				110				
Val	Ser	Gln	Tyr	Ala	Asn	Trp	Leu	Val	Val	Leu	Leu	Leu	Val	Ile	Phe
			115			120					125				
Leu	Leu	Val	Ala	Asn	Ile	Leu	Leu	Val	Asn	Leu	Leu	Ile	Ala	Met	Phe
			130			135					140				

Ser Tyr Thr Phe Gly Lys Val Gln Gly Asn Ser Asp Leu Tyr Trp Lys
 145 150 155 160
 Ala Gln Arg Tyr Arg Leu Ile Arg Glu Phe His Ser Arg Pro Ala Leu
 165 170 175
 Ala Pro Pro Phe Ile Val Ile Ser His Leu Arg Leu Leu Leu Arg Gln
 180 185 190
 Leu Cys Arg Arg Pro Arg Ser Pro Gln Pro Ser Ser Pro Ala Leu Glu
 195 200 205
 His Phe Arg Val Tyr Leu Ser Lys Glu Ala Glu Arg Lys Leu Leu Thr
 210 215 220
 Trp Glu Ser Val His Lys Glu Asn Phe Leu Leu Ala Arg Ala Arg Asp
 225 230 235 240
 Lys Arg Glu Ser Asp Ser Glu Arg Leu Lys Arg Thr Ser Gln Lys Val
 245 250 255
 Asp Leu Ala Leu Lys Gln Leu Gly His Ile Arg Glu Tyr Glu Gln Arg
 260 265 270
 Leu Lys Val Leu Glu Arg Glu Val Gln Gln Cys Ser Arg Val Leu Gly
 275 280 285
 Trp Val Ala Glu Ala Leu Ser Arg Ser Ala Leu Leu Pro Pro Gly Gly
 290 295 300
 Pro Pro Pro Pro Asp Leu Pro Gly Ser Lys Asp
 305 310 315

<210> 113

<211> 553

<212> PRT

<213> Homo sapien

<400> 113

Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala
 1 5 10 15
 Gln Leu Leu Leu Val Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu
 20 25 30
 Ala Ala Gly Ile Thr Tyr Val Pro Leu Leu Leu Glu Val Gly Val
 35 40 45
 Glu Glu Lys Phe Met Thr Met Val Leu Gly Ile Gly Pro Val Leu Gly
 50 55 60
 Leu Val Cys Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly
 65 70 75 80
 Arg Tyr Gly Arg Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile
 85 90 95
 Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu
 100 105 110
 Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly
 115 120 125
 Val Gly Leu Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu
 130 135 140
 Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala
 145 150 155 160
 Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr
 165 170 175
 Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu
 180 185 190
 Gly Thr Gln Glu Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu
 195 200 205
 Thr Cys Val Ala Ala Thr Leu Val Ala Glu Glu Ala Ala Leu Gly
 210 215 220
 Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His

[illegible]

```
<210> 114
<211> 241
<212> PRT
<213> Homo sapien
```

<400> 114															
Met	Gln	Cys	Phe	Ser	Phe	Ile	Lys	Thr	Met	Met	Ile	Leu	Phe	Asn	Leu
1				5					10					15	
Leu	Ile	Phe	Leu	Cys	Gly	Ala	Ala	Leu	Leu	Ala	Val	Gly	Ile	Trp	Val
			20					25					30		
Ser	Ile	Asp	Gly	Ala	Ser	Phe	Leu	Lys	Ile	Phe	Gly	Pro	Leu	Ser	Ser
		35					40					45			
Ser	Ala	Met	Gln	Phe	Val	Asn	Val	Gly	Tyr	Phe	Leu	Ile	Ala	Ala	Gly
	50					55					60				
Val	Val	Val	Phe	Ala	Leu	Gly	Phe	Leu	Gly	Cys	Tyr	Gly	Ala	Lys	Thr
65					70					75					80

Glu Ser Lys Cys Ala Leu Val Thr Phe Phe Phe Ile Leu Leu Leu Ile
 85 90 95
 Phe Ile Ala Glu Val Ala Ala Ala Val Val Ala Leu Val Tyr Thr Thr
 100 105 110
 Met Ala Glu His Phe Leu Thr Leu Leu Val Val Pro Ala Ile Lys Lys
 115 120 125
 Asp Tyr Gly Ser Gln Glu Asp Phe Thr Gln Val Trp Asn Thr Thr Met
 130 135 140
 Lys Gly Leu Lys Cys Cys Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp
 145 150 155 160
 Ser Pro Tyr Phe Lys Glu Asn Ser Ala Phe Pro Pro Phe Cys Cys Asn
 165 170 175
 Asp Asn Val Thr Asn Thr Ala Asn Glu Thr Cys Thr Lys Gln Lys Ala
 180 185 190
 His Asp Gln Lys Val Glu Gly Cys Phe Asn Gln Leu Leu Tyr Asp Ile
 195 200 205
 Arg Thr Asn Ala Val Thr Val Gly Gly Val Ala Ala Gly Ile Gly Gly
 210 215 220
 Leu Glu Leu Ala Ala Met Ile Val Ser Met Tyr Leu Tyr Cys Asn Leu
 225 230 235 240
 Gln

<210> 115
 <211> 366
 <212> DNA
 <213> Homo sapien

<400> 115
 gctctttctc tcccctctc tgaatttaac tctttcaact tgcaatttgc aaggattaca 60
 catttcaactg tgatgtatat tgtgttgcaa aaaaaaaaaa gtgtctttgt ttaaaattac 120
 ttggtttgtg aatccatctt gctttttccc cattggaact agtcattaac ccatctctga 180
 actggtagaa aaacatctga agagctagtc tatcagcatc tgacagggtga attggatggt 240
 tctcagaacc atttcaccca gacagcctgt ttctatcctg ttttaataaat tagtttgggt 300
 tctctacatg cataacaaac cctgctccaa tctgtcacat aaaagtctgt gacttgaagt 360
 ttagtc 366

<210> 116
 <211> 282
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(282)
 <223> n = A,T,C or G
 <400> 116
 acaaagatga accatttcct atattatagc aaaattaaaa tctaccogta ttctaattatt 60
 gagaaatgag atnaaacaca atnttataaa gtctacttag agaagatcaa gtgacctcaa 120
 agactttact attttcatat ttttaagacac atgatttatc ctatttttagt aacctggttc 180
 atacgttaaa caaaggataa tgtgaacagc agagaggatt tgttggcaga aaatctatgt 240
 tcaatctnga actatctana tcacagacat ttctattcct tt 282

<210> 117
 <211> 305
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(305)
 <223> n = A,T,C or G

<400> 117
 acacatgtcg cttcactgcc ttcttagatg cttctggtca acatanagga acagggacca 60
 tattttatcct ccctcctgaa acaattgcaa aataanacaa aatatatgaa acaattgcaa 120
 aataaggcaa aatatatgaa acaacaggtc tcgagatatt ggaaatcagt caatgaagga 180
 tactgatccc tgatcactgt cctaatagcag gatgtgggaa acagatgagg tcacctctgt 240
 gactgcccga gcttactgcc tgtagagagt ttctangctg cagttcagac agggagaaat 300
 tgggt 305

<210> 118
 <211> 71
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(71)
 <223> n = A,T,C or G

<400> 118
 accaaggtgt ntgaatctct gacgtgggga tctctgattc ccgcacaatc tgagtggaaa 60
 aantcctggg t 71

<210> 119
 <211> 212
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(212)
 <223> n = A,T,C or G

<400> 119
 actccggttg gtgtcagcag cacgtggcat tgaacatngc aatgtggagc ccaaaccaca 60
 gaaaatgggg tgaaattggc caactttcta tnaacttatg ttggcaantt tgccaccaac 120
 agtaagctgg cccttctaataaaaagaaaat tgaaagggtt ctcactaanc ggaattaant 180
 aatggantca aganactccc aggcctcagc gt 212

<210> 120
 <211> 90
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(90)
 <223> n = A,T,C or G

<400> 120
 actcgttgca natcaggggc ccccagagt caccgttgca ggagtccttc tggctcttgc 60
 ctccgccggc gcagaacatg ctggggtggg 90

<210> 121
 <211> 218
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(218)
 <223> n = A,T,C or G

<400> 121
 tgtancgtga anacgacaga nagggttgtc aaaaatggag aanccttgaa gtcattttga 60
 gaataagatt tgctaaaaga tttgggggcta aaacatgggtt attgggagac atttctgaag 120
 atatncangt aaattangga atgaattcat ggttcttttg ggaattcctt tacgatngcc 180
 agcatanact tcatgtgggg atancagcta cccttgta 218

<210> 122
 <211> 171
 <212> DNA
 <213> Homo sapien

<400> 122
 taggggtgta tgcaactgta aggacaaaaa ttgagactca actggcttaa ccaataaagg 60
 catttgtag ctcatggaac aggaagtcgg atggtggggc atcttcagtg ctgcatgagt 120
 caccaccccg gcggggtcat ctgtgccaca ggtccctgtt gacagtgcgg t 171

<210> 123
 <211> 76
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(76)
 <223> n = A,T,C or G

<400> 123
 tgtagcgtga agacnacaga atggtgtgtg ctgtgctatc caggaacaca tttattatca 60
 ttatcaanta ttgtgt 76

<210> 124
 <211> 131
 <212> DNA
 <213> Homo sapien

<400> 124
 acctttcccc aaggccaatg tctgtgtgta taactggccg gctgcaggac agctgcaatt 60
 caatgtgctg ggtcatatgg aggggaggag actctaaaat agccaatttt attctcttgg 120
 ttaagatttg t 131

<210> 125
 <211> 432
 <212> DNA
 <213> Homo sapien

<400> 125
 actttatcta ctggctatga aatagatggt ggaaaattgc gttaccaact ataccactgg 60
 cttgaaaaag aggtgatagc tcttcagagg acttgtgact tttgctcaga tgctgaagaa 120

```

ctacagtctg catttggcag aaatgaagat gaatttggat taaatgagga tgctgaagat    180
ttgcctcacc aaacaaaagt gaaacaactg agagaaaatt ttcaggaaaa aagacagtgg    240
ctcttgaagt atcagtcact tttagaatg tttcttagtt actgcatact tcatggatcc    300
catggtgggg gtcttgcacg tgtaagaatg gaattgattt tgcttttgca agaattctcag    360
caggaaacat cagaaccact attttctagc cctctgtcag agcaaaccctc agtgcctctc    420
ctctttgctt gt                                     432

```

```

<210> 126
<211> 112
<212> DNA
<213> Homo sapien

```

```

<400> 126
acacaacttg aatagtaaaa tagaaactga gctgaaattt ctaattcact ttctaacct    60
agtaagaatg atatttcccc ccagggatca ccaaatattt ataaaaattt gt        112

```

```

<210> 127
<211> 54
<212> DNA
<213> Homo sapien

```

```

<400> 127
accacgaaac cacaacaag atggaagcat caatccactt gccaaagcaca gcag      54

```

```

<210> 128
<211> 323
<212> DNA
<213> Homo sapien

```

```

<400> 128
acctcattag taattgtttt gttgtttcat ttttttctaa tgtctcccct ctaccagctc    60
acctgagata acagaatgaa aatggaagga cagccagatt tctcctttgc tctctgctca    120
ttctctctga agtctaggtt acccattttg gggacccatt ataggcaata aacacagttc    180
ccaaagcatt tggacagttt cttgttgtgt tttagaatgg ttttcccttt tcttagcctt    240
ttctcgcaaa aggctcactc agtcccttgc ttgctcagtg gactggggctc cccagggcct    300
aggctgcctt cttttccatg tcc                                     323

```

```

<210> 129
<211> 192
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(192)
<223> n = A,T,C or G

```

```

<400> 129
acatacatgt gtgtatattt ttaaatatca cttttgtatc actctgactt tttagcatatc    60
tgaaaaacaca ctaacataat ttntgtgaac catgatcaga tacaacccaa atcattcatc    120
tagcacattc atctgtgata naaagatagg tgagtttcat ttccttcacg ttggccaatg    180
gataaacaata gt                                     192

```

```

<210> 130
<211> 362
<212> DNA
<213> Homo sapien

```

<220>
 <221> misc_feature
 <222> (1)...(362)
 <223> n = A,T,C or G

<400> 130
 ccctttttta tggaatgagt agactgtatg tttgaanatt tanccacaac ctctttgaca 60
 tataatgacg caacaaaaag gtgctgttta gtcctatggt tcagtttatg cccctgacaa 120
 gtttccattg tgttttgccg atcttctggc taatcgtggg atcctccatg ttattagtaa 180
 ttctgtattc cattttgtta acgcctggta gatgtaacct gctangaggc taactttata 240
 cttatttaaa agctcttatt ttgtggtcat taaaatggca atttatgtgc agcactttat 300
 tgcagcagga agcacgtgtg ggttggttgt aaagctcttt gctaattcta aaaagtaatg 360
 gg 362

<210> 131
 <211> 332
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(332)
 <223> n = A,T,C or G

<400> 131
 ctttttgaag gatcgtgtcc actcctgtgg acatcttgtt ttaatggagt ttcccatgca 60
 gtangactgg tatggttgca gctgtccaga taaaacatt tgaagagctc caaatgaga 120
 gttctcccag gttcgccctg ctgtcccaag tctcagcagc agcctctttt aggaggcatc 180
 ttctgaacta gattaaggca gcttgtaaat ctgatgtgat ttggtttatt atccaactaa 240
 cttccatctg ttatcactgg agaaagccca gactcccan gacnggtacg gattgtgggc 300
 atanaaggat tgggtgaagc tggcgttgtg gt 332

<210> 132
 <211> 322
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(322)
 <223> n = A,T,C or G

<400> 132
 acttttgcca ttttgtatat ataaacaatc ttgggacatt ctctgaaaa ctaggtgtcc 60
 agtggctaag agaactcgat ttcaagcaat tctgaaagga aaaccagcat gacacagaat 120
 ctcaaatcc caaacagggg ctctgtggga aaaaatgagg aggacctttg tatctcgggt 180
 tttagcaagt taaaatgaan atgacaggaa aggcttattt atcaacaaag agaagagttg 240
 ggatgcttct aaaaaaaact ttggtagaga aaataggaat gctnaatcct agggaagcct 300
 gtaacaatct acaattggtc ca 322

<210> 133
 <211> 278
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(278)

<223> n = A,T,C or G

<400> 133

acaagccttc	acaagttaa	ctaaattggg	attaatcttt	ctgtanttat	ctgcataatt	60
cttggttttc	tttccatctg	gtccctgggt	tgacaatttg	tggaacaac	tctattgcta	120
ctatttaaaa	aaaatcacaa	atctttccct	ttaagctatg	ttnaattcaa	actattcctg	180
ctattcctgt	tttgtcaaag	aaattatatt	tttcaaaaata	tgtntatttg	tttgatgggt	240
cccacgaaac	actaataaaa	accacagaga	ccagcctg			278

<210> 134

<211> 121

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(121)

<223> n = A,T,C or G

<400> 134

gtttanaaaa	cttgtttagc	tccatagagg	aaagaatggt	aaactttgta	ttttaaaaca	60
tgattctctg	aggttaaact	tggttttcaa	atgttatatt	tacttgtatt	ttgcttttgg	120
t						121

<210> 135

<211> 350

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(350)

<223> n = A,T,C or G

<400> 135

acttanaacc	atgcctagca	catcagaatc	cctcaaagaa	catcagtata	atcctataacc	60
atancaagtg	gtgactggtt	aagcgtgcga	caaagggtcag	ctggcacatt	acttgtgtgc	120
aaacttgata	cttttggtct	aagtaggaac	tagtatacag	tncctaggan	tggtactcca	180
gggtgcccc	caactcctgc	agccgctcct	ctgtgccagn	ccctgnaagg	aactttcgct	240
ccacctcaat	caagccctgg	gccatgctac	ctgcaattgg	ctgaacaaac	gtttgctgag	300
ttcccaagga	tgcaaagcct	ggtgctcaac	tctgtgggag	tcaactcagt		350

<210> 136

<211> 399

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(399)

<223> n = A,T,C or G

<400> 136

tgtaccgtga	agacgacaga	agttgcatgg	cagggacagg	gcagggccga	ggccagggtt	60
gctgtgattg	tatccgaata	ntcctcgtga	gaaaagataa	tgagatgacg	tgagcagcct	120
gcagacttgt	gtctgccttc	anaagccag	acaggaaggc	cctgcctgcc	ttggctctga	180
cctggcggcc	agccagccag	ccacaggtgg	gcttcttcct	tttgtggtga	caacnccaag	240
aaaactgcag	aggcccaggg	tcaggtgtna	gtgggtangt	gaccataaaa	caccaggtgc	300

tcccaggaaac ccggggcaaag gccatcccca cctacagcca gcatgccac tggcgtgatg	360
ggtgcagang gatgaagcag ccagntgttc tgctgtggt	399

<210> 137

<211> 165

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(165)

<223> n = A,T,C or G

<400> 137

actggtgtgg tnggggtga tgctggtggt anaagttgan gtgacttcan gatggtgtgt	60
ggaggaagtg tgtgaacgta gggatgtaga ngttttggcc gtgctaaatg agcttcggga	120
ttggctggtc ccactggtgg tcactgtcat tgggtggggt cctgt	165

<210> 138

<211> 338

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(338)

<223> n = A,T,C or G

<400> 138

actcactgga atgccacatt cacaacagaa tcagaggtct gtgaaaacat taatggctcc	60
ttaacttctc cagtaagaat cagggacttg aaatggaaac gttacagcc acatgcccaa	120
tgctgggcag tctcccatgc cttccacagt gaaagggtt gagaaaaatc acatccaatg	180
tcattgtgtt ccagccacac caaaagggtc ttgggggtgga gggctggggg catananggt	240
cangcctcag gaagcctcaa gttccattca gctttgccac tgtacattcc ccatntttaa	300
aaaaactgat gccttttttt tttttttttg taaaattc	338

<210> 139

<211> 382

<212> DNA

<213> Homo sapien

<400> 139

gggaatcttg gtttttgga tctggtttgc ctatagccga ggccactttg acagaacaaa	60
gaaagggact tcgagtaaga aggtgattta cagccagcct agtgcccga gtgaaggaga	120
attcaaacag acctcgtcat tcctggtgtg agcctgggtc gctcaccgcc tatcatctgc	180
atttgctta ctcagtgct accggactct ggcccctgat gtctgtagtt tcacaggatg	240
cettatttgt cttctacacc ccacagggcc ccctacttct tcggatgtgt ttttaataat	300
gtcagctatg tgcccatcc tccttcatgc cctccctccc tttcctacca ctgctgagt	360
gcctggaact tgtttaaagt gt	382

<210> 140

<211> 200

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(200)

<223> n = A,T,C or G

<400> 140

acccaaanctt	ctttctgttg	tgtnngattt	tactataggg	gttnngcttn	ttctaaanct	60
acttttcatt	taacancctt	tgtaagtgt	caggetgcac	tttgcctcat	anaattattg	120
ttttcacatt	tcaacttgta	tggtttgtc	tcttanagca	ttggtgaaat	cacataattt	180
atattcagca	ttaaaggagaa					200

<210> 141

<211> 335

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(335)

<223> n = A,T,C or G

<400> 141

actttatttt	caaaacactc	atatgttgca	aaaaacacat	agaaaaataa	agtttggtgg	60
gggtgctgac	taaacttcaa	gtcacagact	tttatgtgac	agattggagc	agggtttggt	120
atgcatgtag	agaaccctaaa	ctaatttatt	aaacaggata	gaaacaggct	gtctgggtga	180
aatggttctg	agaaccatcc	aattcacctg	tcagatgctg	atanactagc	tcttcagatg	240
tttttctacc	agttcagaga	tnggttaatg	actantttcca	atggggaaaa	agcaagatgg	300
attcacaaac	caagtaattt	taaacaaaga	cactt			335

<210> 142

<211> 459

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(459)

<223> n = A,T,C or G

<400> 142

accagggtta	tattgccaca	tatatccttt	ccaattgcgg	gctaaacaga	cgtgtattta	60
gggtgtgtta	aagacaaccc	agcttaatat	caagagaaat	tgtgaccttt	catggagtat	120
ctgatggaga	aaacactgag	ttttgacaaa	tcttatttta	ttcagatagc	agtctgatca	180
cacatgggtcc	aacaacactc	aaataataaa	tcaaataatna	tcagatgtta	aagattggtc	240
ttcaaacatc	atagccaatg	atgccccgct	tgcttataat	ctctccgaca	taaaaccaca	300
tcaaaccttc	agtggccacc	aaaccattca	gcacagcttc	cttaactgtg	agctgtttga	360
agctaccagt	ctgagcacta	ttgactatnt	ttttcangct	ctgaatagct	ctagggatct	420
cagcangggg	gggaggaacc	agctcaacct	tggcgtant			459

<210> 143

<211> 140

<212> DNA

<213> Homo sapien

<400> 143

acatttcctt	ccaccaagtc	aggactcctg	gcttctgtgg	gagttcttat	cacctgaggg	60
aaatccaaac	agtctctcct	agaaggaat	agtgtcacca	acccaccca	tctccctgag	120
accatccgac	ttccctgtgt					140

<210> 144

<211> 164

<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(164)
<223> n = A,T,C or G

<400> 144
acttcagtaa caacatacaa taacaacatt aagtgtatat tgccatcttt gtcattttct 60
atctatacca ctctcccttc tgaaaacaan aatcactanc caatcactta tacaaatttg 120
aggcaattaa tccatatttg ttttcaataa ggaaaaaaag atgt 164

<210> 145
<211> 303
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(303)
<223> n = A,T,C or G

<400> 145
acgtagacca tccaactttg tatttgtaat ggcaaacatc cagnagcaat tcctaaacaa 60
actggagggt atttataccc aattatccca ttcattaaca tgccctcctc ctcaggctat 120
gcaggacagc taticataagt cggcccaggc atccagatac taccatttgt ataaacttca 180
gtaggggagt ccatccaagt gacaggtcta atcaaaggag gaaatggaac ataagcccag 240
tagtaaaatn ttgcttagct gaaacagcca caaaagactt accgccgtgg tgattaccat 300
caa 303

<210> 146
<211> 327
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(327)
<223> n = A,T,C or G

<400> 146
actgcagctc aattagaagt ggtctctgac tttcatcanc ttctccctgg gctccatgac 60
actggcctgg agtgactcat tgctctggtt ggttgagaga gctcctttgc caacaggcct 120
ccaagtcagg gctgggattt gtttccttcc cacattctag caacaatatg ctggccactt 180
cctgaacagg gaggggtgga ggagccagca tggaacaagc tgccactttc taaagtagcc 240
agacttgccc ctgggcctgt cacacctact gatgaccttc tgtgcctgca ggatggaatg 300
taggggtgag ctgtgtgact ctatggt 327

<210> 147
<211> 173
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(173)
<223> n = A,T,C or G

<400> 147

acattgtttt	tttgagataa	agcattgana	gagctctcct	taacgtgaca	caatggaagg	60
actggaacac	ataccacat	ctttgttctg	agggataatt	ttctgataaa	gtcttgctgt	120
atattcaagc	acatatgtta	tatattattc	agttccatgt	ttatagccta	ggt	173

<210> 148

<211> 477

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(477)

<223> n = A,T,C or G

<400> 148

acaaccactt	tatctcatcg	aatttttaac	ccaaactcac	tactgtgcc	tttctatcct	60
atgggatata	ttatttgatg	ctccatttca	tcacacatat	atgaataata	cactcatact	120
gccctactac	ctgctgcaat	aatcacattc	ccttcctgtc	ctgaccctga	agccattggg	180
gtggtcctag	tggccatcag	tccangcctg	caccttgagc	ccttgagctc	cattgctcac	240
nccanccac	ctcacgcacc	ccatcctctt	acacagctac	ctccttgctc	tctaacccca	300
tagattatnt	ccaaattcag	tcaattaagt	tactattaac	actctaccgc	acatgtccag	360
caccactggt	aagccttctc	cagccaacac	acacacacac	acacncacac	acacacatat	420
ccaggcacag	gctacctcat	cttcacaatc	acccctttta	ttaccatgct	atggtgg	477

<210> 149

<211> 207

<212> DNA

<213> Homo sapien

<400> 149

acagttgtat	tataatatca	agaaataaac	ttgcaatgag	agcatttaag	agggagaagac	60
taacgtatnt	tagagagcca	aggaagggtt	ctgtggggag	tgggatgtaa	ggtggggcct	120
gatgataaat	aagagtcagc	caggttaagt	ggtggtgtgg	tatgggcaca	gtgaagaaca	180
tttcaggcag	agggaacagc	agtgaaa				207

<210> 150

<211> 111

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(111)

<223> n = A,T,C or G

<400> 150

accttgattt	cattgctgct	ctgatggaaa	cccaactatc	taatttagct	aaaacatggg	60
cacttaaagt	tggtcagtgt	ttggacttgt	taactantgg	catctttggg	t	111

<210> 151

<211> 196

<212> DNA

<213> Homo sapien

<400> 151

agcgcgagcag	gtcatattga	acattccaga	tacctatcat	tactcgatgc	tgttgataac	60
-------------	------------	------------	------------	------------	------------	----

agcaagatgg ctttgaactc agggtcacca ccagctattg gaccttacta tgaaaaccat	120
ggataccaac cggaaaaccc ctatcccgca cagccactg tgggtcccccac tgtctacgag	180
gtgcatccgg ctgagt	196

<210> 152
 <211> 132
 <212> DNA
 <213> Homo sapien

<400> 152	
acagcacttt cacatgtaag aaggagaaaa ttccctaaatg taggagaaaag ataacagAAC	60
cttccccttt tcatctagtgt gtggaaacct gatgctttat gttgacagga atagaaccag	120
gaggagattt gt	132

<210> 153
 <211> 285
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(285)
 <223> n = A,T,C or G

<400> 153	
acaanaccCa nganaggcca ctggccgtgg tgtcatggcc tccaaacatg aaagtgtcag	60
cttctgctct tatgtcctca tctgacaact ctttaccatt tttatcctcg ctgagcagga	120
gcacatcaat aaagtccaaa gtcttgact tggccttggc ttggaggaag tcatcaacac	180
cctggctagt gaggtgctgg cgccgctcct ggatgacggc atctgtgaag tctgtcacca	240
gtctgcaggc cctgtggaag cgccgtccac acggagtnag gaatt	285

<210> 154
 <211> 333
 <212> DNA
 <213> Homo sapien

<400> 154	
accacagtcc tgttgggcca gggcttcatg accctttctg tgaaaagcca tattatcacc	60
accccaatt tttccttaaa tatctttaac tgaaggggtc agcctcttga ctgcaaagac	120
cctaagccgg ttacacagct aactccact ggccctgatt tgtgaaattg ctgctgctg	180
attggcacag gagtccaagg tgttcagctc ccctcctcgg tggaacgaga ctctgatttg	240
agtttcacaa attctcgggc cacctcgtca ttgtcctct gaaataaaat ccggagaatg	300
gtcaggcctg tctcatccat atggatcttc cgg	333

<210> 155
 <211> 308
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(308)
 <223> n = A,T,C or G

<400> 155	
actggaaata ataaaaccca catcacagtgt ttgtgtcaaa gatcatcagg gcatggatgg	60
gaaagtgcct tgggaactgt aaagtgccta acacatgatc gatgattttt gttataatat	120
ttgaatcacg gtgcatacaa actctcctgc ctgctcctcc tgggccccag cccagcccc	180

atcacagetc actgctctgt tcatccaggc ccagcatgta gtggtgatt cttcttggt	240
gcttttagcc tccanaagtt tctctgaagc caaccaaacc tctangtgta aggcattgctg	300
gccctggg	308

<210> 156
 <211> 295
 <212> DNA
 <213> Homo sapien

<400> 156	
accttgctcg gtgcttgga catattagga actcaaaata tgagatgata acagtgccta	60
ttattgatta ctgagagaac tgtagacat ttagttgaag attttctaca caggaactga	120
gaataggaga ttatgtttgg ccctcatatt ctctcctatc ctcttgctt cattctatgt	180
ctaataatatt ctcaatcaaa taaggtagc ataatcagga aatcgaccaa ataccaatat	240
aaaaccagat gtctatcctt aagattttca aatagaaaac aaattaacag actat	295

<210> 157
 <211> 126
 <212> DNA
 <213> Homo sapien

<400> 157	
acaagtttaa atagtgtgt cactgtgcat gtgctgaaat gtgaaatcca ccacatttct	60
gaagagcaaa acaaattctg tcatgtaatc tctatcttgg gtcgtgggta tatctgtccc	120
cttagt	126

<210> 158
 <211> 442
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(442)
 <223> n = A,T,C or G

<400> 158	
accactgggt cttggaaca cccatcctta atacgatgat ttttctgtcg tgtgaaaatg	60
aanccagcag gctgccccta gtcagtcctt ccttccagag aaaaagagat ttgagaaagt	120
gcctgggtaa ttcaccatta atttccctcc ccaaactctc tgagtcttcc cttaatat	180
ctgggtggtc tgaccaaagc aggtcatggg ttgttgagca tttgggatcc cagtgaagta	240
natgtttgta gccttgcata cttagccctt cccacgcaca aacggagtgg cagagtggg	300
ccaaccctgt tttccagtc cactagaca gattcacagt gcggaattct ggaagctgga	360
nacagacggg ctctttgcag agccgggact ctgagangga catgagggcc tctgcctctg	420
tgttcattct ctgatgtcct gt	442

<210> 159
 <211> 498
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(498)
 <223> n = A,T,C or G

<400> 159	
acttccaggt aacgttggtg tttccgttga gcctgaactg atgggtgacg ttgtaggttc	60

tccaacaaga	actgaggttg	cagagcgggt	aggaagagt	gctgttccag	ttgcacctgg	120
gctgctgtgg	actgttggtg	attcctcact	acggcccaag	gttgtggaac	tggcanaaag	180
gtgtgtgtgt	gganttgagc	tcgggcggct	gtggtaggtt	gtgggctctt	caacaggggc	240
tgctgtggtg	ccgggangtg	aangtgttgt	gtcacttgag	cttggccagc	tctggaaagt	300
antanattct	tcctgaaggc	cagcgcttgt	ggagctggca	ngggtcantg	ttgtgtgtaa	360
cgaaccagtg	ctgctgtggg	tgggtgtana	tcctccacaa	agcctgaagt	tatgggtgcn	420
tcaggtana	atgtggtttc	agtgtccctg	ggcngctgtg	gaaggttgta	nattgtcacc	480
aagggaataa	gctgtggt					498

<210> 160

<211> 380

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(380)

<223> n = A,T,C or G

<400> 160

acctgcatcc	agcttccctg	ccaaactcac	aaggagacat	caacctctag	acagggaaac	60
agcttcagga	tacttccagg	agacagagcc	accagcagca	aaacaaatat	tcccatgcct	120
ggagcatggc	atagaggaag	ctganaaaatg	tggggtctga	ggaagccatt	tgagtctggc	180
cactagacat	ctcatcagcc	acttgtgtga	agagatgccc	catgacccca	gatgcctctc	240
ccacccttac	ctccatctca	cacacttgag	ctttccactc	tgtataattc	taacatcctg	300
gagaaaaatg	gcagtttgac	cgaacctgtt	cacaacggta	gaggctgatt	tctaacgaaa	360
cttgtagaat	gaagcctgga					380

<210> 161

<211> 114

<212> DNA

<213> Homo sapien

<400> 161

actccacatc	ccctctgagc	aggcggttgt	cgttcaaggt	gtatttggcc	ttgcctgtca	60
cactgtccac	tggcccctta	tccacttggt	gcttaatccc	tcgaaagagc	atgt	114

<210> 162

<211> 177

<212> DNA

<213> Homo sapien

<400> 162

actttctgaa	tcgaatcaaa	tgatacttag	tgtagtttta	atatcctcat	atatatcaaa	60
gttttactac	tctgataatt	ttgtaaacca	ggtaaccaga	acatccagtc	atacagcttt	120
tggtgatata	taacttgga	ataaccagct	ctggtgatac	ataaaactac	tcactgt	177

<210> 163

<211> 137

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(137)

<223> n = A,T,C or G

<400> 163

catttataca gacaggcgtg aagacattca cgacaaaaac gcgaaattct atcccgtgac	60
canagaaggc agctacggct actcctacat cctggcgtgg gtggccttcg cctgcacctt	120
catcagcggc atgatgt	137

<210> 164

<211> 469

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(469)

<223> n = A,T,C or G

<400> 164

cttatcacaa tgaatgttct cctgggcagc gttgtgatct ttgccacctt cgtgacttta	60
tgcaatgcat catgctatct cttacctaata gagggagttc caggagattc aaccaggaaa	120
tgcatggatc tcaaaggaaa caaacaccca ataaactcgg agtggcagac tgacaactgt	180
gagacatgca cttgctacga aacagaaatt tcatgttgca cccttggttc tacacctgtg	240
ggttatgaca aagacaactg ccaaagaatc ttcaagaagg aggactgcaa gtatatcgtg	300
gtggagaaga aggacccaaa aaagacctgt tctgtcagtg aatggataat ctaatgtgct	360
tctagtaggc acagggtcc caggccaggc ctcattctcc tctggcctct aatagtcaat	420
gattgtgtag ccattgcctat cagtaaaaag atntttgagc aaacacttt	469

<210> 165

<211> 195

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(195)

<223> n = A,T,C or G

<400> 165

acagtttttt atanatcgc acattgccgg cacttggttt cagtttcata aagctgggtg	60
atccgctgtc atccactatt ccttggctag agtaaaaatt attcttatag cccatgtccc	120
tgcaggccgc ccgcccgtag ttctcgttcc agtcgtcttg gcacacaggg tgccaggact	180
tcctctgaga tgagt	195

<210> 166

<211> 383

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(383)

<223> n = A,T,C or G

<400> 166

acatcttagt agtgtggcac atcagggggc catcagggtc acagtcactc atagcctcgc	60
cgaggctcga gtccacacca ccggtgtagg tgtgtcctaat cttgggcttg gcgcccacct	120
ttggagaagg gatattgtgc acacacatgt ccacaaagcc tgtgaactcg ccaaagaatt	180
tttgacagacc agcctgagca agggggcgat gttcagcttc agctcctcct tcgtcagggtg	240
gatgccaacc tcgtctangg tccgtgggaa gctgggtgct acntcaccta caacctgggc	300
gangatctta taaagaggct ccnagataaa ctccacgaaa cttctctggg agctgctagt	360
nggggccttt ttggtgaact ttc	383

<210> 167
 <211> 247
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(247)
 <223> n = A,T,C or G

<400> 167
 acagagccag accttgGCCa taaatgaanc agagattaag actaaacccc aagtcganat 60
 tggagcagaa actggagcaa gaagtgggcc tggggctgaa gtagagacca aggccactgc 120
 tatanccata cacagagcca actctcaggg caaggcnatg gttggggcag anccagagac 180
 tcaatctgan tccaaagtgg tggctggaac actggctcatg acanaggcag tgactctgac 240
 tgangtc 247

<210> 168
 <211> 273
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(273)
 <223> n = A,T,C or G

<400> 168
 acttctaagt tttctagaag tggaaggatt gtantcatcc tgaaaatggg tttacttcaa 60
 aatccctcan ccttgttctt cacnactgtc tatactgana gtgtcatgtt tccacaaagg 120
 gctgacacct gagcctgnat tttactcat ccctgagaag ccctttccag taggggtggc 180
 aattcccaac ttccttgcca caagcttccc aggcctttctc ccctggaaaa ctccagcttg 240
 agtcccagat acactcatgg gctgccctgg gca 273

<210> 169
 <211> 431
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(431)
 <223> n = A,T,C or G

<400> 169
 acagccttgg cttcccca aa ctccacagtc tcagtgcaga aagatcatct tccagcagtc 60
 agctcagacc agggtc aaag gatgtgacat caacagtttc tggtttcaga acaggttcta 120
 ctactgtcaa atgaccccc atacttcctc aaaggctgtg gtaagttttg cacaggtgag 180
 ggcagcagaa aggggttant tactgatgga caccatcttc tctgtatact ccacactgac 240
 cttgccatgg gcaaaggccc ctaccacaaa aacaatagga tcaactgctgg gcaccagctc 300
 acgcacatca ctgacaaccg ggatggaaaa agaantgcc aactttcatac atccaactgg 360
 aaagtgatct gatactggat tcttaattac cttcaaaagc ttctgggggc catcagctgc 420
 tcgaacactg a 431

<210> 170
 <211> 266
 <212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(266)

<223> n = A,T,C or G

<400> 170

acctgtgggc	tggtctgtta	tgctgtgcc	ggctgtgaa	agggagttca	gaggtggagc	60
tcaaggagct	ctgcaggcat	tttgccaanc	ctctccanag	canagggagc	aacctacact	120
ccccgctaga	aagacaccag	attggagtc	tggtggggg	agttggggg	ggcatttgat	180
gtatacttgt	cacctgaatg	aangagccag	agaggaanga	gacgaanatg	anattggcct	240
tcaaagctag	gggtctggca	ggtgga				266

<210> 171

<211> 1248

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(1248)

<223> n = A,T,C or G

<400> 171

ggcagccaaa	tcataaacgg	cgaggactgc	agcccgcact	cgcagccctg	gcaggcggca	60
ctggtcatgg	aaaacgaatt	gttctgctcg	ggcgtcctgg	tgcatccgca	gtgggtgctg	120
tcagccgcac	actgtttcca	gaagtgaatg	cagagctcct	acaccatcgg	gctgggcctg	180
cacagtcttg	agggcgacca	agagccagg	agccagatgg	tgagggccag	cctctccgta	240
cggcaccag	agtacaacag	acccttgctc	gctaaccgacc	tcagtctcat	caagttggac	300
gaatccgtgt	ccgagtctga	caccatccgg	agcatcagca	ttgcttcgca	gtgccctacc	360
gcggggaaact	cttgccctcg	ttctggctgg	ggtctgctgg	cgaacggcag	aatgcctacc	420
gtgctgcagt	gcgtgaacgt	gtcgggtggtg	tctgaggagg	tctgcagtaa	gctctatgac	480
ccgctgtacc	accccgagcat	gttctgcgcc	ggcggaggggc	aagaccagaa	ggactcctgc	540
aacggtgact	ctggggggcc	cctgatctgc	aacgggtact	tgaggggcct	tgtgtctttc	600
ggaaaagccc	cgtgtggcca	agttggcgtg	ccagggtgtct	acaccaacct	ctgcaaattc	660
actgagtggg	tagagaaaac	cgtccaggcc	agttaactct	ggggactggg	aacccatgaa	720
attgaccccc	aaatacatcc	tgcggaagga	attcaggaat	atctgttccc	agcccctcct	780
ccctcaggcc	caggagtcca	ggccccagc	ccctcctccc	tcaaaccaag	ggtacagatc	840
cccagcccct	cctccctcag	acccaggagt	ccagaccccc	cagcccctcc	tccctcagac	900
ccaggagtcc	agcccctcct	ccctcagacc	caggagtcca	gacccccag	cccctcctcc	960
ctcagaccga	ggggtccagg	cccccaaccc	ctcctccctc	agactcagag	gtccaagccc	1020
ccaaccntc	attcccaga	cccagaggtc	cagggtccag	cccctcntcc	ctcagaccga	1080
gcggtccaat	gccacctaga	ctntccctgt	acacagtgcc	cccttggtggc	acgttgaccc	1140
aaccttacca	gttggttttt	catttttngt	ccctttcccc	tagatccaga	aataaagttt	1200
aagagaagng	caaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa		1248

<210> 172

<211> 159

<212> PRT

<213> Homo sapien

<220>

<221> VARIANT

<222> (1)...(159)

<223> Xaa = Any Amino Acid

<400> 172


```

Met Val Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro
 1           5           10           15
Leu Leu Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser
           20           25           30
Glu Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr
           35           40           45
Ala Gly Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly
 50           55           60
Arg Met Pro Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu
 65           70           75           80
Glu Val Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe
           85           90           95
Cys Ala Gly Gly Gly Gln Xaa Gln Xaa Asp Ser Cys Asn Gly Asp Ser
           100          105          110
Gly Gly Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe
           115          120          125
Gly Lys Ala Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn
           130          135          140
Leu Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser
145           150           155

```

```

<210> 173
<211> 1265
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(1265)
<223> n = A,T,C or G

```

```

<400> 173
ggcagcccgcc actcgccagcc ctggcaggcg gcaactgggtca tggaaaacga attgttctgc      60
tcgggcggtcc tgggtgcatcc gcagtgggtg ctgtcagccg cacactgttt ccagaactcc      120
tacaccatcg ggctgggcct gcacagtctt gaggccgacc aagagccagg gagccagatg      180
gtggaggcca ccctctccgt acggcaccca gactacaaca gaccttgct cgctaacgac      240
ctcatgctca tcaagttgga cgaatccgtg tccgagtctg acaccatccg gagcatcagc      300
attgcttcgc agtgccttac cgcggggaac tcttgctctg tttctggctg gggctctgctg      360
gcgaacggtg agctcacggg tgtgtgtctg ccctcttcaa ggaggtcttc tgcccagtcg      420
cgggggctga ccagagctc tgcgtcccag gcagaatgcc taccgtgctg cagtgcgtga      480
acgtgtcggg ggtgtctgag gaggtctgca gtaagctcta tgaccgctg taccaccca      540
gcatgttctg cgccggcgga gggcaagacc agaaggactc ctgcaacggt gactctgggg      600
ggccctgat ctgcaacggg tacttgagg gtctacacca acctctgcaa attcactgag tggatagaga      660
gccaagttgg cgtgccaggt gtctacacca acctctgcaa attcactgag tggatagaga      720
aaaccgtcca ggccagttaa ctctggggac tgggaaccca tgaaattgac ccccaaatac      780
atcctgcgga aggaattcag gaatatctgt tcccagcccc tcctccctca ggcccaggag      840
tccaggcccc cagcccctcc tccctcaaac caagggtaca gatccccagc ccctcctccc      900
tcagaccagc gaggccagac cccccagccc ctccctccctc agaccagga gtccagcccc      960
tcctccntca gaccaggag tccagacccc ccagcccctc ctccctcaga cccaggggtt     1020
gaggccccc acccctctc ctccagagtc agaggtccaa gcccacaacc cctcgttccc     1080
cagaccagga ggtnnaggtc ccagcccctc ttccntcaga cccagngtc caatgccacc     1140
tagattttcc gtgnacacag tgcccccttg tggngangttg acccaacctt accagttggt     1200
ttttcatttt tngtcccttt cccctagatc cagaaataaa gtttaagaga ngngcaaaaa     1260
aaaaa                                           1265

```

```

<210> 174
<211> 1459
<212> DNA

```

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(1459)

<223> n = A,T,C or G

<400> 174

```

ggtcagccgc acactgtttc cagaagttag tgcagagctc ctacaccatc gggctgggccc 60
tgcacagtct tgaggccgac caagagccag ggagccagat ggtggaggcc agcctctccg 120
tacggcacc agagtacaac agacccttgc tcgctaacga cctcatgctc atcaagttgg 180
acgaatccgt gtccgagtct gacaccatcc ggagcatcag cattgcttcg cagtgcctta 240
ccgcggggaa ctcttgccct gtttctggct ggggtctgct ggcgaacggt gagctcacgg 300
gtgtgtgtct gccctcttca aggaggtcct ctgcccagtc gcgggggctg acccagagct 360
ctgcgtccca ggcagaatgc ctaccgtgct gcagtgcgtg aacgtgtcgg tgggtgtctga 420
ngaggtctgc antaagctct atgaccgct gtaccacccc ancatgttct gcgcggcg 480
agggcaagac cagaaggact cctgcaacgt gagagagggg aaaggggagg gcaggcgact 540
caggggaagg tggagaagg ggagacagag acacacaggg ccgcatggcg agatgcagag 600
atggagagac acacagggag acagtgacaa cttagagagag aaactgagag aaacagagaa 660
ataaacacag gaataaagag aagcaaagga agagagaaac agaaacagac atggggaggc 720
agaaacacac acacatagaa atgcagttga ccttccaaca gcatggggcc tgagggcggt 780
gacctccacc caatagaaaa tcctcttata acttttgact ccccaaaaac ctgactagaa 840
atagcctact gttgacgggg agccttacca ataacataaa tagtcgattt atgcatacgt 900
tttatgcatt catgatatac ctttgttga attttttgat atttctaagc tacacagttc 960
gtctgtgaat ttttttaa atgttgcaact ctctaaaat ttttctgatg tgtttattga 1020
aaaaatccaa gtataaagtgg acttgtgcat tcaaaccagg gttgttcaag ggtcaactgt 1080
gtaccagag ggaaacagt acacagattc atagaggtga aacacgaaga gaaacaggaa 1140
aaatcaagac tctacaaaga ggctgggcag ggtggctcat gcctgtaatc ccagcacttt 1200
gggaggcgag gcaggcagat cacttgaggt aaggagttca agaccagcct ggccaaaatg 1260
gtgaaatcct gtctgtacta aaaatacaaa agttagctgg atatgggtggc aggcgcctgt 1320
aatccagct acttgggagg ctgaggcagg agaattgctt gaatatggga ggcagaggtt 1380
gaagttagtt gagatcacac cactatactc cagctggggc aacagagtaa gactctgtct 1440
caaaaaaaaa aaaaaaaaaa 1459

```

<210> 175

<211> 1167

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(1167)

<223> n = A,T,C or G

<400> 175

```

gcgcagccct ggcaggcggc actggtcatg gaaaacgaat tgttctgctc gggcgctcctg 60
gtgcatccgc agtgggtgct gtcagccgca cactgtttcc agaactccta caccatcg 120
ctgggcctgc acagtcttga ggccgaccaa gagccaggga gccagatggt ggaggccagc 180
ctctccgtac ggcaccaga gtacaacaga ctcttctcgc ctaacgacct catgtctc 240
aagttggagc aatccgtgct cgagtctgac accatccgga gcatcagcat tgcttcgag 300
tgccctaccg cggggaactc ttgcctcgtn tctggctggg gtctgctggc gaacggcaga 360
atgcctaccg tgctgcactg cgtgaacgtg tcggtgggtg ctgaggangt ctgcagtaag 420
ctctatgacc cgctgtacca cccagcatg ttctgcgcgc gcggagggca agaccagaag 480
gactcctgca acggtgactc tggggggccc ctgatctgca acgggtactt gcagggcctt 540
gtgtctttcg gaaaagcccc gtgtggccaa cttggcgtgc caggtgtcta caccaacctc 600
tgcaaattca ctgagtgat agagaaaacc gtccagncca gtttaactctg gggactggga 660
acccatgaaa ttgaccccca aatacatcct gcggaangaa ttcaggaata tctgttccca 720
gcccctcctc cctcaggccc aggagtccag gccccagcc cctcctccct caaaccaagg 780

```

```

gtacagatcc ccagcccctc ctccctcaga cccaggagtc cagacccccc agcccctcnt      840
ccntcagacc caggagtcca gccctcctc cntcagacgc aggagtccag acccccacgc      900
ccntcntccg tcagaccagc ggggtgcagc cccaacccc tcntccntca gagtcagagg      960
tccaagcccc caaccctcg ttccccagac ccagaggtnc aggtcccagc cctctctccc     1020
tcagaccagc cggccaatg ccacctagan tntccctgta cacagtgcc ccttggtgca     1080
ngttgacca accttaccag ttggtttttc attttttgtc cctttcccct agatccagaa     1140
ataaagtnta agagaagcgc aaaaaaa                                1167

```

<210> 176
 <211> 205
 <212> PRT
 <213> Homo sapien

<220>
 <221> VARIANT
 <222> (1)...(205)
 <223> Xaa = Any Amino Acid

```

<400> 176
Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp
 1          5          10          15
Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu
          20          25          30
Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val
          35          40          45
Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Leu Leu Leu
          50          55          60
Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser
          65          70          75          80
Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly
          85          90          95
Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg Met
          100          105          110
Pro Thr Val Leu His Cys Val Asn Val Ser Val Val Ser Glu Xaa Val
          115          120          125
Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys Ala
          130          135          140
Gly Gly Gly Gln Asp Gln Lys Asp Ser Cys Asn Gly Asp Ser Gly Gly
          145          150          155          160
Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly Lys
          165          170          175
Ala Pro Cys Gly Gln Leu Gly Val Pro Gly Val Tyr Thr Asn Leu Cys
          180          185          190
Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Xaa Ser
          195          200          205

```

<210> 177
 <211> 1119
 <212> DNA
 <213> Homo sapien

```

<400> 177
gcgcactcgc agccctggca ggcggcactg gtcattgaaa acgaattgtt ctgctcgggc      60
gtcctggtgc atccgcagtg ggtgctgtca gccgcacact gttccagaa ctctacacc      120
atcgggctgg gctgcacag tcttgaggcc gaccaagagc cagggagcca gatggtggag      180
gccagcctct ccgtacggca cccagagtac aacagaccct tgctcgctaa cgacctcatg      240
ctcatcaagt tggacgaatc cgtgtccgag tctgacacca tccggagcat cagcattgct      300
tcgcagtgcc ctaccgcggg gaactcttgc ctcttttctg gctggggtct gctggcgaac      360

```

```

gatgctgtga ttgccatcca gtcccagact gtgggaggct gggagtgtga gaagctttcc 420
caaccctggc agggttgtac catttcggca acttccagtg caaggacgtc ctgctgcatc 480
ctcactgggt gtcactact gtcactgca tcaccggaa cactgtgatc aactagccag 540
caccatagtt ctccgaagtc agactatcat gattactgtg ttgactgtgc tgtctattgt 600
actaaccatg ccgatgttta ggtgaaatta gcgtcacttg gcctcaacca tcttggtatc 660
cagttatcct cactgaattg agatttcctg cttcagtgtc agccattccc acataatttc 720
tgacctacag aggtgagggg tcatatagct cttcaaggat gctgggtactc ccctcacaaa 780
ttcatttctc ctggtgtagt gaaagggtgc ccctctggag cctcccaggg tgggtgtgca 840
ggtcacaatg atgaatgtat gatcgtgttc ccattaccca aagcctttaa atccctcatg 900
ctcagtacac cagggcaggt ctagcatttc ttcatttagt gtatgctgtc cattcatgca 960
accacctcag gactcctgga ttctctgcct agttgagctc ctgcatgctg cctccttggg 1020
gaggtgaggg agagggccca tggttcaatg ggatctgtgc agttgtaaca cattaggtgc 1080
ttaataaaca gaagctgtga tgttaaaaaa aaaaaaaaa 1119

```

<210> 178
 <211> 164
 <212> PRT
 <213> Homo sapien

<220>
 <221> VARIANT
 <222> (1) ... (164)
 <223> Xaa = Any Amino Acid

<400> 178

```

Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp
1      5      10      15
Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu
20     25     30
Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val
35     40     45
Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu Leu
50     55     60
Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser
65     70     75     80
Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly
85     90     95
Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Asp Ala Val
100    105    110
Ile Ala Ile Gln Ser Xaa Thr Val Gly Gly Trp Glu Cys Glu Lys Leu
115    120    125
Ser Gln Pro Trp Gln Gly Cys Thr Ile Ser Ala Thr Ser Ser Ala Arg
130    135    140
Thr Ser Cys Cys Ile Leu Thr Gly Cys Ser Leu Leu Leu Thr Ala Ser
145    150    155    160
Pro Gly Thr Leu

```

<210> 179
 <211> 250
 <212> DNA
 <213> Homo sapien

<400> 179

```

ctggagtgcc ttggtgtttc aagcccctgc aggaagcaga atgcaccttc tgaggcacct 60
ccagctgccc ccggccgggg gatgcgagggc tcggagcacc cttgcccggc tgtgattgct 120
gccaggcact gttcatctca gcttttctgt ccctttgctc ccggcaagcg cttctgtga 180
aagttcatat ctggagcctg atgtcttaac gaataaaggt cccatgctcc acccgaaaaa 240

```

aaaaaaaaaa

250

<210> 180
 <211> 202
 <212> DNA
 <213> Homo sapien

<400> 180

actagtccag	tgtggtggaa	ttccattgtg	ttggggcccaa	cacaatggct	acctttaaca	60
tcacccagac	cccgccctg	cccggtgccc	acgtgctgc	taacgacagt	atgatgctta	120
ctctgctact	cggaactat	ttttatgtaa	ttaatgtatg	ctttcttggt	tataaatgcc	180
tgatttaaaa	aaaaaaaaaa	aa				202

<210> 181
 <211> 558
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc_feature
 <222> (1)...(558)
 <223> n = A,T,C or G

<400> 181

tccytttgkt	naggtttkkg	agacamccck	agacctwaan	ctgtgtcaca	gacttcyngg	60
aatgttttag	cagtgttagt	aatttcytcg	taatgattct	gttattactt	tcctnattct	120
ttattcctct	ttcttctgaa	gattaatgaa	gttgaaaatt	gaggtggata	aatacaaaaa	180
ggtagtgtga	tagtataagt	atctaagtgc	agatgaaagt	gtgttatata	tatccattca	240
aaattatgca	agtttagtaat	tactcagggt	taactaaaatt	actttaatat	gctgttgaac	300
ctactctgtt	ccttggctag	aaaaaattat	aaacaggact	ttgttagttt	gggaagccaa	360
attgataata	ttctatgttc	taaaagttgg	gctatacata	aattattaag	aaatatggaw	420
ttttattccc	aggaatatgg	kgttcatttt	atgaatatta	cscrggatag	awgtwtgagt	480
aaaaycagtt	ttggtwaata	ygtwaatatg	tcmtaaataa	acaakgcttt	gacttatttc	540
caaaaaaaaa	aaaaaaaaa					558

<210> 182
 <211> 479
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc_feature
 <222> (1)...(479)
 <223> n = A,T,C or G

<400> 182

acagggwttk	grggatgcta	agscceerga	rwtygtttga	tccaaccctg	gcttwttttc	60
agaggggaaa	atggggccta	gaagttacag	mecatytagy	tgggtgcgmg	gcacccctgg	120
cstcacacag	astcccaggt	agctgggact	acaggcacac	agtcactgaa	gcaggccctg	180
ttwgcaattc	acgttgccac	ctccaactta	aacattcttc	atatgtgatg	tccttagtca	240
ctaagggtta	actttcccac	ccagaaaagg	caacttagat	aaaatcttag	agtactttca	300
tactmttcta	agtcctcttc	cagcctcact	kkgagtcctm	cytggggggt	gataggaant	360
ntctcttggc	tttctcaata	aartctctat	ycatctcatg	tttaatttgg	tacgcataara	420
awtgstgata	aaattaaaat	gttctggtty	macttttaaaa	araaaaaaaaa	aaaaaaaaaa	479

<210> 183
 <211> 384
 <212> DNA

<213> Homo sapien

<400> 183

aggcgggagc	agaagctaaa	gccaaagccc	aagaagagtg	gcagtgccag	cactggtgcc	60
agtaccagta	ccaataacag	tgccagtgcc	agtgccagca	ccagtgggtg	cttcagtgtc	120
ggtgccagcc	tgaccgccac	tctcacattt	gggtctctcg	ctggccttgg	tggagctggt	180
gccagcacca	gtggcagctc	tggtgcctgt	ggtttctcct	acaagtgaga	ttttagatat	240
tgttaatcct	gccagtcttt	ctcttcaagc	caggggtgcat	cctcagaaac	ctactcaaca	300
cagcactcta	ggcagccact	atcaatcaat	tgaagttgac	actctgcatt	aratctattt	360
gccatttcaa	aaaaaaaaaa	aaaa				384

<210> 184

<211> 496

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(496)

<223> n = A,T,C or G

<400> 184

accgaattgg	gaccgctggc	ttataagcga	tcatgttynt	ccrgtatcac	ctcaacgagc	60
aggagatcg	agttatatac	ctgaagaaat	ttgaccgat	gggacaacag	acctgctcag	120
cccacctgc	tcggttctcc	ccagatgaca	aatactctsg	acaccgaatc	accatcaaga	180
aacgcttcaa	ggtgctcatg	accagcaaac	cgcgccctgt	cctctgaggg	tcccttaaac	240
tgatgtcttt	tctgccacct	gttacccttc	ggagactccg	taaccaaact	cttcggactg	300
tgagccctga	tgcttttttg	ccagccatac	tctttggcat	ccagtctctc	gtggcgattg	360
attatgcttg	tgtgaggcaa	tcatggtggc	atcacccata	aagggaacac	atttgacttt	420
tttttctcat	attttaaat	actacmagaw	tattwmagaw	waaatgawtt	gaaaaactst	480
taaaaaaaaa	aaaaaa					496

<210> 185

<211> 384

<212> DNA

<213> Homo sapien

<400> 185

gctggtagcc	tatggcgkkg	cccacggagg	ggctcctgag	gccacggrac	agtgacttcc	60
caagtatcyt	gcgcsgcgtc	ttctaccgtc	cctacctgca	gatcttcggg	cagattcccc	120
aggaggacat	ggacgtggcc	ctcatggagc	acagcaactg	ytcgctcgag	cccggcttct	180
gggcacaccc	tcttgggggc	caggcgggca	cctgcgtctc	ccagtatgcc	aactggctgg	240
tggtgctgct	cctcgctcatc	ttcctgctcg	tggccaacat	cctgctggtc	aacttgctca	300
ttgccatggt	cagttacaca	ttcggcaaa	tacagggcaa	cagcgatctc	tactgggaag	360
gcgcagcggt	accgcctcat	ccgg				384

<210> 186

<211> 577

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(577)

<223> n = A,T,C or G

<400> 186

gagttagctc	ctccacaacc	ttgatgaggt	cgtctgcagt	ggcctctcgc	ttcataccgc	60
------------	------------	------------	------------	------------	------------	----

tnccatcgtc	atactgtagg	tttgccacca	cytcctggca	tcttggggcg	gcntaatatt	120
ccaggaaact	ctcaatcaag	tcaccgtoga	tgaacctgt	gggctgggtc	tgtcttccgc	180
tcggtgtgaa	aggatctccc	agaaggagtg	ctcgatcttc	cccacacttt	tgatgacttt	240
attgagtcga	ttctgcatgt	ccagcaggag	gttgtaccag	ctctctgaca	gtgaggtcac	300
cagccctatc	atgccgttga	mcgtgccgaa	garcaccgag	ccttgtgtgg	gggkkgaagt	360
ctcaccaga	ttctgcatta	ccagagagcc	gtggcaaaa	acattgacaa	actcgcccag	420
gtggaaaaag	amcamctcct	ggargtgctn	gccgctcctc	gtcmgttgg	ggcagcgctw	480
tccttttgac	acacaaacaa	gttaaaggca	ttttcagccc	ccagaaantt	gtcatcatcc	540
aagatntcgc	acagcactna	tccagttggg	attaaat			577

<210> 187

<211> 534

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(534)

<223> n = A,T,C or G

<400> 187

aacatcttcc	tgtataatgc	tgtgtaatat	cgatccgatn	ttgtctgstg	agaatycatw	60
actkggaaaa	gmaacattaa	agcctggaca	ctggtattaa	aattcacaat	atgcaacact	120
ttaaacagtg	tgtcaatctg	ctcccyynac	tttgcacatc	ccagtctggg	aakaagggtg	180
tgccctattc	acacctgtta	aaagggcgct	aagcattttt	gattcaacat	cttttttttt	240
gacacaagtc	cgaaaaaagc	aaaagtaaac	agttatyaat	ttgttagcca	attcactttc	300
ttcatgggac	agagccatyt	gatttaaaaa	gcaaattgca	taatattgag	cttygggagc	360
tgatatttga	gcggaagagt	agcctttcta	cttcaccaga	cacaactccc	tttcatattg	420
ggatgttnac	naaagtwatg	tctctwacag	atgggatgct	tttgtggcaa	ttctgttctg	480
aggatctccc	agtttatitta	ccacttgcac	aagaaggcgt	tttcttcttc	aggc	534

<210> 188

<211> 761

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(761)

<223> n = A,T,C or G

<400> 188

agaaaccagt	atctctnaaa	acaacctctc	ataccttggt	gacctaat	ttgtgtgcgtg	60
tgtgtgtgcg	cgcatattat	atagacaggc	acatcttttt	tacttttgta	aaagcttatg	120
cctctttggt	atctatatct	gtgaaagttt	taatgatctg	ccataatgtc	ttggggacct	180
ttgtcttctg	tgtaaatggt	actagagaaa	acacctatnt	tatgagtcaa	tctagttngt	240
tttattcgac	atgaaggaaa	tttccagatn	acaacactna	caaactctcc	ctkgackarg	300
ggggacaaa	aaaagcaaaa	ctgamcataa	raaacaatwa	cctgggtgaga	arttgcataa	360
acagaaatwr	ggtagtatat	tgaarnacag	catcattaaa	rmgttwtktt	wttctccctt	420
gcacaaaaaca	tgtacngact	tcccgttgag	taatgccaa	ttgttttttt	tatnataaaa	480
cttgcccttc	attacatggt	tnaaagtgg	gtgggtggcc	aaaatattga	aatgatggaa	540
ctgactgata	aagctgtaca	aataagcagt	gtgcctaaca	agcaacacag	taatgttgac	600
atgcttaatt	cacaaatgct	aatttcatta	taaatgtttg	ctaaaataca	ctttgaacta	660
ttttctgtgn	ttcccagagc	tgagatntta	gattttatgt	agtatnaagt	gaaaaantac	720
gaaaataata	acattgaaga	aaaananaaa	aaanaaaaaa	a		761

<210> 189

<211> 482

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(482)

<223> n = A,T,C or G

<400> 189

tttttttttt	tttgccgatn	ctactat	ttt	attgcaggan	gtgggggtgt	atgcaccgca	60
caccggggct	atnagaagca	agaaggaagg	agggagggca	cagccccttg	ctgagcaaca		120
aagccgcctg	ctgccttctc	tgtctgtctc	ctgggtgcagg	cacatgggga	gaccttcccc		180
aaggcagggg	ccaccagtc	aggggtggga	atacagggg	tgggangtgt	gcataagaag		240
tgataggcac	aggccaccg	gtacagaccc	ctcggctcct	gacaggtnga	tttcgaccag		300
gtcattgtgc	cctgccagg	cacagcgtan	atctggaaaa	gacagaatgc	tttccttttc		360
aaatttggct	ngtcatngaa	ngggcanttt	tccaantng	gctnggtctt	ggtacncttg		420
gttcggccca	gtccncgtc	caaaaantat	tcaccnct	ccnaattgct	tgcnngnccc		480
cc							482

<210> 190

<211> 471

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(471)

<223> n = A,T,C or G

<400> 190

tttttttttt	ttttaaaaca	gtttttcaca	acaaaattta	ttagaagaat	agtgggtttg	60
aaaactctcg	catccagtga	gaactaccat	acaccacatt	acagctngga	atgtntctcca	120
aatgtctggt	caaatgatac	aatggaacca	ttcaatctta	cacatgcacg	aaagaacaag	180
cgcttttgac	atacaatgca	caaaaaaaaa	aggggggggg	gaccacatgg	attaaaattt	240
taagtaactca	tcacatacat	taagacacag	ttctagtcca	gtcnaaaatc	agaactgcnt	300
tgaaaaattt	catgtatgca	atccaacca	agaacttnat	tggtgatcat	gantnctcta	360
ctacatcnac	cttgatcatt	gccaggaacn	aaaagttnaa	ancacncngt	acaaaaanaa	420
tctgtaattn	anttcaacct	ccgtacngaa	aaatnttntt	tatacactcc	c	471

<210> 191

<211> 402

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(402)

<223> n = A,T,C or G

<400> 191

gagggattga	aggtctgttc	tastgtcggm	ctgttcagcc	accaactcta	acaagttgct	60
gtcttccact	cactgtctgt	aagcttttta	accagacwg	tatcttcata	aatagaacaa	120
attcttcacc	agtcacatct	tctaggacct	ttttggattc	agttagtata	agctottcca	180
cttcctttgt	taagacttca	tctggtaaag	tcttaagttt	tgtagaaagg	aattyaattg	240
ctcgttctct	aacaatgtcc	tctccttgaa	gtatttggct	gaacaacca	cctaaagtcc	300
ctttgtgcat	ccatttttaa	tatacttaat	agggcattgk	tnactaggt	taaattctgc	360
aagagtcatc	tgcttgcaaa	agttgcgtta	gtatatctgc	ca		402

<210> 192
 <211> 601
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(601)
 <223> n = A,T,C or G

<400> 192
 gagctcggat ccaataatct ttgtctgagg gcagcacaca tatncagtgc catggnaact 60
 ggtctacccc acatgggagc agcatgccgt agntatataa ggtcattccc tgagtcagac 120
 atgcytyttt gaytaccgtg tgccaagtgc tgggtgattct yaacacacyt ccatcccgyt 180
 cttttgtgga aaaactggca cttktctgga actagcarga catcacttac aaattcaccc 240
 acgagacact tgaaggtgt aacaaagcga ytccttgcat gctttttgtc cctccggcac 300
 cagttgtcaa tactaaccgg ctggtttgcc tccatcacat ttgtgatctg tagctctgga 360
 tacatctcct gacagtactg aagaacttct tcttttgttt caaaagcarg tcttggtgcc 420
 tgttgatca ggttcccatt tcccagtcyg aatgttcaca tggecatatt wacttcccac 480
 aaaacattgc gatttgaggc tcagcaacag caaatcctgt tccggcattg gctgcaagag 540
 cctcgatgta gccggccagc gccaaaggcag gcgccgtgag cccaccagc agcagaagca 600
 g 601

<210> 193
 <211> 608
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(608)
 <223> n = A,T,C or G

<400> 193
 atacagccca natcccacca cgaagatgcg cttgttgact gagaacctga tgcggtcact 60
 ggtcccgtg tagccccagc gactctccac ctgctggaag cggttgatgc tgcactcytt 120
 cccaacgcag gcagmagcgg gscgggtcaa tgaactccay tcgtggcttg gggtkgacgg 180
 tkaagtgcag gaagaggctg accacctcgc ggtccaccag gatgcccgac tgtgcgggac 240
 ctgcagcgaa actcctcgat ggtcatgagc gggaagcgaa tgaggcccag ggccttgccc 300
 agaaccttcc gctgtttctc tggcgtcacc tgcagctgct gccgctgaca ctccggcctcg 360
 gaccagcgga caaacggcrt tgaacagccg cacctcacgg atgcccagtg tgtcgcgctc 420
 caggammgsc accagcgtgt ccaggtcaat gtcggtgaag ccctccgcgg gtrattggcg 480
 ctgcagtgtt ttgtcgtatg ttctccaggc acaggctggc cagctgcggt tcatcgaaga 540
 gtcgcgcctg cgtgagcagc atgaaggcgt tgtcggctcg cagttcttct tcaggaactc 600
 cacgcaat 608

<210> 194
 <211> 392
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(392)
 <223> n = A,T,C or G

<400> 194
 gaacggctgg accttgccctc gcattgtgct tgctggcagg gaataccttg gcaagcagyt 60

```

ccagtcgag cagccccaga ccgctgccgc ccgaagctaa gcctgcctct ggccttcccc 120
tccgcctcaa tgcagaacca gtagtgggag cactgtgttt agagttaaga gtgaacactg 180
tttgatttta ctgggaatt tcctctgtta tatagctttt cccaatgcta atttccaaac 240
aacaacaaca aaataacatg tttgcctgtt aagttgtata aaagtaggtg attctgtatt 300
taaagaaaat attactgtta catatactgc ttgcaatttc tgtatttatt gktinctstgg 360
aaataaatat agttattaaa ggtgtcant cc 392

```

```

<210> 195
<211> 502
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(502)
<223> n = A,T,C or G

```

```

<400> 195
ccsttkgagg ggtkaggkyc cagttyccga gtggaagaaa caggccagga gaagtgcgtg 60
ccgagctgag gcagatgttc ccacagtgc cccagagacc stgggstata gtytctgacc 120
cctcncaagg aaagaccacs ttctggggac atgggctgga gggcaggacc tagaggcacc 180
aagggaagge ccattccgg ggstgttccc cgaggaggaa gggaaggggc tctgtgtgcc 240
ccccasgagg aagaggccct gagtccctgg atcagacacc cttcacgtg tatccccaca 300
caaatgcaag ctcaccaagg tcccctctca gtccccttcc stacaccctg amcggccact 360
gscscacacc caccagagc acgccaccgc ccatggggar tgtgtcaag gartcgcnng 420
gcrcgtgga catctngtcc cagaaggggg cagaatctcc aatagangga ctgarcmstt 480
gctnanaaaa aaaaanaaaa aa 502

```

```

<210> 196
<211> 665
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(665)
<223> n = A,T,C or G

```

```

<400> 196
ggttacttg tttcattgcc accacttagt ggatgtcatt tagaaccatt ttgtctgctc 60
cctctggaag ccttgccgag agcggacttt gtaattgttg gagaataact gctgaatttt 120
wagctgtttk gatttgatts gcaccactgc acccacaact tcaatatgaa aacyawttga 180
actwatttat tatcttgtga aaagtataac aatgaaaatt ttgttcatac tgtattkac 240
aagtatgatg aaaagcaawa gatatatatt cttttattat gttaaattat gattgccatt 300
attaatcggc aaaatgtgga gtgtatgttc ttttcacagt aatatatgcc ttttgtaact 360
tcacttggtt attttattgt aaatgartta caaaattctt aatttaagar aatggatgt 420
watatttatt tcattaattt ctttcctkgt ttacgtwaat ttgaaaaga wtgcatgatt 480
tcttgacaga aatcgatctt gatgctgttg aagtagtttg acccacatcc ctatgagttt 540
ttcttagaat gtataaagggt ttagacccat cnaacttcaa agaaaaaat gaccacatac 600
tttgcaatca ggctgaaatg tggcatgctn ttctaattcc aactttataa actagcaaan 660
aagtg 665

```

```

<210> 197
<211> 492
<212> DNA
<213> Homo sapien

```

```

<220>

```

<221> misc_feature
 <222> (1)...(492)
 <223> n = A,T,C or G

<400> 197
 tttntttttt ttttttttgc aggaaggatt ccattttattg tggatgcatt ttcacaatat 60
 atgttttattg gagcgatcca ttatcagtga aaagtatcaa gtgtttataa natttttagg 120
 aaggcagatt cacagaacat gctngtcngc ttgcagtttt acctcgtana gatnacagag 180
 aattatagtc naaccagtaa acnaggaatt tacttttcaa aagattaaat ccaaactgaa 240
 caaaattcta ccctgaaact tactccatcc aaatattgga ataanagtca gcagtgtac 300
 attctcttct gaactttaga ttttctagaa aaatatgtaa tagtgatcag gaagagctct 360
 tgttcaaaag tacaacnaag caatgttccc ttaccatagg ccttaattca aactttgatc 420
 catttcactc ccatacagg agtcaatgct acctgggaca cttgtatttt gttcatnctg 480
 ancntggctt aa 492

<210> 198
 <211> 478
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(478)
 <223> n = A,T,C or G

<400> 198
 tttnttttgn atttcantct gtannaanta ttttcattat gtttattana aaaatatnaa 60
 tgtntccacn acaaatcatn ttacntnagt aagaggccan ctacattgta caacatacac 120
 tgagtatttt ttgaaaagga caagttttaa gtanacncat attgccganc atancacatt 180
 tatacatggc ttgattgata tttagcacag canaaactga gtgagttacc agaaanaaat 240
 natatatgtc aatcngattt aagatacaaa acagatccta tggtagatan catcntgtag 300
 gagttgtggc tttatgttta ctgaaagtca atgcagttcc tgtacaaaga gatggccgta 360
 agcattctag tacctctact ccatgggttaa gaatcgtaca cttatgttta catatgtnca 420
 gggtaagaat tgtgttaagt naanttattg agaggtccan gagaaaaatt tgaatnca 478

<210> 199
 <211> 482
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(482)
 <223> n = A,T,C or G

<400> 199
 agtgacttgt cctccaacaa aacccttga tcaagtttgt ggcaactgaca atcagacctta 60
 tgctagtcc tgctatctat tcgctactaa atgcagactg gaggggacca aaaaggggca 120
 tcaactccag ctggattatt ttggagcctg caaatctatt cctacttgta cggactttga 180
 agtgactcag tttcctctac ggatgagaga ctggctcaag aatatcctca tgcagcttta 240
 tgaagccnac tctgaacacg ctggttatct nagatgagaa ncagagaaat aaagtcnaga 300
 aaatttacct ggangaaaag aggccttngg ctggggacca tccattgaa ccttctctta 360
 anggacttta agaanaaact accacatgtn tgtngtatcc tgggtgccngg ccgtttantg 420
 aacntngacn ncacccttnt ggaatanant cttgacngcn tcctgaactt gctcctctgc 480
 ga 482

<210> 200
 <211> 270

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(270)

<223> n = A,T,C or G

<400> 200

cggccgcaag tgcaactcca gctggggccg tgcggacgaa gattctgcca gcagttggtc	60
cgactgcgac gacggcgcg ggcacagtcg caggtgcagc gcgggcgcct ggggtcttgc	120
aaggctgagc tgacgccgca gaggtcgtgt cacgtcccac gacctgacg ccgtcgggga	180
cagccggaac agagcccggt gaangcggga ggcctcgggg agcccctcgg gaagggcggc	240
ccgagagata cgcaggtgca ggtggccgcc	270

<210> 201

<211> 419

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(419)

<223> n = A,T,C or G

<400> 201

tttttttttt ttttgaatc tactgcgagc acagcaggtc agcaacaagt ttattttgca	60
gctagcaagg taacagggtt gggcatggtt acatgttcag gtcaacttcc ttgtcgtgg	120
ttgattggtt tgtctttatg ggggcggggt ggggtagggg aaancgaagc anaantaaca	180
tggagtgggt gcaccctccc tgtagaacct ggttacnaaa gcttggggca gttcacctgg	240
tctgtgacgg tcatTTTTtT gacatcaatg ttattagaag tcaggatatc ttttagagag	300
tccactgtnt ctggaggag attagggttt cttgccana tccaancaa atccacntga	360
aaaagtTgga tgatncangt acngaatacc ganggcatan ttctcatant cggTggcca	419

<210> 202

<211> 509

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(509)

<223> n = A,T,C or G

<400> 202

tttntttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt	60
tggcacttaa tccattttta tttcaaaatg tctacaaant ttnaatncnc cattatacng	120
gtntttttnc aaaatctaaa nnttattcaa attnagcca aantccttac ncaaattnaa	180
tacnncnaaa aatcaaaaat atacnttct ttcagcaaac ttngttacat aaattaaaaa	240
aatatatacg gctgggtgtt tcaaagtaca attatcttaa cactgcaaac atnttttnaa	300
ggaactaaaa taaaaaaaaa cactnccgca aagggttaaag ggaacaacaa attcntttta	360
caacancnnc nattataaaa atcatatctc aaatcttagg ggaatatata cttcacacng	420
ggatcttaac ttttactnca ctttgtttat ttttttanaa ccattgtntt gggcccaaca	480
caatggnaat nccnccnccncc tggactagt	509

<210> 203

<211> 583

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(583)

<223> n = A,T,C or G

<400> 203

tttttttttt	ttttttttga	ccccctctt	ataaaaaaca	agttaccatt	ttattttact	60
tacacatatt	tattttataa	ttggtattag	atattcaaaa	ggcagctttt	aaaatcaaac	120
taaaatgaaa	ctgccttaga	tacataattc	ttaggaatta	gcttaaaatc	tgccataaagt	180
gaaaatcttc	tctagctctt	ttgactgtaa	atttttgact	cttgtaaaac	atccaaattc	240
atttttcttg	tctttaaaaa	tatctaattc	ttccattttt	tccctattcc	aagtcaattt	300
gcttctctag	cctcatttcc	tagctcttat	ctactattag	taagtggctt	ttttcctaaa	360
agggaaaaca	ggaagagana	atggcacaca	aaacaaacat	tttatattca	tatttctacc	420
tacgttaata	aaatagcatt	ttgtgaagcc	agctcaaaag	aaggcttaga	tccttttatg	480
tccattttag	tcactaaacg	atatcnaaag	tgccagaatg	caaaagggtt	gtgaacattt	540
attcaaaagc	taatataaga	tatttcacat	actcatcttt	ctg		583

<210> 204

<211> 589

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(589)

<223> n = A,T,C or G

<400> 204

ttttttttnt	tttttttttt	ttttttntct	ttcttttttt	ttganaatga	ggatcgagtt	60
tttcaactct	tagatagggc	atgaagaaaa	ctcatctttc	cagcttttaa	ataacaatca	120
aatctcttat	gctatatcat	attttaagtt	aaactaatga	gtcactggct	tatcttctcc	180
tgaaggaaat	ctgttcattc	ttctcattca	tatagttata	tcaagtacta	ccttgcatat	240
tgagagggtt	ttcttctcta	tttacacata	tatttccatg	tgaatttgta	tcaaaccctt	300
attttcatgc	aaactagaaa	ataatgtntt	cttttgcata	agagaagaga	acaatatnag	360
cattacaaaa	ctgctcaaat	tgtttgtaa	gnttatccat	tataattagt	tnggcaggag	420
ctaatacaaa	tcacattttac	ngacnagcaa	taataaaact	gaagtaccag	ttaaatatcc	480
aaaataatta	aaggaacatt	tttagcctgg	gtataattag	ctaattcact	ttacaagcat	540
ttattnagaa	tgaattcaca	tgttattatt	cntagccca	acacaatgg		589

<210> 205

<211> 545

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(545)

<223> n = A,T,C or G

<400> 205

ttttnttttt	ttttttcagt	aataatcaga	acaatattta	tttttatatt	taaaattcat	60
agaaaagtgc	cttacattta	ataaaaagttt	gtttctcaaa	gtgatcagag	gaattagata	120
tngtcttgaa	caccaatatt	aatttgagga	aaatacacca	aaatacatta	agtaaattat	180
ttaagatcat	agagcttgta	agtgaaga	taaaatttga	cctcagaaac	tctgagcatt	240
aaaaatccac	tattagcaaa	taaattacta	tggaacttct	gctttaattt	tgtgatgaat	300
atgggggtgc	actggtaa	caacacattc	tgaaggatac	attacttagt	gatagattct	360

```

tatgtacttt gctanatnac gtggatatga gttgacaagt ttctctttct tcaatctttt 420
aaggggcnga ngaaatgagg aagaaaagaa aaggattacg catactgttc tttctatngg 480
aaggattaga tatgtttcct ttgccaatat taaaaaata ataatgttta ctactagtga 540
aacc 545

```

```

<210> 206
<211> 487
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(487)
<223> n = A,T,C or G

```

```

<400> 206
tttttttttt ttttttagtc aagtttctna tttttattat aattaaagtc ttggtcattt 60
catttattag ctctgcaact tacatattta aattaaagaa acgttnttag acaactgtna 120
caatttataa atgtaagggt ccattattga gtanatatat tcctccaaga gtggatgtgt 180
cccttctccc accaactaat gaancagcaa cattagtta attttattag tagatnatac 240
actgctgcaa acgctaattc tcttctccat ccccatgtng atattgtgta tatgtgtgag 300
ttggtnagaa tgcatacanca atctnacaat caacagcaag atgaagctag gcntgggctt 360
tcggtgaaaa tagactgtgt ctgtctgaat caaatgatct gacctatcct cggtggcaag 420
aactcttoga accgcttcct caaaggcngc tgccacattt gtggcntctn ttgcacttgt 480
ttcaaaa 487

```

```

<210> 207
<211> 332
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(332)
<223> n = A,T,C or G

```

```

<400> 207
tgaattggct aaaagactgc atttttanaa ctagcaactc ttatttcttt cctttaaaaa 60
tacatagcat taaatcccaa atcctattta aagacctgac agcttgagaa ggtcactact 120
gcatttatag gaccttctgg tggttctgct gttacntttg aantctgaca atccttgana 180
atctttgcat gcagaggagg taaaagggtat tggattttca cagaggaana acacagcgca 240
gaaatgaagg ggccaggctt actgagcttg tccactggag ggctcatggg tgggacatgg 300
aaaagaaggc agcctaggcc ctggggagcc ca 332

```

```

<210> 208
<211> 524
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(524)
<223> n = A,T,C or G

```

```

<400> 208
agggcggtgt gcgaggggcg ttactgtttt gtctcagtaa caataaatac aaaaagactg 60
gttgtgttcc ggcccatcc aaccacgaag ttgatttctc ttgtgtgcag agtgactgat 120
tttaaaggac atggagcttg tcacaatgtc acaatgtcac agtgtgaagg gcacactcac 180

```

tcccgctga ttcacattta gcaaccaaca atagctcatg agtcataact tgtaaataact	240
tttggcagaa tacttnttga aacttgcaga tgataactaa gatccaagat atttcccaaa	300
gtaaatagaa gtgggtcata atattaatta cctgttcaca tcagcttcca tttacaagtc	360
atgagcccag acactgacat caaactaagc ccacttagac tcctcaccac cagtctgtcc	420
tgatcatcaga caggaggctg tcaccttgac caaattctca ccagtcaatc atctatccaa	480
aaaccattac ctgatccact tccggtaatg caccaccttg gtga	524

<210> 209
 <211> 159
 <212> DNA
 <213> Homo sapien

<400> 209	
gggtgaggaa atccagagtt gccatggaga aaattccagt gtcagcattc ttgctccttg	60
tggccctctc ctacactctg gccagagata ccacagtcaa acctggagcc aaaaaggaca	120
caaaggactc tcgacccaaa ctgcccaga ccctctcca	159

<210> 210
 <211> 256
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(256)
 <223> n = A,T,C or G

<400> 210	
actccctggc agacaaaggc agaggagaga gctctgttag ttctgtgttg ttgaactgcc	60
actgaatttc tttccaattg gactattaca tgccanttga gggactaatg gaaaaacgta	120
tggggagatt ttanccaatt tangtntgta aatggggaga ctggggcagg cgggagagat	180
ttgcaggggtg naaatgggan ggctggtttg ttanatgaac agggacatag gaggtaggca	240
ccaggatgct aaatca	256

<210> 211
 <211> 264
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(264)
 <223> n = A,T,C or G

<400> 211	
acattgtttt tttagataaa agcattgaga gagctctcct taacgtgaca caatggaagg	60
actggaacac ataccacat ctttgttctg agggataatt ttctgataaa gtcttgctgt	120
atattcaagc acatattgta tatattattc agttccatgt ttatagccta gttaaggaga	180
ggggagatac attcngaaag aggactgaaa gaaatactca agtnggaaaa cagaaaaaga	240
aaaaaaggag caaatgagaa gcct	264

<210> 212
 <211> 328
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature

<222> (1)...(328)

<223> n = A,T,C or G

<400> 212

acccaaaaat ccaatgctga atatttggtc	tcattattcc canattcttt gattgtcaaa	60
ggatttaatg ttgtctcagc ttgggcactt	cagttaggac ctaaggatgc cagccggcag	120
gtttatatat gcagcaacaa tattcaagcg	cgacaacagg ttattgaact tgcccgccag	180
ttnaatttca ttccattga cttgggatcc	ttatcatcag ccagagagat tgaaaattta	240
cccctacnac tctttactct ctgganaggg	ccagtgggtg tagctataag cttggccaca	300
tttttttttc cttttattcct ttgtcaga		328

<210> 213

<211> 250

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(250)

<223> n = A,T,C or G

<400> 213

acttatgagc agagcgacat atccnagtgt	agactgaata aaactgaatt ctctccagtt	60
taaagcattg ctactgaag ggatagaagt	gactgccagg agggaaagta agccaaggct	120
cattatgccca aagganatat acatttcaat	tctccaaact tcttcctcat tccaagagtt	180
ttcaatattt gcatgaacct gctgataanc	catgttaana aacaaatato tctctnacct	240
tctcatcggt		250

<210> 214

<211> 444

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(444)

<223> n = A,T,C or G

<400> 214

accagaatc caatgctgaa tatttggtt	cattattccc agattctttg attgtcaaag	60
gatttaatgt tgtctcagct tgggcacttc	agttaggacc taaggatgcc agccggcagg	120
tttatatatg cagcaacaat attcaagcgc	gacaacaggc tattgaactt gcccgccagt	180
tgaatttcat toccattgac ttgggatcct	tatcatcagc canagagatt gaaaatttac	240
ccctacgact ctttactctc tggagagggc	cagtgggtgt agctataagc ttggccacat	300
ttttttttcc tttattcctt tgtcagagat	gcgattcatc catatgctan aaaccaacag	360
agtgactttt acaaaattcc tataganatt	gtgaataaaa ccttacctat agttgccatt	420
actttgctct ccctaataata cctc		444

<210> 215

<211> 366

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(366)

<223> n = A,T,C or G


```

<400> 215
acttatgagc agagcgacat atccaagtgt anactgaata aaactgaatt ctctccagtt      60
taaagcattg ctactgaag ggatagaagt gactgccagg agggaaagta agccaaggct      120
cattatgcca aagganatat acatttcaat tctccaaact tcttcctcat tccaagagtt      180
ttcaatattt gcatgaacct gctgataagc catgttgaga aacaaatata tctctgacct      240
tctcatcggg aagcagaggc tgtaggcaac atggaccata gcgaanaaaa aacttagtaa      300
tccaagctgt tttctacact gtaaccagggt ttccaaccaa ggtggaaatc tcctatactt      360
ggtgcc

```

```

<210> 216
<211> 260
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(260)
<223> n = A,T,C or G

```

```

<400> 216
ctgtataaac agaactccac tgcangaggg agggccgggc caggagaatc tccgcttgtc      60
caagacaggg gcctaaggag ggtctccaca ctgctnntaa gggctnttnc atttttttat      120
taataaaaaag tnnaaaaggc ctctttctcaa cttttttccc ttnggctgga aaatttaaaa      180
atcaaaaatt tctnaagtt ntcaagctat catatatact ntatcctgaa aaagcaacat      240
aattcttctt tccctccttt

```

```

<210> 217
<211> 262
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(262)
<223> n = A,T,C or G

```

```

<400> 217
acctacgtgg gtaagtttan aaatgttata atttcaggaa naggaacgca tataattgta      60
tcttgccat aattttctat ttaataagg aaatagcaaa ttgggggtggg gggaatgtag      120
ggcattctac agtttgagca aaatgcaatt aaatgtggaa ggacagcact gaaaaatttt      180
atgaataatc tgtatgatta tatgtctcta gagtagattt ataattagcc acttacccta      240
atatccttca tgcttgtaaa gt

```

```

<210> 218
<211> 205
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(205)
<223> n = A,T,C or G

```

```

<400> 218
accaaggtgg tgcattaccg gaantggatc aangacacca tegtggccaa cccctgagca      60
cccctatcaa ctcccctttg tagtaaactt ggaaccttgg aaatgaccag gccaaagactc      120
aggcctcccc agttctactg acctttgtcc ttangtntna ngtccagggt tgctaggaaa      180
anaaatcagc agacacaggt gtaaa

```

<210> 219
 <211> 114
 <212> DNA
 <213> Homo sapien

<400> 219
 tactgttttg tctcagtaac aataaatata aaaagactgg ttgtgttccg gcccaccca 60
 accacgaagt tgatttctct tgtgtgcaga gtgactgatt ttaaaggaca tgga 114

<210> 220
 <211> 93
 <212> DNA
 <213> Homo sapien

<400> 220
 actagccagc acaaaaaggca gggtagcctg aattgctttc tgctctttac atttctttta 60
 aaataagcat ttagtgctca gtccctactg agt 93

<210> 221
 <211> 167
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(167)
 <223> n = A,T,C or G

<400> 221
 actangtgca ggtg'gcaca aatatttgct gatattccct tcatcttgga ttccatgagg 60
 tcttttgccc agcctgtggc tctactgtag taagtttctg ctgatgagga gccagnatgc 120
 ccccactac cttccctgac gtcgccana aatcacccaa cctctgt 167

<210> 222
 <211> 351
 <212> DNA
 <213> Homo sapien

<400> 222
 agggcggtggt gcggagggcg gtactgacct cattagtagg aggatgcatt ctggcacccc 60
 gttcttcacc tgtccccca tcttaaaag gccatactgc ataaagtcaa caacagataa 120
 atgtttgctg aattaaagga tggatgaaaa aaattaataa tgaatttttg cataatccaa 180
 ttttctcttt tatatttcta gaagaagttt ctttgagcct attagatccc gggaatcttt 240
 taggtgagca tgattagaga gctttaggt tgcttttaca tatatctggc atatttgagt 300
 ctcgtatcaa aacaatagat tggtaaaggt ggtattattg tattgataag t 351

<210> 223
 <211> 383
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(383)
 <223> n = A,T,C or G

<400> 223

aaaacaaaca aacaaaaaaa acaattcttc attcagaaaa attatcttag ggactgatat	60
tggttaattat ggtcaattta atwrtttkt ggggcatttc cttacattgt cttgacaaga	120
ttaaaaatgtc tgtgccaaaa ttttgtatth tatttgagaga cttcttatca aaagtaatgc	180
tgccaaagga agtctaagga attagtagtg ttcccmccac ttgtttggag tgtgctattc	240
taaaagattt tgatttcctg gaatgacaat tatattttaa ctttggtggg ggaaanagtt	300
ataggaccac agtcttcact tctgatactt gtaaattaat cttttattgc acttgttttg	360
accattaagc tatatgttta aaa	383

<210> 224

<211> 320

<212> DNA

<213> Homo sapien

<400> 224

cccctgaagg cttcttggtta gaaaatagta cagttacaac caataggaac aacaaaaaga	60
aaaagtttgt gacattgtag tagggagtgt gtaccocctta ctcccatca aaaaaaaat	120
ggatacatgg ttaaaggata raagggaat attttatcat atgttctaaa agagaaggaa	180
gagaaaatac tactttctcr aaatggaagc ccttaaaggt gctttgatac tgaaggacac	240
aaatgtggcc gtccatcctc ctttaragtt gcatgacttg gacacggtaa ctgttgcaat	300
tttaractcm gcattgtgac	320

<210> 225

<211> 1214

<212> DNA

<213> Homo sapien

<400> 225

gaggactgca gcccgcactc gcagccctgg caggcggcac tggatcatgga aaacgaattg	60
ttctgctcgg gcgtcctggt gcatccgcag tgggtgctgt cagccgcaca ctgtttccag	120
aactcctaca ccattcgggt gggcctgcac agtcttgagg ccgaccaaga gccagggagc	180
cagatgggtg aggccagcct ctccgtacgg caccagaggt acaacagacc ctgtctcgct	240
aacgacctca tgcctcatca gttggacgaa tccgtgtccg agtctgacac catccggagc	300
atcagcattg cttcgcagtg ccctaccgag gggaaactctt gctcgtttc tggctgggggt	360
ctgctggcga acggcagaat gcctaccgtg ctgcagtgcg tgaacgtgtc ggtggtgtct	420
gaggaggtct gcagtaagct ctatgaccgg ctgtaccacc ccagcatgtt ctgcccgggc	480
ggagggaag accagaagga ctccctgcaac ggtgactctg gggggcccct gatctgcaac	540
gggtacttgc agggccttgt gtctttcgga aaagcccgt gtggccaagt tggcgtgcca	600
ggtgtctaca ccaacctctg caaattcact gagtggatag agaaaaccgt ccaggccagt	660
taactctggg gactgggaac ccataaatt gacccccaaa tacatcctgc ggaaggaatt	720
caggaatata tgttcccagc ccctcctccc tcaggcccag gactccaggc cccagcccc	780
tcctccctca aaccaagggt acagatcccc agcccctcct ccctcagacc caggagtcca	840
gacccccag cccctcctcc ctccagacca ggagtccagc ccctcctccc tcagaccag	900
gagtccagac cccccagccc ctccctccctc agaccaggg gtccaggccc ccaaccctc	960
ctccctcaga ctccagagtc caagccccc acccctcctt cccagacc' agagggtccag	1020
gtcccagccc ctccctccctc agaccagcg gtccaatgcc acctagactc tccctgtaca	1080
cagtgcctcc ttgtggcagc ttgacccaac cttaccagtt ggtttttcat tttttgtccc	1140
tttcccttag atccagaaat aaagtctaag agaagcgcaa aaaaaaaaaa aaaaaaaaaa	1200
aaaaaaaaaa aaaa	1214

<210> 226

<211> 119

<212> DNA

<213> Homo sapien

<400> 226

accagtatg tgcagggaga cggaacccca tgtgacagcc cactccacca gggttcccaa	60
agaacctggc ccagtcataa tcattcatcc tgacagtggc aataatcacg ataaccagt	119

<210> 227
 <211> 818
 <212> DNA
 <213> Homo sapien

<400> 227
 acaattcata gggacgacca atgaggacag ggaatgaacc cggctctccc ccagccctga 60
 tttttgctac atatggggtc ctttttcatt ctttgcaaaa aactggggtt ttctgagaac 120
 acggacggtt cttagcaciaa tttgtgaaat ctgtgtaraa ccgggctttg caggggagat 180
 aattttcctc ctctggagga aaggtgggtga ttgacaggca gggagacagt gacaaggcta 240
 gaaaaagcca cgctcggcct tctctgaaac aggatggaac ggagacccc tgaaaacgaa 300
 gcttgctccc ttccaatcag ccacttctga gaacccccat ctaacttcct actggaaaag 360
 agggcctcct caggagcagt ccaagagttt tcaaagataa cgtgacaact accatctaga 420
 ggaaaagggtg caccctcagc agagaagccg agaacttaac tctggctcgtt tccagagaca 480
 acctgctggc tgtcttgga tgcccccagc ctttgagagg ccactacccc atgaacttct 540
 gccatccact ggacatgaag ctgaggacac tgggcttcaa cactgagttg tcatgagagg 600
 gacaggctct gccctcaagc cggctgaggg cagcaaccac tctcctccc tttctcacgc 660
 aaagccattc ccacaaatcc agaccatacc atgaagcaac gagacccaaa cagtttggt 720
 caagaggata tgaggactgt ctgagcctgg ctttgggctg acaccatgca cacacacaag 780
 gtccacttct aggttttcag cctagatggg agtcgtgt 818

<210> 228
 <211> 744
 <212> DNA
 <213> Homo sapien

<400> 228
 actggagaca ctgtgaact tgatcaagac ccagaccacc ccaggtctcc ttcgtgggat 60
 gtcattgacgt ttgacatacc tttggaacga gcctcctcct tggaagatgg aagaccgtgt 120
 tcgtggccga cctggcctct cctggcctgt ttcttaagat gggagtcac atttcaatgg 180
 taggaaaagt ggcttcgtaa aatagaagag cagtcactgt ggaactacca aatggcgaga 240
 tgctcgggtc acattggggt gctttgggat aaaagattta tgagccaact attctctggc 300
 accagattct aggcagttt gttccactga agcttttccc acagcagtc accctctgcag 360
 gctggcagct gaattggctt cgggtggctc tgtggcaaga tcacactgag atcgatgggt 420
 gagaaggcta ggatgcttgt ctagtgttct tagctgtcac gttggctcct tccaggttgg 480
 ccagacggtg ttggccactc ctttctaaaa cacaggcgcc ctctggtga cagtgaacccg 540
 ccgtggtatg ccttgcccca ttccagcagt ccagttatg catttcaagt ttggggtttg 600
 ttcttttctg taatgttct ctgtgttgc agctgtcttc atttcctggg ctaagcagca 660
 ttgggagatg tggaccagag atccactcct taagaaccag tggcgaaaga cactttcttt 720
 cttcactctg aagtagctgg tgg 744

<210> 229
 <211> 300
 <212> DNA
 <213> Homo sapien

<400> 229
 cgagtcctggg ttttgtctat aaagtttgat ccctcctttt ctcacccaaa tcatgtgaac 60
 cattacacat cgaaataaaa gaaagtggtc agacttgccc aacgccaggc tgacatgtgc 120
 tgcagggttg ttgtttttta attattattg ttagaacagt caccacagt ccctgttaat 180
 ttgtatgtga cagccaactc tgagaaggtc ctatttttcc acctgcagag gatccagtct 240
 cactaggctc ctcttgccc tcacactgga gtctccgcca gtgtgggtgc ccactgacat 300

<210> 230
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 230

cagcagaaca aatacaata tgaagagtgc aaagatctca taaaatctat gctgaggaat	60
gagcgacagt tcaaggagga gaagcttgca gagcagctca agcaagctga ggagctcagg	120
caatataaag tcctggttca cactcaggaa cgagagctga cccagttaag ggagaagttg	180
cgggaaggga gagatgcctc cctctcattg aatgagcatc tccaggccct cctcactccg	240
gatgaaccgg acaagtccca ggggcaggac ctccaagaaa cagacctcgg ccgcgaccac	300
g	301

<210> 231

<211> 301

<212> DNA

<213> Homo sapien

<400> 231

gcaagcacgc tggcaaatct ctgtcaggtc agctccagag aagccattag tcatttttagc	60
caggaactcc aagtccacat ccttggaac tggggacttg cgcaggttag ccttgaggat	120
ggcaacacgg gacttctcat caggaagtgg gatgtagatg agctgatcaa gacggccagg	180
tctgaggatg gcaggatcaa tgatgtcagg ccggttggtta ccgccaatga tgaacacatt	240
tttttttggtg gacatgccat ccatttctgt caggatctgg ttgatgactc ggtcagcagc	300
c	301

<210> 232

<211> 301

<212> DNA

<213> Homo sapien

<400> 232

agtaggtatt tcgtgagaag ttcaacacca aaactggaac atagttctcc ttcaagtgtt	60
ggcgacacgg gggcttcctg attctggaat ataactttgt gtaaattaac agccacctat	120
agaagagtcc atctgctgtg aaggagagac agagaactct gggttccgtc gtcctgtcca	180
cgtgctgtac caagtgtctg tgccagcctg ttacctgttc tactgaaaa tctggctaatt	240
gctcttgtgt atcacttctg attctgacaa tcaatcaatc aatggcctag agcactgact	300
g	301

<210> 233

<211> 301

<212> DNA

<213> Homo sapien

<400> 233

atgactgact tcccagtaag gctctctaag gggtaagtag gaggatccac aggatttgag	60
atgctaaggc cccagagatc gtttgatcca accctcttat tttcagaggg gaaaatgggg	120
cctagaagtt acagagcatc tagctggtgc gctggcacc cttggcctcac acagactccc	180
gagtagctgg gactacaggc acacagtcac tgaagcaggc cctgttagca attctatgcg	240
tacaaattaa catgagatga gtagagactt tattgagaaa gcaagagaaa atcctatcaa	300
c	301

<210> 234

<211> 301

<212> DNA

<213> Homo sapien

<400> 234

aggctctaca catcgagact catccatgat tgatatgaat ttaaaaatta caagcaaaga	60
cattttattc atcatgatgc tttcttttgt ttcttctttt cgtttttctt tttttctttt	120
tcaatttcag caacatactt ctcaatttct tcaggattta aaatcttgag ggattgatct	180
cgcctcatga cagcaagttc aatgtttttg ccacctgact gaaccacttc caggagtgcc	240
ttgatcacca gcttaatggg cagatcatct gcttcaatgg cttcgtcagt atagtcttc	300

t

301

<210> 235
 <211> 283
 <212> DNA
 <213> Homo sapien

<400> 235

tggggctgtg	catcaggcgg	gtttgagaaa	tattcaattc	tcagcagaag	ccagaatttg	60
aattccctca	tcttttaggg	aatcatttac	caggtttgga	gaggattcag	acagctcagg	120
tgctttcact	aatgtctctg	aacttctgtc	cctctttgtt	catggatagt	ccaataaata	180
atgttatctt	tgaactgatg	ctcataggag	agaatataag	aactctgagt	gatatcaaca	240
ttagggattc	aaagaaatat	tagatttaag	ctcacactgg	tca		283

<210> 236
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 236

aggtcctcca	ccaactgcct	gaagcacggg	taaaattggg	aagaagtata	gtgcagcata	60
aatactttta	aatcgatcag	atttccctaa	cccacatgca	atcttcttca	ccagaagagg	120
tcgggacgac	atcatataa	ccaagcagaa	tgcgtaatag	ataaatacaa	tggtatatag	180
tgggtagacg	gcttcatgag	tacagtgtac	tgtggatcgc	taatctggac	ttgggttgta	240
aagcatcgtg	taccagtcag	aaagcatcaa	tactcgacat	gaacgaatat	aaagaacacc	300
a						301

<210> 237
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 237

cagtggtagt	ggtggtggac	gtggcggttg	tcgtggtgcc	tttttgggtg	cccgtcacaa	60
actcaatttt	tgctcgctcc	tttttggcct	tttccaattt	gtccatctca	attttctggg	120
ccttggctaa	tgctcatag	taggagtcct	cagaccagcc	atggggatca	aacatatcct	180
ttgggtagtg	ggtgccaagc	tcgtcaatgg	cacagaatgg	atcagcttct	cgtaaatcta	240
gggttccgaa	attctttctt	cctttggata	atgtagttca	tatccattcc	ctcctttatc	300
t						301

<210> 238
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 238

gggcagggtt	tttttttttt	ttttttgatg	gtgcagaccc	ttgctttatt	tgtctgactt	60
gttcacagtt	cagccccctg	ctcagaaaac	caacgggcca	gctaaggaga	ggaggaggca	120
ccttgagact	tccggagtcg	aggctctcca	gggttcccca	gcccatcaat	cattttctgc	180
acccccctgc	tgggaagcag	ctccctgggg	ggtgggaatg	ggtgactaga	agggatttca	240
gtgtgggacc	cagggctctg	tcttcacagt	aggaggtgga	agggatgact	aatttcttta	300
t						301

<210> 239
 <211> 239
 <212> DNA
 <213> Homo sapien

<400> 239

ataagcagct aggggaattct ttatttagta atgtcctaac ataaaagttc acataactgc	60
ttctgtcaaa ccatgatact gagctttgtg acaaccaga aataactaag agaaggcaaa	120
cataatacct tagagatcaa gaaacattta cacagttcaa ctgtttaaaa atagctcaac	180
attcagccag tgagtagagt gtgaatgcca gcatacacag tatacaggtc cttcaggga	239

<210> 240

<211> 300

<212> DNA

<213> Homo sapien

<400> 240

ggtcctaag aagcagcagc ttccacattt taacgcaggt ttacgggtgat actgtccttt	60
gggatctgcc ctccagtga accttttaag gaagaagtgg gcccaagcta agttccacat	120
gctgggtgag ccagatgact tctgttccct ggtcactttc ttcaatgggg cgaatggggg	180
ctgccaggtt tttaaaatca tgcttcatct tgaagcacac ggtcacttca ccctcctcac	240
gctgtgggtg tactttgatg aaaataccca ctttgttggc ctttctgaag ctataatgtc	300

<210> 241

<211> 301

<212> DNA

<213> Homo sapien

<400> 241

gaggtctggt gctgaggtct ctgggctagg aagaggaggt ctgtggagct ggaagccaga	60
cctctttgga ggaaactcca gcagctatgt tgggtgtctct gaggggaatgc aacaaggctg	120
ctctccatg tattggaaaa ctgcaactg gactcaactg gaagggaagtg ctgctgccag	180
tgtgaagaac cagcctgagg tgacagaaac ggaagcaaac aggaacagcc agtcttttct	240
tcctcctcct gtcatacggg ctctctcaag catcctttgt tgtcaggggc ctaaaaggga	300

g

<210> 242

<211> 301

<212> DNA

<213> Homo sapien

<400> 242

ccgaggctct gggatgcaac caatcactct gtttcacgtg actttttatca ccatacaatt	60
tgtggcattt cctcattttc tacattgtag aatcaagagt gtaaataaat gtatatcgat	120
gtcttcaaga atatatcatt cttttttcac tagaaccat tcaaatata agtcaagaat	180
cttaatatca acaaatatat caagcaaaact ggaaggcaga ataactacca taatttagta	240
taagtaccca aagttttata aatcaaaagc cctaatagata accattttta gaattcaatc	300

a

<210> 243

<211> 301

<212> DNA

<213> Homo sapien

<400> 243

aggtaaagtc cagtttgaag ctcaaaagat ctggtatgag cataggctca tcgacgacat	60
ggtggcccaa gctatgaaat cagagggagg cttcatctgg gcctgtaaaa actatgatgg	120
tgacgtgcag tcggactctg tggcccaagg gtatggctct ctcggcatga tgaccagcgt	180
gctggtttgt ccagatggca agacagtaga agcagaggct gccacaggga ctgtaaccgc	240
tcactaccgc atgttcacaga aaggacagga gacgtccacc aatcccattg cttccatttt	300

t

<210> 244

<211> 300
 <212> DNA
 <213> Homo sapien

<400> 244
 gctggtttgc aagaatgaaa tgaatgattc tacagctagg acttaacctt gaaatggaaa 60
 gtcattgcaat cccatttgca ggatctgtct gtgcacatgc ctctgtagag agcagcattc 120
 ccagggacct tggaaacagt tgacactgta aggtgcttgc tccccaaagac acatcctaaa 180
 aggtgttgta atggtgaaaa cgtcttcctt ctttattgcc ccttcttatt tatgtgaaca 240
 actggttgc ttttgtgtat cttttttaa ctgtaaagtt caattgtgaa aatgaatatc 300

<210> 245
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 245
 gtctgagtat ttaaaatggt attgaaatta tccccacca atgttagaaa agaaagaggt 60
 tatatactta gataaaaaat gaggtgaatt actatccatt gaaatcatgc tcttagaatt 120
 aaggccagga gatattgtca ttaatgtara cttcaggaca ctagagtata gcagccctat 180
 gttttcaaag agcagagatg caattaaata ttgttttagca tcaaaaaggc cactcaatac 240
 agctaataaa atgaaagacc taatttctaa agcaattctt tataatttac aaagttttaa 300
 g 301

<210> 246
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 246
 ggtctgtcct acaatgcctg cttcttgaaa gaagtcggca ctttctagaa tagctaaata 60
 acctgggctt attttaaaga actatttgta gtcagattg gttttcctat ggctaaaata 120
 agtgcttctt gtgaaaatta aataaaacag ttaattcaaa gccttgatat atgttaccac 180
 taacaatcat actaaatata ttttgaagta caaagtttga catgctctaa agtgacaacc 240
 caaatgtgtc ttacaaaaca cgttcctaac aaggtatgct ttacactacc aatgcagaaa 300
 c 301

<210> 247
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 247
 aggtcctttg gcagggtcga tggatcagag ctcaaactgg agggaaaggc atttcgggta 60
 gcctaagagg gcgactggcg gcagcacaac caaggaaggc aaggttggtt cccccacgct 120
 gtgtcctgtg ttcagggtcg acacacaatc ctcatgggaa caggatcacc catgcgctgc 180
 ccttgatgat caaggttggg gcttaagtgg attaagggag gcaagttctg gggttccttg 240
 cttttcaaac catgaagtca ggctctgtat ccctcctttt cctaactgat attctaacta 300
 a 301

<210> 248
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 248
 aggtccttgg agatgccatt tcagccgaag gactcttctw ttcggaagta caccctcact 60
 attaggaaga ttcttagggg taatttttct gaggaaggag aactagccaa cttaagaatt 120

acaggaagaa agtggtttgg aagacagcca aagaaataaa agcagattaa attgtatcag 180
gtacattcca gcctgttggc aactccataa aaacatttca gattttaatc ccgaatttag 240
ctaagagac tggatttttg ttttttatgt tgtgtgtcgc agagctaaaa actcagttcc 300
c 301

<210> 249
<211> 301
<212> DNA
<213> Homo sapien

<400> 249
gtccagagga agcacctggt gctgaactag gcttgccctg ctgtgaactt gcaacttgag 60
ccctgacgct gctgttctcc ccgaaaaacc cgaccgacct ccgcgatctc cgtcccgcgc 120
ccaggagac acagcagtga ctcagagctg gtgcacact gtgcctccct cctcaccgcc 180
catcgtaatg aattattttg aaaattaatt ccaecatcct ttcagattct ggatggaaag 240
actgaatctt tgactcagaa ttgtttgctg aaaagaatga tgtgactttc ttagtcattt 300
a 301

<210> 250
<211> 301
<212> DNA
<213> Homo sapien

<400> 250
ggtctgtgac aaggacttgc aggctgtggg aggcaagtga cccttaacac tacacttctc 60
cttatcttta ttggcttgat aaacataatt atttctaaca ctagcttatt tccagttgcc 120
cataagcaca tcagtacttt tctctggctg gaatagtaaa cttaaagtatg gtacatctac 180
ctaaaagact actatgtgga ataatacata ctaatgaagt attacatgat ttaaagacta 240
caataaaacc aaacatgctt ataacattaa gaaaaacaat aaagatacat gattgaaacc 300
a 301

<210> 251
<211> 301
<212> DNA
<213> Homo sapien

<400> 251
gccgaggtcc tacatttggc ccagtttccc cctgcacccct ctccagggcc cctgcctcat 60
agacaacctc atagagcata ggagaactgg ttgccctggg ggcaggggga ctgtctggat 120
ggcaggggtc ctcaaaaatg ccactgtcac tgccaggaaa tgcttctgag cagtacacct 180
cattgggata aatgaaaagc ttcaagaaat cttcaggctc actctcttga aggcccggaa 240
cctctggagg ggggcagtgg aatcccagct ccaggacgga tcctgtcgaa aagatatcct 300
c 301

<210> 252
<211> 301
<212> DNA
<213> Homo sapien

<400> 252
gcaaccaatc actctgtttc acgtgacttt tatcaccata caatttgttg catttcctca 60
ttttctacat tgtagaatca agagtgtaaa taaatgtata tcgatgtctt caagaatata 120
tcattccttt ttcactagga acccattcaa aatataagtc aagaatctta atatcaacaa 180
atatatcaag caaactggaa ggcagaataa ctaccataat ttagtataag taccctaaagt 240
tttataaatc aaaagcccta atgataacca tttttagaat tcaatcatca ctgtagaatc 300
a 301

<210> 253

<211> 301
 <212> DNA
 <213> Homo sapien

<400> 253
 ttccctaaga agatgttatt ttgttgggtt ttgttccccc tccatctcga ttctcgtacc 60
 caactaaaaa aaaaaataa agaaaaaatg tgctgcgttc tgaaaaataa ctcccttagct 120
 tggcttgatt gttttcagac cttaaaatat aaacttgttt cacaagcttt aatccatgtg 180
 gatttttttt cttagagaac cacaaaacat aaaaggagca agtcggactg aatacctgtt 240
 tccatagtgc ccacagggta ttcctcacat tttctccata ggaaaatgct ttttcccaag 300
 g 301

<210> 254
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 254
 cgctgcgcct ttcccttggg ggaggggcaa ggccagaggg ggtccaagtg cagcacgagg 60
 aacttgacca attcccttga agcgggtggg ttaaaccctg taaatgggaa caaatccccc 120
 ccaaatctct tcatcttacc ctggtggact cctgactgta gaattttttg gttgaaacaa 180
 gaaaaaata aagctttgga cttttcaagg ttgcttaaca ggtactgaaa gactggcctc 240
 acttaactg agccaggaaa agctgcagat ttattaatgg gtgtgttagt gtgcagtgcc 300
 t 301

<210> 255
 <211> 302
 <212> DNA
 <213> Homo sapien

<400> 255
 agcttttttt tttttttttt tttttttttt ttcattaaaa aatagtgtct tttattataa 60
 attactgaaa tgtttctttt ctgaatataa atataaatat gtgcaaagt tgaactggat 120
 tgggattttg ttgagttctt caagcatctc ctaataccct caagggcctg agtagggggg 180
 aggaaaaagg actggagggtg gaatctttat aaaaaacaag agtgattgag gcagattgta 240
 aacattatta aaaaacaaga acaaaacaaa aaaatagaga aaaaaaccac cccaacacac 300
 aa 302

<210> 256
 <211> 301
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(301)
 <223> n = A,T,C or G

<400> 256
 gttccagaaa acattgaagg tggcttccca aagtotaact agggataccc cctctagcct 60
 aggaccctcc tccccacacc tcaatccacc aaaccatcca taatgcaccc agataggccc 120
 acccccaaaa gcctggacac cttgagcaca cagttatgac caggacagac tcatctctat 180
 aggcaaatag ctgctggcaa actggcatta cctggtttgt ggggatgggg gggcaagtgt 240
 gtggcctctc ggcttggtta gcaagaacat tcagggtagg cctaagttan tcgtgttagt 300
 t 301

<210> 257
 <211> 301

<212> DNA

<213> Homo sapien

<400> 257

gttgtggagg aactctggct tgctcattaa gtctactga ttttcactat cccctgaatt	60
tccccactta tttttgtctt tcaactatcgc aggccttaga agaggtctac ctgcctccag	120
tcttacctag tccagtctac cccctggagt tagaatggcc atcctgaagt gaaaagtaat	180
gtcacattac tcccttcagt gattttctgt agaagtgcc atccctgaat gccaccaaga	240
tcttaattctt cacatcttta atcttatctc ttgtactcct ctttacaccg gagaaggctc	300
c	301

<210> 258

<211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(301)

<223> n = A,T,C or G

<400> 258

cagcagtagt agatgccgta tgccagcacg cccagcactc ccaggatcag caccagcacc	60
aggggccag ccaccaggcg cagaagcaag ataaacagta ggctcaagac cagagccacc	120
cccagggcaa caagaatcca ataccaggac tgggcaaaat cttcaaagat cttaacactg	180
atgtctcggt cattgaggct gtcaataana cgctgatccc ctgctgtatg gtggtgtcat	240
tggatgccc tgggagcgcc ggtggagtaa cgttggtcca tggaaagcag cgcccacaac	300
t	301

<210> 259

<211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(301)

<223> n = A,T,C or G

<400> 259

tcatatatgc aaacaaatgc agactangcc tcaggcagag actaaaggac atctcttggg	60
gtgtcctgaa gtgatttga ccctgaggg cagacaccta agtaggaatc ccagtgggaa	120
gcaaagccat aaggaagccc aggattcctt gtgatcagga agtgggcccag gaaggctctgt	180
tccagctcac atctcatctg catgcagcac ggaccggatg cgcccactgg gtcttggctt	240
ccctcccatc ttctcaagca gtgtccttgt tgagccattt gcaccccttg ctccagggtg	300
c	301

<210> 260

<211> 301

<212> DNA

<213> Homo sapien

<400> 260

tttttttct ccctaaggaa aaagaaggaa caagtctcat aaaaccaa at aagcaatgg	60
aagggtgtctt aacttgaaaa agattaggag tcaactgggtt acaagttata attgaatgaa	120
agaactgtaa cagccacagt tggccatttc atgccaatgg cagcaaaca caggattaac	180
tagggcaaaa taaataagtg tgtggaagcc ctgataagtg ctttaataaac agactgattc	240
actgagacat cagtacctgc ccgggcggcc gctcgagccg aattctgcag atatccatca	300

c

301

<210> 261
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 261

aaatattcga gcaaattcctg taactaatgt gtctccataa aaggctttga actcagtga	60
tctgcttcca tccacgattc tagcaatgac ctctcggaca tcaaagctcc tcttaagggt	120
agcaccact attccataca attcatcagc aggaataaaa ggctcttcag aagggtcaat	180
ggtgacatcc aatttcttct gataatttag attcctcaca accttcctag ttaagtgaag	240
ggcatgatga tcatccaaag ccagtggtc acttactcca gactttctgc aatgaagatc	300
a	301

<210> 262
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 262

gaggagagcc tggtacagca tttgtaagca cagaatactc caggagtatt tgtaattgtc	60
tgtgagcttc ttgccgcaag tctctcagaa atttaaaaag atgcaaattc ctgagtcacc	120
cctagacttc ctaaaccaga tcctctgggg ctggaacctg gactctgca tttgtaatga	180
gggctttctg gtgcacacct aattttgtgc atctttgccc taaatcctgg attagtgcc	240
catcattacc cccacattat aatgggatag attcagagca gatactctcc agcaaagaat	300
c	301

<210> 263
 <211> 301
 <212> DNA
 <213> Homo sapien

<220>

<221> misc_feature

<222> (1)... (301)

<223> n = A,T,C or G

<400> 263

tttagcttgt ggtaaatgac tcacaaaact gattttaaaa tcaagttaat gtgaattttg	60
aaaattacta cttaatccta attcacaata acaatggcat taagggttga cttgagttgg	120
ttcttagtat tatttatggt aaataggctc ttaccacttg caataactg gccacatcat	180
taatgactga cttccagta aggctctcta aggggtaagt angaggatcc acaggatttg	240
agatgctaag gccccagaga tcgtttgatc caaccctctt attttcagag gggaaaatgg	300
g	301

<210> 264
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 264

aaagacgtta aaccactcta ctaccacttg tggaactctc aaagggtaaa tgacaaascc	60
aatgaatgac tctaaaaaca atatttacat ttaatgggtt gtagacaata aaaaaacaag	120
gtggatagat ctagaattgt aacattttta gaaaaccata scatttgaca gatgagaaag	180
ctcaattata gatgcaaagt tataactaaa ctactatagt agtaaagaaa tacatttcac	240
acccttcata taaattcact atcttggctt gaggcactcc ataaaatgta tcacgtgcac	300
a	301

<210> 265
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 265
 tgcccaagtt atgtgtaagt gtatccgcac ccagaggtaa aactacactg tcattctttgt 60
 cttcttctga cgcagtattt cttctctggg gagaagccgg gaagtcttct cctggctcta 120
 catattcttg gaagtctcta atcaactttt gttccatttg tttcatttct tcaggaggga 180
 ttttcagttt gtcaacatgt tctctaacaa cacttgccca tttctgtaaa gaatccaaag 240
 cagtccaagg ctttgacatg tcaacaacca gcataactag agtatccttc agagatacgg 300
 c 301

<210> 266
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 266
 taccgtctgc ctttctctcc atccaggcca tctgcgaatc tacatgggtc ctcctattcg 60
 acaccagatc actcttttct ctaccacacag gcttgctatg agcaagagac acaacctcct 120
 ctcttctgtg ttccagcttc ttttctgtt cttccacccc cttaagtctt attcctgggg 180
 atagagacac caatacccat aacctctctc ctaagcctcc ttataaccca ggggtgcacag 240
 cacagactcc tgacaactgg taaggccaat gaactgggag ctcacagctg gctgtgcctg 300
 a 301

<210> 267
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 267
 aaagagcaca ggccagctca gcctgccttg gccatctaga ctcagcctgg ctccatgggg 60
 gttctcagtg ctgagtcctat ccaggaaaag ctcacctaga ctttctgagg ctgaatcttc 120
 atcttcacag gcagcttctg agagcctgat attcctagcc ttgatgggtc ggagtaaaag 180
 ctcaattctga ttctctctct tcttttcttt caagttggct ttcttcacat cctctgttc 240
 aattcgtctc agcttgcttg ctttagccct catttcaga agcttcttct ctttggcatc 300
 t 301

<210> 268
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 268
 aatgtctcac tcaactactt ccagcctac cgtggcctaa ttctgggagt tttcttctta 60
 gatcttggga gagctgggtc ttctaaggag aaggaggaag gacagatgta actttggatc 120
 tcgaagagga agtctaattg aagtaattag tcaacgggtc ttgtttagac tcttggata 180
 tgctgggttg ctcagtgagc ctttttgag aaagcaagta ttattcttaa ggagtaacca 240
 ctccccattg ttctactttc taccatcatc aattgtatat tatgtattct ttggagaact 300
 a 301

<210> 269
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 269

taacaatata	cactagctat	ctttttaact	gtccatcatt	agcaccaatg	aagattcaat	60
aaaattacct	ttattcacac	atctcaaaac	aattctgcaa	attcttagtg	aagtttaact	120
atagtcacag	accttaaata	ttcacattgt	tttctatgtc	tactgaaaat	aagttcacta	180
cttttctgga	tattctttac	aaaatcttat	taaaattcct	ggtattatca	cccccaatta	240
tacagtagca	caaccacctt	atgtagtttt	tacatgatag	ctctgtagaa	gtttcacatc	300
t						301

<210> 270

<211> 301

<212> DNA

<213> Homo sapien

<400> 270

cattgaagag	cttttgcgaa	acatcagaac	acaagtgcct	ataaaattaa	ttaagcctta	60
cacaagaata	catattcctt	ttatttctaa	ggagttaaac	atagatgtag	ctgatgtggg	120
gagcttgctg	gtgcagtgc	tattggataa	cactattcat	ggccgaattg	atcaagtcaa	180
ccaactcctt	gaactggatc	atcagaagaa	gggtggtgca	cgatatactg	cactagataa	240
tggaccaacc	aactaaattc	tctcaccagg	ctgtatcagt	aaactggcct	aacagaaaac	300
a						301

<210> 271

<211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc feature

<222> (1)...(301)

<223> n = A,T,C or G

<400> 271

aaaaggttct	cataagatta	acaatttaaa	taaatatttg	atagaacatt	ctttctcatt	60
tttatagctc	atcttttagg	ttgatattca	gttcattgct	cccttgctgt	tcttgatcca	120
gaattgcaat	cacttcatca	gcctgtattc	gctccaattc	tctataaagt	gggtccaagg	180
tgaaccacag	agccacagca	cacctctttc	ccttggtgac	tgccttcacc	ccatganggt	240
tctctctccc	agatganaac	tgatcatgcg	cccacatttt	gggttttata	gaagcagtca	300
c						301

<210> 272

<211> 301

<212> DNA

<213> Homo sapien

<400> 272

taaattgcta	agccacagat	aacaccaatc	aaatggaaca	aatcactgtc	ttcaaagtgc	60
ttatcagaaa	accaaagtag	cctggaatct	tcataatacc	ttaaactgcc	gtatttagga	120
tccaataatt	ccctcatgat	gagcaagaaa	aattctttgc	gcacccctcc	tgcattccaca	180
gcatcttctc	caacaaatat	aaccttgagt	ggcttcttgt	aatctatgtt	ctttgttttc	240
ctaaggactt	ccattgcata	tcctacaata	ttttctctac	gcaccactag	aattaagcag	300
g						301

<210> 273

<211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature
 <222> (1)...(301)
 <223> n = A,T,C or G

<400> 273
 acatgtgtgt atgtgtatct ttgggaaaan aanaagacat cttgtttayt atttttttgg 60
 agagangctg ggacatggat aatcacwtaa tttgctayta tyactttaat ctgactygaa 120
 gaaccgtcta aaaataaaat ttacatgtc dtatatctct tatagtatgc ttatttcacc 180
 ttytttctgt ccagagagag tatcagtgac ananatttma ggggtgaamac atgmattggg 240
 gggacttnty tttaacngam accctgcccg sgcgccctcg makcngantt ccgcsananc 300
 t 301

<210> 274
 <211> 301
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(301)
 <223> n = A,T,C or G

<400> 274
 cttatatact ctttctcaga ggcaaaagag gagatgggta atgtagacaa ttcttttgagg 60
 aacagtaaatt gattattaga gagaangaat ggaccaagga gacagaaatt aacttgtaaa 120
 tgattctctt tggaaatctga atgagatcaa gaggccagct ttagcttctg gaaaagtcca 180
 tctaggtagt gttgcattct cgtcttcttt tctgcagtag ataatgaggt aaccgaaggc 240
 aattgtgctt cttttgataa gaagctttct tggtcataac aggaaattcc aganaaagtc 300
 c 301

<210> 275
 <211> 301
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(301)
 <223> n = A,T,C or G

<400> 275
 tcggtgtcag cagcacgtgg cattgaacat tgcaatgtgg agcccaaacc acagaaaatg 60
 gggtgaaatt ggccaacttt ctattaactt atgttggcaa ttttgccacc aacagtaagc 120
 tggcccttct aataaaagaa aattgaaagg tttctcacta aacggaatta agtagtgag 180
 tcaagagact cccaggcctc agcgtacctg cccgggcggc cgctcgaagc cgaattctgc 240
 agatatccat cacactggcg gncgctcgan catgcatcta gaaggnccaa ttcgccctat 300
 a 301

<210> 276
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 276
 tgtacacata ctcaataaat aaatgactgc attgtggtat tattactata ctgattatat 60
 ttatcatgtg acttctaatt agaaaatgta tccaaaagca aaacagcaga tatacaaaat 120
 taaagagaca gaagatagac attaacagat aaggcaactt atacattgag aatccaaatc 180
 caatacattt aaacatttgg gaaatgaggg ggacaaatgg aagccagatc aaatttgtgt 240

aaaactattc agtatgtttc ccttgcttca tgtctgagaa ggctctcctt caatggggat 300
g 301

<210> 277
<211> 301
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

<400> 277
tttgttgatg tcagtatttt attacttgcg ttatgagtgc tcacctggga aattctaaag 60
atacagagga cttggaggaa gcagagcaac tgaatttaat ttaaaagaag gaaaacattg 120
gaatcatggc actcctgata ctttcccaaa tcaacactct caatgccccca ccctcgctcct 180
caccatagtg gggagactaa agtggccacg gatttgcctt angtgtgcag tgcgttctga 240
gttcnctgtc gattacatct gaccagtctc ctttttccga agtcnctccg ttcaatcttg 300
c 301

<210> 278
<211> 301
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

<400> 278
taccactaca ctccagcctg ggcaacagag caagacctgt ctcaaagcat aaaatggaat 60
aacatatcaa atgaaacagg gaaaatgaag ctgacaattt atggaagcca gggcttgtca 120
cagtctctac tgttattatg cattacctgg gaatttatat aagcccttaa taataatgcc 180
aatgaacatc tcattgtgtg tcacaatggt ctggcactat tataagtgtc tcacaggttt 240
tatgtgttct tcgtaacttt atggantagg tactcggccg cgaacacgct aagccgaatt 300
c 301

<210> 279
<211> 301
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

<400> 279
aaagcaggaa tgacaaagct tgcttttctg gtatgttcta ggtgtattgt gacttttact 60
gttatattaa ttgccaatat aagtaaatat agattatata tgtatagtgt ttcacaaagc 120
ttagaccttt accttccagc caccacacag tgcttgatat ttcagagtca gtcattgggt 180
atacatgtgt agttccaaag cacataagct agaanaanaa atatttctag ggagcactac 240
catctgtttt cacatgaaat gccacacaca tagaactcca acatcaattt cattgcacag 300
a 301

<210> 280

<211> 301
 <212> DNA
 <213> Homo sapien

<400> 280
 ggtactggag ttttctctcc ctgtgaaaac gtaactactg ttgggagtga attgaggatg 60
 tagaaagggtg gtggaaccaa attgtggtca atggaaatag gagaatatgg ttctcactct 120
 tgagaaaaaa acctaagatt agcccaggta gttgcctgta acttcagttt ttctgcctgg 180
 gtttgatata gtttaggggtt ggggttagat taagatctaa attacatcag gacaaagaga 240
 cagactatta actccacagt taattaagga ggtatgttcc atgtttattt gttaaagcag 300
 t 301

<210> 281
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 281
 aggtacaaga aggggaatgg gaaagagctg ctgctgtggc attgttcaac ttggatatctc 60
 gccgagcaat ccaaactcctg aatgaagggg catcttctga aaaaggagat ctgaatctca 120
 atgtggtagc aatggcttta tcgggttata cggatgagaa gaactccctt tggagagaaa 180
 tgtgtagcac actgcgatta cagctaaata acccgatttt gtgtgtcatg ttgcatcttc 240
 tgacaagtga aacaggatct tacgatggag ttttgtatga aaacaaagtt gcagtacctc 300
 g 301

<210> 282
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 282
 caggtactac agaattaaaa tactgacaag caagtagttt cttggcgtgc acgaattgca 60
 tccagaaccc aaaaattaaag aaattcaaaa agacattttg tgggcacctg ctgacacaga 120
 agcgcagaag caaagcccag gcagaacat gctaacctta cagctcagcc tgacagaag 180
 cgcagaagca aagcccaggc agaaccatgc taaccttaca gctcagcctg cacagaagcg 240
 cagaagcaaa gcccaggcag aacatgctaa ccttacagct cagcctgcac agaagcacag 300
 a 301

<210> 283
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 283
 atctgtatac ggcagacaaa ctttatarag tgtagagagg tgagcgaaag gatgcaaaag 60
 cactttgagg gctttataat aatatgctgc ttgaaaaaaa aaatgtgtag ttgatactca 120
 gtgcatctcc agacatagta aggggttgct ctgaccaatc aggtgatcat tttttctatc 180
 acttcccagg ttttatgcaa aaattttgtt aaattctata atggtgatat gcattcttta 240
 ggaaacatat acatttttta aaatctattt tatgtaagaa ctgacagacg aatttgcttt 300
 g 301

<210> 284
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 284
 caggtacaaa acgctattaa gtggcttaga atttgaacat ttgtggtctt tatttacttt 60

```

gcttcgtgtg tgggcaaagc aacatcttcc ctaaatatat attaccaaga aaagcaagaa    120
gcagattagg tttttgacaa aacaaacagg ccaaaagggg gctgacctgg agcagagcat    180
ggtgagaggc aaggcatgag agggcaagtt tgttgtggac agatctgtgc ctactttatt    240
actggagtaa aagaaaacaa agttcattga tgtcgaagga tatatacagt gttagaaatt    300
a                                                                    301

```

```

<210> 285
<211> 301
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

```

```

<400> 285
acatcaccat gatcggatcc cccacccatt atacgttgta tgtttacata aatactcttc    60
aatgatcatt agtggttttaa aaaaaatact gaaaactcct tctgcatccc aatctctaac    120
caggaaagca aatgctatct acagacctgc aagccctccc tcaaacnaaa ctatttctgg    180
attaaatatg tctgacttct tttgaggtca cagcactagg caaatgctat ttacgatctg    240
caaaagctgt ttgaagagtc aaagcccca tgtgaacacg atttctggac cctgtaacag    300
t                                                                    301

```

```

<210> 286
<211> 301
<212> DNA
<213> Homo sapien

```

```

<400> 286
taccaactgca ttccagcctg ggtgacagag tgagactccg tctccaaaaa aaactttgct    60
tgtatattat ttttgacctta cagtggatca ttctagtagg aaaggacagt aagatttttt    120
atcaaaatgt gtcattgccag taagagatgt tatattcttt tctcatttct tccccacca    180
aaaaaagct accatatagc ttataagtct caaatttttg ccttttacta aaatgtgatt    240
gtttctgttc attgtgtatg cttcatcacc tatattaggc aaattccatt ttttcccttg    300
t                                                                    301

```

```

<210> 287
<211> 301
<212> DNA
<213> Homo sapien

```

```

<400> 287
tacagatctg ggaactaaat attaaaaatg agtgtggctg gatatatgga gaatgttggg    60
cccagaagga acgtagagat cagatattac aacagctttg ttttgagggt tagaaatatg    120
aaatgatttg gttatgaacg cacagtttag gcagcagggc cagaatcctg accctctgcc    180
ccgtgggttat ctccctccca gcttggctgc ctcatgttat cacagtatc cattttgttt    240
gttgcattgc ttgtgaagcc atcaagattt tctcgtctgt tttcctctca ttggtaatgc    300
t                                                                    301

```

```

<210> 288
<211> 301
<212> DNA
<213> Homo sapien

```

```

<400> 288
gtacacctaa ctgcaaggac agctgaggaa tgtaatgggc agccgctttt aaagaagtag    60
agtcaatagg aagacaaatt ccagttccag ctcatgtctg gtatctgcaa agctgcaaaa    120

```

gatctttaaa gacaatttca agagaatatt tccttaaagt tggcaatttg gagatcatac 180
aaaagcatct gcttttgtga tttaatttag ctcatctggc cactggaaga atccaaacag 240
tctgccttaa ttttgatga atgcatgatg gaaattcaat aatttagaaa gttaaaaaaa 300
a 301

<210> 289
<211> 301
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

<400> 289
ggtacactgt ttccatgtta tgtttctaca cattgctacc tcagtgtctcc tggaaactta 60
gcttttcatg tctccaagta gtccaccttc atttaactct ttgaaactgt atcatctttg 120
ccaagtaaga gtggtggcct atttcagctg ctttgacaaa atgactggct cctgacttaa 180
cgttctataa atgaatgtgc tgaagcaaag tgcccatggt ggccggcgaan aagagaaaga 240
tgtgttttgt tttgactct ctgtggtccc ttccaatgct gtgggtttcc aaccagnnga 300
a 301

<210> 290
<211> 301
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

<400> 290
acactgagct cttcttgata aatatacaga atgcttggca tatacaagat tctatactac 60
tgactgatct gttcatttct ctccacagctc ttaccccca aagcttttcc accctaagtg 120
ttctgacctc cttttctaata cacagtaggg atagaggcag anccacctac aatgaacatg 180
gagttctatc aagaggcaga aacagcacag aatcccagtt ttaccattcg cttagcagtgc 240
tgccttgaac aaaaacattt ctccatgtct cattttcttc atgectcaag taacagtga 300
a 301

<210> 291
<211> 301
<212> DNA
<213> Homo sapien

<400> 291
caggtaccaaa tttcttctat cctagaaaca tttcatttta tgttgttgaa acataacaac 60
tatatcagct agattttttt tctatgcttt acctgctatg gaaaatttga cacattctgc 120
tttactcttt tgtttatagg tgaatcacia aatgtatttt tatgtattct gtagttcaat 180
agccatggct gtttacttca tttaatttat ttagcataaa gacattatga aaaggcctaa 240
acatgagctt cacttcccca ctaactaatt agcatctgtt atttcttaac cgtaatgcct 300
a 301

<210> 292
<211> 301
<212> DNA
<213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(301)
 <223> n = A,T,C or G

<400> 292
 accttttagt agtaatgtct aataataaat aagaaatcaa ttttataagg tccatatagc 60
 tgtatttaaat aatttttaag tttaaaagat aaaataccat catttttaaat gttgggtattc 120
 aaaaccaaag natataaccg aaaggaaaaa cagatgagac ataaaatgat ttgcnagatg 180
 ggaaatatag tasttyatga atgttnatta aattccagtt ataatagtgg ctacacactc 240
 tcactacaca cacagacccc acagtcctat atgccacaaa cacattttcca taacttgaaa 300
 a 301

<210> 293
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 293
 ggtaccaagt gctgggtgcc gctgttacc tgttctcact gaaaagtctg gctaattgctc 60
 ttgtgtagtc acttctgatt ctgacaatca atcaatcaat ggcctagagc actgactgtt 120
 aacacaaacg tctactagca agtagcaaca gctttaagtc taaatacaaa gctgttctgt 180
 gtgagaattt tttaaaaggc tacttgtata ataacccttg tcatttttaa tgtacctcgg 240
 ccgcgaccac gctaagccga attctgcaga tatccatcac actggcggcc gctcgagcat 300
 g 301

<210> 294
 <211> 301
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(301)
 <223> n = A,T,C or G

<400> 294
 tgaccataa caatatacac tagctatctt ttttaactgtc catcattagc accaatgaag 60
 attcaataaa attaccttta ttcacacatc tcaaaaacat tctgcaaat cttagtgaag 120
 ttttaactata gtcacaganc ttaaattatc acattgtttt ctatgtctac tgaaaataag 180
 ttcactactt ttctgggata ttctttacaa aatcttatta aaattcctgg tattatcacc 240
 cccaattata cagtagcaca accaccttat gtagttttta catgatagct ctgtagagggt 300
 t 301

<210> 295
 <211> 305
 <212> DNA
 <213> Homo sapien

<400> 295
 gtactctttc tctccctcc tctgaattta attctttcaa cttgcaattt gcaaggatta 60
 cacatttcac tgtgatgtat attgtgttgc aaaaaaaaaa gtgtctttgt ttaaaattac 120
 ttggtttgtg aatccatctt gctttttccc cattggaact agtcattaac ccatctctga 180
 actggtagaa aaacrtctga agagctagtc tatcagcatc tgacagggtga attggatggg 240
 tctcagaacc atttcaccca gacagcctgt ttctatcctg ttttaataaat tagtttgggt 300
 tctct 305

<210> 296
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 296
 aggtactatg ggaagctgct aaaataatat ttgatagtaa aagtatgtaa tgtgctatct 60
 cacctagtag taaactaaaa ataaactgaa actttatgga atctgaagtt attttccttg 120
 attaaataga attaataaac caatatgagg aaacatgaaa ccatgcaatc tactatcaac 180
 tttgaaaaag tgattgaacg aaccacttag ctttcagatg atgaacactg ataagtcatt 240
 tgtcattact ataaatttta aaatctgtta ataagatggc ctatagggag gaaaaagggg 300
 c 301

<210> 297
 <211> 300
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(300)
 <223> n = A,T,C or G

<400> 297
 actgagtttt aactggacgc caagcaggca aggctggaag gttttgctct ctttgtgcta 60
 aaggttttga aaaccttgaa ggagaatcat ttgacaaga agtacttaag agtctagaga 120
 acaaagangt gaaccagctg aaagctctcg ggggaanctt acatgtgttg ttaggcctgt 180
 tccatcattg ggagtgcact ggccatccct caaaatttgt ctgggctggc ctgagtggc 240
 accgcaoctc ggccgcgacc acgctaagcc gaattctgca gatatccatc aactggcgc 300

<210> 298
 <211> 301
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(301)
 <223> n = A,T,C or G

<400> 298
 tatggggttt gtcacccaaa agctgatgct gagaaaggcc tccctggggc ccctcccgcg 60
 ggcatctgag agacctggtg ttccagtgtt tctggaaatg ggtcccagtg ccgccggctg 120
 tgaagctctc agatcaatca cgggaagggc ctggcgggtg tggccacctg gaaccacct 180
 gtccgtgtctg ttacatttc actaycaggt tttctctggg cattacnatt tgttccccta 240
 caacagtgac ctgtgcattc tgctgtggcc tgctgtgtct gcagggtggc ctcagcgagg 300
 t 301

<210> 299
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 299
 gttttgagac ggagtttcac tcttgttgcc cagactggac tgcaatggca gggctctctgc 60
 tcaactgcacc ctctgcctcc caggttcgag caattctcct gcctcagcct ccaggttagc 120
 tgggattgca ggctcagcc accataccca gctaattttt ttgtattttt agtagagacg 180
 gagtttcgcc atgttgcca gctggctcga aactcctgac ctcaagcgac ctgcctgcct 240

cggcctccca aagtgcctgga attataggca tgagtcaaca cgcccagcct aaagatatatt 300
t 301

<210> 300
<211> 301
<212> DNA
<213> Homo sapien

<400> 300
attcagtttt atttgcctgcc ccagtatctg taaccaggag tgccacaaaa tcttgccaga 60
tatgtccac acccactggg aaaggctccc acctggctac ttcctctatc agctgggtca 120
gctgcattcc acaaggttct cagcctaata agtttacta cctgccagtc tcaaaactta 180
gtaaagcaag accatgacat tccccacgg aaatcagagt ttgccccacc gtcttggtac 240
tataaagcct gcctctaaca gtccttgctt cttcacacca atcccgagcg catcccccat 300
g 301

<210> 301
<211> 301
<212> DNA
<213> Homo sapien

<400> 301
ttaaattttt gagaggataa aaaggacaaa taatctagaa atgtgtcttc ttcagctctgc 60
agaggacccc aggtctccaa gcaaccacat ggtcaagggc atgaataatt aaaagttggt 120
gggaactcac aaagaccctc agagctgaga caccacaaac agtgggagct cacaaagacc 180
ctcagagctg agacaccac aacagtggga gctcacaag accctcagag ctgagacacc 240
cacaacagca cctcgttcag ctgccacatg tgtgaataag gatgcaatgt ccagaagtgt 300
t 301

<210> 302
<211> 301
<212> DNA
<213> Homo sapien

<400> 302
aggtagacat ttagcttggt gtaaattgact caaaaaactg attttaaaat caagttaatg 60
tgaattttga aaattactac ttaattcctaa ttcacaataa caatggcatt aaggtttgac 120
ttgagttggt tottagtatt atttatggta aataggctct taccacttgc aaataactgg 180
ccacatcatt aatgactgac ttcccagtaa ggctctctaa ggggtaagta ggaggatcca 240
caggatttga gatgctaagg ccccagagat cgtttgatcc aaccctctta ttttcagagg 300
g 301

<210> 303
<211> 301
<212> DNA
<213> Homo sapien

<400> 303
aggtagcaac tgtggaaata ggtagaggat ctttttttct ttccatatca actaagttgt 60
atattgtttt ttgacagttt aacacatctt cttctgtcag agattctttc acaatagcac 120
tggtaatg aactaccgct tgcattgtaa aaatgggtgt ttgtgaaatg atcataggcc 180
agtaacgggt atgtttttct aactgatctt ttgctcgttc caaagggacc tcaagacttc 240
catcgatttt atatctgggg tctagaaaaa gagttaatct gttttccctc ataaattcac 300
c 301

<210> 304
<211> 301
<212> DNA

<213> Homo sapien

<400> 304

acatggatgt	tattttcag	actgtcaacc	tgaatttgta	tttgcttgac	attgccta	60
tattagtttc	agtttcagct	taccactttt	ttgtctgcaa	catgcaraas	agacagtgcc	120
cttttttagtg	tatcatatca	ggaatcatct	caatttggtt	tgtgccatta	ctgggtgcagt	180
gactttcagc	cacttggtga	aggtggagtt	ggccatatgt	ctccactgca	aaattactga	240
ttttcctttt	gtaattaata	agtgtgtgtg	tgaagattct	ttgagatgag	gtatataatct	300
c						301

<210> 305

<211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(301)

<223> n = A,T,C or G

<400> 305

gangtacagc	gtggtcaagg	taacaagaag	aaaaaatgt	gagtggcatc	ctgggatgag	60
cagggggaca	gacctggaca	gacacgttgt	catttgctgc	tgtgggtagg	aaaatgggag	120
taaaggagga	gaaacagata	caaatctcc	aactcagtat	taaggatttc	tcatgcctag	180
aatatttgta	gaaacaagaa	tacattcata	tggcaaataa	ctaaccatgg	tgggaacaaa	240
ttctgggatt	taagttggat	accaangaaa	ttgtattaaa	agagctgttc	atggaataag	300
a						301

<210> 306

<211> 8

<212> PRT

<213> Homo sapien

<400> 306

Val	Leu	Gly	Trp	Val	Ala	Glu	Leu
1				5			

<210> 307

<211> 637

<212> DNA

<213> Homo sapien

<400> 307

acaggggratg	aagggaaagg	gagaggatga	ggaagccccc	ctggggattt	ggtttgggtcc	60
ttgtgatcag	gtggtctatg	gggcttatcc	ctacaaagaa	gaatccagaa	ataggggcac	120
attgaggaat	gatacttgag	cccaaagagc	attcaatcat	tgttttattt	gccttmtttt	180
cacaccattg	gtgagggagg	gattaccacc	ctgggggttat	gaagatggtt	gaacacccca	240
cacatagcac	cggagatatg	agatcaacag	tttcttagcc	atagagattc	acagcccaga	300
gcaggaggac	gcttgccacac	catgcaggat	gacatggggg	atgcgctcgg	gattgggtgtg	360
aagaagcaag	gactgttaga	ggcaggcttt	atagtaacaa	gacgggtggg	caaactctga	420
tttccgtggg	ggaatgtcat	ggtcttgctt	tactaagttt	tgagactggc	aggtagtgaa	480
actcattagg	ctgagaacct	tgtggaatgc	acttgaccca	sctgatagag	gaagtagcca	540
ggtgggagcc	tttcccagtg	ggtgtgggac	atatctggca	agattttgtg	gcactcctgg	600
ttacagatac	tgggggcagca	aataaaaactg	aatcttg			637

<210> 308

<211> 647

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (647)

<223> n = A,T,C or G

<400> 308

acgattttca	ttatcatgta	aatcgggtca	ctcaaggggc	caaccacagc	tgggagccac	60
tgctcagggg	aaggttcata	tgggactttc	tactgcccaa	ggttctatac	aggatataaa	120
ggngcctcac	agtatagatc	tggtagcaaa	gaagaagaaa	caaacactga	tctctttctg	180
ccaccctct	gaccctttgg	aactcctctg	accctttaga	acaagcctac	ctaatatctg	240
ctagagaaaa	gaccaacaac	ggcctcaaag	gatctcttac	catgaaggtc	tcagctaatt	300
cttggctaag	atgtgggttc	cacattaggt	tctgaatatg	gggggaaggg	tcaatttgct	360
cattttgtgt	gtggataaag	tcaggatgcc	caggggccag	agcagggggc	tgcttgcttt	420
gggaacaatg	gctgagcata	taaccatagg	ttatggggaa	caaaacaaca	tcaaagtcac	480
tgtatcaatt	gccatgaaga	cttgagggac	ctgaatctac	cgattcatct	taaggcagca	540
ggaccagttt	gagtggcaac	aatgcagcag	cagaatcaat	ggaaacaaca	gaatgattgc	600
aatgtccttt	ttttctctct	gcttctgact	tgataaaagg	ggaccgt		647

<210> 309

<211> 460

<212> DNA

<213> Homo sapien

<400> 309

actttatagt	ttaggctgga	cattggaaaa	aaaaaaaagc	cagaacaaca	tgtgatagat	60
aatatgattg	gctgcacact	tccagactga	tgaatgatga	acgtgatgga	ctattgtatg	120
gagcacatct	tcagcaagag	ggggaaatac	tcattcattt	tggccagcag	ttgtttgatc	180
accaaacatc	atgccagaat	actcagcaaa	ccttcttagc	tcttgagaag	tcaaagtccg	240
ggggaattta	tttctggcaa	ttttaattgg	actccttatg	tgagagcagc	ggctaccag	300
ctggggtggt	ggagcgaacc	cgtcactagt	ggacatgcag	tggcagagct	cctggtaacc	360
acctagagga	atacacaggc	acatgtgtga	tgccaagcgt	gacacctgta	gcactcaa	420
ttgtcttggt	tttgcctttc	ggtgtgtaag	attcttaagt			460

<210> 310

<211> 539

<212> DNA

<213> Homo sapien

<400> 310

acgggactta	tcaaataaag	ataggaaaag	aagaaaactc	aaatattata	ggcagaaatg	60
ctaaagggtt	taaaatatgt	caggattgga	agaaggcatg	gataaagaac	aaagttcagt	120
taggaaagag	aaacacagaa	ggaagagaca	caataaaagt	cattatgtat	tctgtgagaa	180
gtcagacagt	aagatttggt	ggaaatgggt	tggtttgttg	tatgggtatg	attttagcaa	240
taatctttat	ggcagagaaa	gctaaaatcc	tttagcttgc	gtgaatgatc	acttgctgaa	300
ttcctcaagg	taggcatgat	gaaggagggt	ttagaggaga	cacagacaca	atgaactgac	360
ctagatagaa	agccttagta	tactcagcta	ggaatagtga	ttctgagggc	acactgtgac	420
atgattatgt	cattacatgt	atggtagtga	tggggatgat	aggaaggaag	aacttatggc	480
atattttcac	ccccacaaaa	gtcagttaaa	tattgggaca	ctaaccatcc	aggtcaaga	539

<210> 311

<211> 526

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(526)

<223> n = A,T,C or G

<400> 311

caaatttgag ccaatgacat agaattttac aaatcaagaa gcttattctg gggccatttc	60
ttttgacgtt ttctctaaac tactaaagag gcattaatga tccataaatt atattatcta	120
catttacagc atttaaaatg tggtcagcat gaaatattag ctacagggga agctaaataa	180
attaaacatg gaataaagat ttgtccttaa atataatcta caagaagact ttgatatttg	240
tttttcacaa gtgaagcatt cttataaagt gtcataacct ttttggggaa actatgggaa	300
aaaatgggga aactctgaag ggttttaagt atcttacctg aagctacaga ctccataacc	360
tctctttaca gggagctcct gcagccccta cagaaatgag tggtgagat tcttgattgc	420
acagcaagag cttctcatct aaaccctttc cttttttagt atctgtgtat caagtataaa	480
agttctataa actgtagtnt acttatitta atccccaag cacagt	526

<210> 312

<211> 500

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(500)

<223> n = A,T,C or G

<400> 312

cctctctctc cccaccccct gactctagag aactggggtt tctcccagta ctccagcaat	60
tcatttctga aagcagtga gccactttat tccaaagtac actgcagatg ttcaaactct	120
ccatttctct ttcccttcca cctgccagtt ttgctgactc tcaacttgtc atgagtgtaa	180
gcattaagga cattatgctt cttcgattct gaagacaggc cctgctcatg gatgactctg	240
gcttcttagg aaaatatttt tcttccaaaa tcagtaggaa atctaaactt atccccctct	300
tgcagatgtc tagcagcttc agacatttgg ttaagaacct atgggaaaaa aaaaaatcct	360
tgctaattgtg gtttcctttg taaaccanga ttcttatttg nctggtatag aatatcagct	420
ctgaacgtgt ggtaaagatt tttgtgtttg aatataggag aaatcagttt gctgaaaagt	480
tagtcttaat tatctattgg	500

<210> 313

<211> 718

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(718)

<223> n = A,T,C or G

<400> 313

ggagatttgt gtggtttgca gccgaggag accaggaaga tctgcatggt gggaaggacc	60
tgatgataca gaggtgagaa ataagaaagg ctgctgactt taccatctga ggccacacat	120
ctgctgaaat ggagataatt aacatcacta gaaacagcaa gatgacaata taatgtctaa	180
gtagtgacat gtttttgca atttccagcc cttttaaata tccacacaca caggaagcac	240
aaaagggaagc acagagatcc ctgggagaaa tgcccggccg ccactctggg tcatcgatga	300
gcctcgccct gtgctgntc ccgcttggtg gggaaggaca ttagaaaatg aattgatgtg	360
ttccttaaa gattgagcaga aaacagatcc tgggtgtgat atttatttga acgggattac	420
agatttgaaa tgaagtcaca aagtgagcat taccaatgag aggaaaacag acgagaaaat	480
cttgatggtt cacaagacat gcaacaaaca aaatggaata ctgtgatgac acgagcagcc	540
aactggggag gagataccac ggggcagagg tcaggattct ggccctgctg cctaactgtg	600
cgttatacca atcatttcta tttctaccct caaacaagct gtngaataatc tgacttacgg	660
ttctnttggc ccacattttc atnatccacc ccntcntttt aannttantc caaantgt	718

<210> 314
 <211> 358
 <212> DNA
 <213> Homo sapien

<400> 314
 gtttattttac attacagaaa aaacatcaag acaatgtata ctattttcaaa tatatccata 60
 cataatcaaa tatagctgta gtacatgttt tcattgggtg agattaccac aaatgcaagg 120
 caacatgtgt agatctcttg tcttatttctt ttgtctataa tactgtattg tgtagtccaa 180
 gctctcggtg gtccagccac tgtgaaacat gtcaccttta gattaacctc gtggacgctc 240
 ttgtgtgatt gctgaactgt agtgccctgt attttgcttc tgtctgtgaa ttctgttgct 300
 tctggggcat ttcttgtga tgcagaggac caccacacag atgacagcaa tctgaatt 358

<210> 315
 <211> 341
 <212> DNA
 <213> Homo sapien

<400> 315
 taccacctcc ccgctggcac tgatgagccg catcaccatg gtcaccagca ccatgaaggc 60
 ataggtgatg atgaggacat ggaatgggcc cccaaggatg gtctgtccaa agaagcgagt 120
 gaccccatc ctgaagatgt ctggaacctc taccagcagg atgatgatg cccaatgac 180
 agtcaccagc tccccgacca gccggatata gtccttaggg gtcatgtagg cttcctgaag 240
 tagctctgc tgtaagaggg tgttgtcccg ggggctcgtg cggttattgg tectgggctt 300
 gagggggcgg tagatgcagc acatggtgaa gcagatgatg t 341

<210> 316
 <211> 151
 <212> DNA
 <213> Homo sapien

<400> 316
 agactgggca agactcttac gcccacact gcaatttggt cttgttgccg tatccattta 60
 tgtgggcctt tctcgagttt ctgattataa acaccactgg agcgatgtgt tgactggact 120
 cattcaggga gctctggttg caatattagt t 151

<210> 317
 <211> 151
 <212> DNA
 <213> Homo sapien

<400> 317
 agaactagtg gatcctaata aaatacctga aacatatatt ggcatttatc aatggctcaa 60
 atcttcattt atctctggcc ttaacctggg ctctgagggc tgcggccagc agatcccagg 120
 ccagggctct gttcttgcca cacctgcttg a 151

<210> 318
 <211> 151
 <212> DNA
 <213> Homo sapien

<400> 318
 actggtggga ggcgctgttt agttggctgt ttccagaggg gtctttcgga gggacctcct 60
 gctgcaggct ggagtgtctt tattcctggc gggagaccgc acattccact gctgaggctg 120
 tgggggcggg ttatcaggca gtgataaaca t 151

<210> 319

<211> 151
 <212> DNA
 <213> Homo sapien

<400> 319
 aactagtggg tccagagcta taggtacagt gtgatctcag ctttgcaaac acattttcta 60
 catagatagt actaggtatt aatagatatg taaagaaaga aatcacacca ttaataatgg 120
 taagattggg tttatgtgat tttagtgggt a 151

<210> 320
 <211> 150
 <212> DNA
 <213> Homo sapien

<400> 320
 aactagtggg tccactagtc cagtgtgggt gaattccatt gtgttggggt tctagatcgc 60
 gagcggctgc cttttttttt tttttttttg ggggggaatt tttttttttt aatagttatt 120
 gagtgttcta cagcttacag taaataccat 150

<210> 321
 <211> 151
 <212> DNA
 <213> Homo sapien

<400> 321
 agcaactttg tttttcatcc aggttatattt aggccttagga tttcctctca cactgcagtt 60
 taggggtggc ttgtaaccag ctatggcata ggtgttaacc aaaggctgag taaacatggg 120
 tgccctctgag aaatcaaagt cttcatacac t 151

<210> 322
 <211> 151
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(151)
 <223> n = A,T,C or G

<400> 322
 atccagcadc ttctcctggt tcttgccctc ctttttcttc ttcttasatt ctgcttgagg 60
 tttgggcttg gtcagtttgc cacagggtt ggagatggtg acagtcttct ggcattcggc 120
 attgtgcagg gctcgttca nacttcagtt 151

<210> 323
 <211> 151
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(151)
 <223> n = A,T,C or G

<400> 323
 tgaggacttg tktttttttt ctttatattt aatcctctta ckttgtaaatt atattgccta 60
 nagactcant tactacccag tttgtggtt twtgggagaa atgtaactgg acagtttagct 120
 gttcaatyaa aaagacactt ancccatgtg g 151

<210> 324
<211> 461
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(461)
<223> n = A,T,C or G

<400> 324
acctgtgttg aatttcagct ttctcatgc aaaaggattt tgtatccccg gcctacttga 60
agaagtgggc agctaaagga atccagggtg ttgggtggac tgtaataacc tttgatgaaa 120
agagttacta cgaatcccat cttggttcca gctatatcac tgacagcatg gtagaagact 180
gcgaacctca cttctagact ttcacgggtg gacgaaacgg gttcagaaac tgccaggggc 240
ctcatacagg gatatacaaaa taccctttgt gctaccagg ccctggggaa tcagggtgact 300
cacacaaatg caatagttgg tctactgcatt ttacctgaa ccaaagctaa acccggtgtt 360
gccaccatgc accatggcat gccagagttc aacactgttg ctcttgaaaa ttgggtctga 420
aaaaacgcac aagagccccct gccctgccct agctgangca c 461

<210> 325
<211> 400
<212> DNA
<213> Homo sapien

<400> 325
acactgtttc catgttatgt ttctacacat tgctacctca gtgctcctgg aaacttagct 60
tttgatgtct ccaagtagtc caccttcatt taactctttg aaactgtatc atctttgcca 120
agtaagatg gtggcctatt tcagctgctt tgacaaaatg actggctcct gacttaacgt 180
tctataaatg aatgtgctga agcaaagtgc ccatgggtggc ggcgaagaag agaaagatgt 240
gttttgtttt ggactctctg tggctccctc caatgctgtg gggtttccaac caggggaagg 300
gtcccttttg cattgccaag tgccataacc atgagcacta cgctaccatg gttctgcctc 360
ctggccaagc aggtctggtt gcaagaatga aatgaatgat 400

<210> 326
<211> 1215
<212> DNA
<213> Homo sapien

<400> 326
ggaggactgc agcccgcact cgcagccctg gcaggcggca ctggtcatgg aaaacgaatt 60
gttctgctcg ggcgtcctgg tgcacccgca gtgggtgctg tcagccgcac actgtttcca 120
gaactcctac accatcgggc tgggcctgca cagtcttgag gccgaccaag agccagggag 180
ccagatgggtg gaggccagcc tctccgtacg gcccccagag tacaacagac ccttgctcgc 240
taacgacctc atgctcatca agttggacga atccgtgtcc gactctgaca ccatccggag 300
catcagcatt gcttcgcagt gccctaccgc ggggaactct tgctcgttt ctggctgggg 360
tctgctggcg aacggcagaa tgcctaccgt gctgcagtgc gtgaacgtgt cgggtggtgc 420
tgaggaggtc tgcagtaagc tctatgacct gctgtaccac cccagcatgt tctgcgccgg 480
cggagggcaa gaccagaagg actcctgcaa cgggtgactct ggggggcccc tgatctgcaa 540
cgggtacttc cagggccttg tgtctttcgg aaaagccccg tgtggccaag ttggcgtgcc 600
agggtgtctac accaactct gcaaatccac tgagtggata gagaaaaccg tccaggccag 660
ttaactctgg ggactgggaa cccatgaaat tgacccccaa atacatcctg cggaagggaat 720
tcaggaatat ctgttcccag cccctcctcc ctcaggccca ggagtccagg cccccagccc 780
ctcctccctc aaaccaaggg tacagatccc cagccctcc tccctcagac ccaggagtcc 840
agacccccca gccctcctc cctcagacct aggagtccag cccctcctcc ctcagaccca 900
ggagtccaga cccccagcc cctcctccct cagacccagg ggtccaggcc cccaaccct 960
ctcctccctc actcagaggt ccaagcccc aaccctcct tccccagacc cagaggtcca 1020

```

gggtccagcc cctcctccct cagaccagc ggtccaatgc cacctagact ctccctgtac 1080
acagtgcgcc cttgtggcac gttgacccaa ccttaccagt tggtttttca ttttttgtcc 1140
ctttcccta gatccagaaa taaagtctaa gagaagcgca aaaaaaaaaa aaaaaaaaaa 1200
aaaaaaaaaa aaaaaa 1215

```

<210> 327
 <211> 220
 <212> PRT
 <213> Homo sapien

<400> 327

```

Glu Asp Cys Ser Pro His Ser Gln Pro Trp Gln Ala Ala Leu Val Met
 1          5          10          15
Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp Val
          20          25          30
Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu Gly
          35          40          45
Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val Glu
          50          55          60
Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu Leu Ala
          65          70          75          80
Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser Asp
          85          90          95
Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly Asn
          100          105          110
Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg Met Pro
          115          120          125
Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu Glu Val Cys
          130          135          140
Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys Ala Gly
          145          150          155          160
Gly Gly Gln Asp Gln Lys Asp Ser Cys Asn Gly Asp Ser Gly Gly Pro
          165          170          175
Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly Lys Ala
          180          185          190
Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn Leu Cys Lys
          195          200          205
Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser
          210          215          220

```

<210> 328
 <211> 234
 <212> DNA
 <213> Homo sapien

<400> 328

```

cgctcgtctc tggtagctgc agccaatca taaacggcga ggactgcagc ccgcactcgc 60
agccctggca ggcggcactg gtcattgaaa acgaattgtt ctgctcgggc gtcctgggtgc 120
atccgcagtg ggtgctgtca gccacacact gttccagaa ctctacacc atcgggctgg 180
gctgcacag tcttgaggcc gaccaagagc cagggagcca gatggtggag gcca 234

```

<210> 329
 <211> 77
 <212> PRT
 <213> Homo sapien

<400> 329

```

Leu Val Ser Gly Ser Cys Ser Gln Ile Ile Asn Gly Glu Asp Cys Ser

```

105

1	5	10	15
Pro His Ser Gln Pro Trp Gln Ala Ala Leu Val Met Glu Asn Glu Leu			
	20	25	30
Phe Cys Ser Gly Val Leu Val His Pro Gln Trp Val Leu Ser Ala Thr			
	35	40	45
His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu Gly Leu His Ser Leu			
	50	55	60
Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val Glu Ala			
65	70	75	

<210> 330
 <211> 70
 <212> DNA
 <213> Homo sapien

<400> 330
 cccaacacaa tggcccgatc ccatccctga ctccgccctc aggatcgctc gtctctggta 60
 gctgcagcca 70

<210> 331
 <211> 22
 <212> PRT
 <213> Homo sapien

<400> 331
 Gln His Asn Gly Pro Ile Pro Ser Leu Thr Pro Pro Ser Gly Ser Leu
 1 5 10 15
 Val Ser Gly Ser Cys Ser
 20

<210> 332
 <211> 2507
 <212> DNA
 <213> Homo sapien

<400> 332
 tgggtgcgct gcagccggca gagatgggtg agctcatgtt cccgctgttg ctccctcttc 60
 tgcccttcct tctgtatatg gctgcgcccc aaatcaggaa aatgctgtcc agtgggggtg 120
 gtacatcaac tgttcagctt cctgggaaag tagttgtggt cacaggagct aatacaggta 180
 tcgggaagga gacagccaaa gagctggctc agagaggagc tcgagtatat ttagcttgcc 240
 gggatgtgga aaagggggaa ttggtggcca aagagatcca gaccacgaca gggaaccagc 300
 aggtgttggg gcggaaaactg gacctgtctg atactaagtc tattcgagct tttgctaagg 360
 gcttcttagc tgaggaaaag cacctccacg ttttgatcaa caatgcagga gtgatgatgt 420
 gtccgtactc gaagacagca gatggctttg agatgcacat aggagtcaac cacttgggtc 480
 acttccctct aaccatctg ctgctagaga aactaaagga atcagcccca tcaaggatag 540
 taaatgtgtc ttccctcgca catcacctgg gaaggatcca ctccataac ctgcaggggc 600
 agaaattcta caatgcaggc ctggcctact gtcacagcaa gctagccaac atcctcttca 660
 cccaggaact ggcccgagga ctaaaaggct ctggcggttac gacgtattct gtacaccctg 720
 gcacagtcca atctgaactg gttcggcact catctttcat gagatggatg tgggtggcttt 780
 tctccttttt catcaagact cctcagcagg gagcccagac cagcctgcac tgtgccttaa 840
 cagaaggtct tgagattcta agtgggaatc atttcagtga ctgtcatgtg gcatgggtct 900
 ctgcccgaagc tcgtaattgag actatagcaa ggccgctgtg ggacgtcagt tgtgacctgc 960
 tgggcctccc aatagactaa caggcagtgc cagttggacc caagagaaga ctgcagcaga 1020
 ctacacagta cttcttgtca aaatgattct ccttcaaggt tttcaaaacc tttagcacia 1080
 agagagcaaa accttccagc cttgcctgct tgggtgtccag ttaaaactca gtgtactgcc 1140
 agattcgtct aaatgtctgt catgtccaga tttactttgc ttctgttact gccagagtta 1200
 ctagagatat cataatagga taagaagacc ctcatatgac ctgcacagct cattttcctt 1260
 ctgaaagaaa ctactaccta ggagaatcta agctatagca gggatgattt atgcaaat 1320

gaactagctt	ctttgttcac	aattcagttc	ctcccaacca	accagtcttc	acttcaagag	1380
ggccacactg	caacctcagc	ttaacatgaa	taacaaagac	tggtcagga	gcagggcttg	1440
cccaggcatg	gtggatcacc	ggaggtcagt	agttcaagac	cagcctggcc	aacatgggtga	1500
aacccccact	ctactaaaaa	tttgttatat	ctttgtgtgt	cttcctgttt	atgtgtgccca	1560
agggagtatt	ttcacaagt	tcaaaacagc	cacaataatc	agagatggag	caaaccagt	1620
ccatccagtc	tttatgcaaa	tgaatgctg	caaagggag	cagattctgt	atatgttggt	1680
aactaccac	caagagcaca	tggtagcag	ggaagaagta	aaaaaagaga	aggagaatac	1740
tggaagataa	tgcacaaaat	gaagggacta	gttaaggatt	aactagccct	ttaaggatta	1800
actagttaag	gattaatagc	aaaagayatt	aaatatgcta	acatagctat	ggaggaattg	1860
agggcaagca	cccaggactg	atgaggtctt	aacaaaaacc	agtgtggcaa	aaaaaaaaaa	1920
aaaaaaaaaa	aaaaatccta	aaaacaaaca	aacaaaaaaa	acaattcttc	attcagaaaa	1980
attatcttag	ggactgatat	tggttaattat	ggtcaattta	ataatatttt	ggggcatttc	2040
cttacattgt	cttgacaaga	ttaaaatgtc	tgtgccaaaa	ttttgtattt	tatttgagga	2100
cttcttatca	aaagtaatgc	tgccaaagga	agtctaagga	attagtagtg	ttcccatcac	2160
ttgtttggag	tgtgctattc	taaaagattt	tgatttcttg	gaatgacaat	tatatattta	2220
ctttgtgtgg	ggaaagagtt	ataggaccac	agtcttcact	tctgatactt	gtaaattaat	2280
cttttattgc	acttgttttg	accattaagc	tatatgttta	gaaatggtca	ttttacggaa	2340
aaattagaaa	aattctgata	atagtgcaga	ataaatgaat	taatgtttta	cttaatttat	2400
attgaactgt	caatgacaaa	taaaattctt	ttttgattat	ttttgttttt	catttaccag	2460
aataaaaacg	taagaattaa	aagtttgatt	acaaaaaaa	aaaaaaa		2507

<210> 333

<211> 3030

<212> DNA

<213> Homo sapien

<400> 333

gcaggcgact	tgcgagctgg	gagcgattta	aaacgctttg	gattcccccg	gcctgggtgg	60
ggagagcgag	ctgggtgccc	cctagattcc	ccgccccgc	acctcatgag	ccgacctcg	120
gctccatgga	gcccggaat	tatgccacct	tgtagggagc	caaggatata	gaaggcttgc	180
tgggagcggg	agggggcg	aatctggctg	ccactcccc	tctgaccagc	cacccagcgg	240
cgctacgct	gatgctgct	gtcaactatg	cccccttga	tctgccaggc	tcggcggagc	300
cgccaaagca	atgccacca	tgccctggg	tgccccagg	gacgtcccca	gctcccgctc	360
cttatggtta	ctttggaggc	gggtactact	cctgccgagt	gtcccgagc	tcgctgaaac	420
cctgtgccc	ggcagccacc	ctggccgct	accocgagg	gactccacg	gccggggag	480
agtaccccag	ycgccccact	gagtttgct	tctatccgg	atatccggga	acctaccagc	540
ctatggcag	ttacctggac	gtgtctgtg	tcgagactct	gggtgtcct	ggagaaccgc	600
gacatgactc	ctctgtgct	gtggacagtt	accagctttg	ggctctcgct	ggtggctgga	660
acagccagat	gtgttgccag	ggagaacaga	accaccagg	tcccttttgg	aaggcagcat	720
ttgcagactc	cagcgggcag	caccctcctg	acgcctgcgc	ctttcgtcgc	ggccgcaaga	780
aacgcattcc	gtacagcaag	gggcagttgc	gggagctgga	gcgggagtat	gcggctaaca	840
agttcatcac	caaggacaag	aggcgaaga	tctcggcagc	caccagcctc	tcggagcgcc	900
agattaccat	ctggtttcag	aaccgccggg	tcaaagagaa	gaaggttctc	gccaagggtga	960
agaacagcgc	tacccttaa	gagatctct	tgctgggtg	ggaggagcga	aagtgggggt	1020
gtcctgggga	gaccaggaac	ctgccaaagc	caggctgggg	ccaaggactc	tgctgagagg	1080
cccctagaga	caacacctt	cccaggccac	tggctgctgg	actgttcctc	aggagcggcc	1140
tgggtaccca	gtatgtgcag	ggagacggaa	ccccatgtga	cagccactc	caccagggtt	1200
cccaaagaac	ctggcccagt	cataatcatt	catcctgaca	gtggcaataa	tcacgataac	1260
cagtactagc	tgccatgatc	gttagcctca	tattttctat	ctagagctct	gtagagcact	1320
ttagaaaccg	ctttcatgaa	ttgagctaat	tatgaataaa	tttggagggc	gatccctttg	1380
caggggaagct	ttctctcaga	cccccttcca	ttacacctct	caccctggta	acagcaggaa	1440
gactgaggag	aggggaacgg	gcagattcgt	ttgtggctg	tgatgtccgt	ttagcatttt	1500
tctcagctga	cagctgggta	ggtggacaat	tgtagaggct	gtctcttctc	ccctccttgt	1560
ccaccccata	gggtgtaccc	actggctctg	gaagcaccca	tccttaatac	gatgattttt	1620
ctgtcgtgtg	aaaatgaagc	cagcaggctg	cccctagtca	gtccttctct	ccagagaaaa	1680
agagatttga	gaaagtgcct	gggtaattca	ccattaattt	cctcccccaa	actctctgag	1740
tcttccctta	atattttctg	tggttctgac	caaagcaggt	catgggttgt	tgagcatttg	1800
ggatcccagt	gaagtagatg	ttgttagcct	tgcatactta	gcccttccca	ggcacaacg	1860

gagtggcaga	gtggtgccaa	ccctgttttc	ccagtccacg	tagacagatt	cacagtgcgg	1920
aattctggaa	gctggagaca	gacgggctct	ttgcagagcc	gggactctga	gagggacatg	1980
agggcctctg	cctctgtgtt	cattctctga	tgtcctgtac	ctgggctcag	tgcccgggtg	2040
gactcatctc	ctggccgcgc	agcaaagcca	gcgggttcgt	gctggtcctt	cctgcacctt	2100
aggtctgggg	tggtgggctt	gccggcgcat	tctccacgat	tgagcgca	ggcctgaagt	2160
ctggacaacc	cgagaaaccg	aagctccgag	cagcgggtcg	gtggcgagta	gtggggtcgg	2220
tggcgagcag	ttggtgtgtg	gccgcggccg	ccactacctc	gaggacattt	ccctcccggg	2280
gccagctctc	ctagaaaccc	cgcgcgccgc	gccgcagcca	agtgtttatg	gcccgcggtc	2340
gggtggggtc	ctagccctgt	ctcctctcct	gggaaggagt	gaggggtgga	cgtgacttag	2400
acacctacaa	atctatttac	caaagaggag	cccgggactg	agggaaaagg	ccaaagagtg	2460
tgagtgcagt	cgactggggg	gttcaggagg	agaggacgag	gaggaggaag	atgaggtcga	2520
tttcctgatt	taaaaaatcg	tccaagcccc	gtggtccagc	ttaaggtcct	cggttacatg	2580
cgccgctcag	agcaggtcac	tttctgcctt	ccacgtcctc	cttcaaggaa	gccccatgtg	2640
ggtagctttc	aatatcgag	gttcttactc	ctctgcctct	ataagctcaa	accaccaaac	2700
gatcgggcaa	gtaaaccccc	tccctcgccg	acttcggaac	tggcgagagt	tcagcgagga	2760
tggtgctgtg	gggagggggc	aagatagatg	agggggagcg	gcatggtgcg	gggtgacccc	2820
ttggagagag	gaaaaaggcc	acaagagggg	ctgccaccgc	cactaacgga	gatggccctg	2880
gtagagacct	ttgggggtct	ggaacctctg	gactcccat	gctctaactc	ccacactctg	2940
ctatcagaaa	cttaaaactg	aggattttct	ctgtttttca	ctcgcaataa	aytcagagca	3000
aacaaaaaaa	aaaaaaaaaa	aaaactcgag				3030

<210> 334

<211> 2417

<212> DNA

<213> Homo sapien

<400> 334

ggcgccgct	ctagagctag	tggtatcccc	cgggctgcac	gaattcggca	cgagtgagtt	60
ggagttttac	ctgtattgtt	ttaattttcaa	caagcctgag	gactagccac	aaatgtaccc	120
agttttacaa	tgaggaaaca	ggtgcaaaaa	ggttgttacc	tgtcaaaagt	cgtatgtggc	180
agagccaaga	tttgagccca	gttatgtctg	atgaacttag	cctatgctct	ttaaacttct	240
gaatgctgac	cattgaggat	atctaaactt	agatcaattg	cattttccct	ccaagactat	300
ttacttatca	atacaataat	accaccttta	ccaatctatt	gttttgatac	gagactcaa	360
tatgccagat	atatgtaaaa	gcaacctaca	agctctctaa	tcatgctcac	ctaaaagatt	420
cccgggatct	aataggctca	aagaaaactt	ttctagaaat	ataaaaagaga	aaattggatt	480
atgcaaaaat	tcattattaa	tttttttcat	ccatccttta	attcagcaaa	catttatctg	540
ttgttgactt	tctcagtat	ggccttttaa	ggattggggg	acagggtgaag	aacgggggtgc	600
cagaatgcatt	cctcctacta	atgaggtcag	tacacatttg	catttttaaaa	tgccctgtcc	660
agctgggcat	ggtggatcat	gcctgtaatc	tcaacattgg	aaggccaagg	caggaggatt	720
gcttcagccc	aggagttcaa	gaccagcctg	ggcaacatag	aaagacccca	tctctcaatc	780
aatcaatcaa	tgccctgtct	ttgaaaaata	aactctttaa	gaaagggtta	atgggcaggg	840
tgtggtagct	catgcctata	atacagcaat	ttgggaggct	gaggcaggag	gatcacttta	900
gccagaagt	tcaagaccag	cctgggcaac	aagtgcaccc	tcatctcaat	tttttaataa	960
aatgaatata	tacataagga	aagataaaaa	gaaaagttaa	atgaaagaat	acagtataaa	1020
acaaatctct	tggacctaaa	agtatttttg	ttcaagccaa	atattgtgaa	tcacctctct	1080
gtgttgagga	tacagaatat	ctaagcccag	gaaactgagc	agaaagttca	tgtactaact	1140
aatcaaccgg	aggcaaggca	aaaatgagac	taactaatca	atccgaggca	aggggcaaat	1200
tagacggaac	ctgactctgg	tctattaagc	gacaactttc	cctctgttgt	atttttcttt	1260
tattcaatgt	aaaaggataa	aaactctcta	aaactaaaaa	caatgtttgt	caggagttac	1320
aaacctgac	caactaatta	tggtgaatca	taaaatatga	ctgtatgaga	tcttgatggt	1380
ttacaaagt	taccactgt	taactacttt	aaacttaaat	gaacttaaaa	atgaatttac	1440
ggagattgga	atgtttcttt	cctgttgtat	tagttggctc	aggctgccat	aacaaaatac	1500
cacagactgg	gaggcttaag	taacagaaat	tcatttctca	cagttctggg	ggctggaagt	1560
ccacgatcaa	ggtgcaggaa	aggcaggctt	cattctgagg	cccctctctt	ggctcacatg	1620
tggtccacct	cccactgcgt	gctcacatga	cctctttgtg	ctcctggaaa	gaggggtgtg	1680
gggacagagg	gaaagagaa	gagagggaac	tctctgttgt	ctcgtcttct	aaggacccta	1740
acctgggcca	ctttggccca	ggcactgtgg	ggtggggggt	tgtggctgct	ctgctctgag	1800
tggtcaagat	aaagcaacag	aaaaatgtcc	aaagctgtgc	agcaaaagaca	agccaccgaa	1860

cagggatctg	ctcatcagtg	tggggacctc	caagtcggcc	accctggagg	caagccccc	1920
cagagcccat	gcaaggtggc	agcagcagaa	gaagggatt	gtccctgtcc	ttggcacatt	1980
cctcaccgac	ctggtgatgc	tggacactgc	gatgaatgg	aatgtggatg	agaatatgat	2040
ggactcccag	aaaaggagac	ccagctgctc	aggtggctgc	aatcattac	agccttcac	2100
ctggggagga	actggggggc	tggttctggg	tcagagagca	gccagtgag	ggtgagagct	2160
acagcctgtc	ctgccagctg	gatccccagt	cccggtcaac	cagtaataca	ggctgagcag	2220
atcaggcttc	ccggagctgg	tcttgggaag	ccagccctgg	ggtgagttgg	ctcctgctgt	2280
ggtactgaga	caatatgtgc	ataaattcaa	tgcgcccctg	tatccctttt	tcttttttat	2340
ctgtctacat	ctataatcac	tatgcatact	agtctttgtt	agtgtttcta	ttcmacttaa	2400
tagagatatg	ttatact					2417

<210> 335

<211> 2984

<212> DNA

<213> Homo sapien

<400> 335

atccctcctt	ccccactctc	ctttccagaa	ggcacttggg	gtcttatctg	ttggactctg	60
aaaacacttc	agggcgccct	ccaaggcttc	cccaaacc	taagcagccg	cagaagcgct	120
cccagctgc	cttctccac	actcaggtga	tcgagttgga	gaggaagttc	agccatcaga	180
agtacctgtc	ggccccetgaa	cgggcccacc	tggccaagaa	cctcaagctc	acggagaccc	240
aagtgaagat	atggttccag	aacagacgct	ataagactaa	gcgaaagcag	ctctcctcgg	300
agctgggaga	cttggaag	cactcctctt	tgcggccct	gaaagaggag	gccttctccc	360
gggcctccct	ggtctccgtg	tataacagct	atccttacta	ccataacctg	tactgcgtgg	420
gcagctggag	cccagctttt	tggtaatgcc	agctcaggtg	acaaccatta	tgatcaaaaa	480
ctgccttccc	caggtgtct	ctatgaaaag	cacaaggggc	caaggtcagg	gagcaagagg	540
tgtgcacacc	aaagctattg	gagatttgcg	tggaaatctc	asattcttca	ctggtgagac	600
aatgaaacaa	cagagacagt	gaaagtttta	atacctaagt	cattccccca	gtgcatactg	660
taggtcattt	tttttgcttc	tggctacctg	tttgaagggg	agagagggaa	aatcaagttg	720
tatttccag	ccttctgtat	gattttggat	gagctgtaca	cccaaggatt	ctgttctgca	780
actccatcct	cctgtgtcac	tgaatatcaa	ctctgaaaga	gcaaaccctaa	caggagaaag	840
gacaaccagg	atgaggatgt	caccaactga	attaaactta	agtccagaag	cctcctgttg	900
gccttggaa	atggccaagg	ctctctctgt	ccctgtaaaa	gagaggggca	aatagagagt	960
ctccaagaga	acgccctcat	gctcagcaca	tatttgcattg	ggagggggag	atgggtggga	1020
ggagatgaaa	atatcagctt	ttcttattcc	tttttattcc	ttttaaatag	gtatgccaac	1080
ttaagtattt	acaggtggc	ccaaatagaa	caagatgcac	tcgctgtgat	tttaagacaa	1140
gctgtataaa	cagaactcca	ctgcaagagg	ggggccggg	ccaggagaat	ctcgcgttgt	1200
ccaagacagg	ggcctaagga	gggtctccac	actgtgcta	ggggctgttg	cattttttta	1260
ttagtagaaa	gtggaaaggc	ctcttctcaa	cttttttccc	ttgggctgga	gaatttagaa	1320
tcagaagttt	cctggagttt	tcaggctatc	atatatactg	tatcctgaaa	ggcaacataa	1380
ttcttccttc	cctcctttta	aaattttgtg	ttcctttttg	cagcaattac	tcactaaagg	1440
gcttcatttt	agtccagatt	tttagtctgg	ctgcacctaa	cttatgcctc	gcttatttag	1500
cccagatct	ggtctttttt	ttttttttt	ttttccgtc	tcccaaagc	tttatctgtc	1560
ttgacttttt	aaaaaagttt	gggggcagat	tctgaattgg	ctaaaagaca	tgcattttta	1620
aaactagcaa	ctcttatttc	tttcctttaa	aaatacatag	cattaaatcc	caaactctat	1680
ttaaagacct	gacagcttga	gaaggtcact	actgcattta	taggaccttc	tgggtggttct	1740
gctgttacgt	ttgaagtctg	acaatccttg	agaatctttg	catgcagagg	aggtaagagg	1800
tattggattt	tcacagagga	agaacacagc	gcagaatgaa	gggccaggct	tactgagctg	1860
tccagtggag	ggctcatggg	tgggacatgg	aaaagaaggc	agcctaggcc	ctggggagcc	1920
cagtccactg	agcaagcaag	ggactgagtg	agccttttgc	aggaaaaggc	taagaaaaag	1980
gaaaaccatt	ctaaaacaca	acaagaaact	gtccaaatgc	tttgggaact	gtgtttattg	2040
cctataatgg	gtccccaaaa	tggtaacct	agacttcaga	gagaatgagc	agagagcaaa	2100
ggagaaatct	ggctgtcctt	ccattttcat	tctgttatct	caggtgagct	ggtagagggg	2160
agacattaga	aaaaaatgaa	acaacaaaac	aattactaat	gaggtagcgt	gaggcctggg	2220
agtctcttga	ctccactact	taattccgtt	tagtgagaaa	cctttcaatt	ttcttttatt	2280
agaagggcca	gcttactgtt	ggtggcaaaa	ttgccaacat	aagttaatag	aaagtgggcc	2340
aatttcaccc	cattttctgt	ggtttgggct	ccacattgca	atgttcaatg	ccacgtgctg	2400
ctgacaccga	ccggagtact	agccagcaca	aaaggcaggg	tagcctgaat	tgctttctgc	2460

```

tctttacatt tcttttaaaa taagcattta gtgctcagtc cctactgagt actctttctc 2520
tcccctcctc tgaatttaat tctttcaact tgcaatttgc aaggattaca catttcactg 2580
tgatgtatat tgtgttgcaa aaaaaaaaaa aagtgtcttt gtttaaaatt acttggtttg 2640
tgaatccatc ttgctttttc cccattggaa ctatgcatta acccatctct gaactggtag 2700
aaaaacatct gaagagctag tctatcagca tctgacaggt gaattggatg gttctcagaa 2760
ccatttcacc cagacagcct gtttctatcc tgtttaataa attagtttgg gttctctaca 2820
tgcataacaa accctgctcc aatctgtcac ataaaagtct gtgacttgaa gtttagtcag 2880
caccgccacc aaactttatt tttctatgtg ttttttgcaa catatgagtg ttttgaaaat 2940
aaagtaccca tgtctttatt agaaaaaaaa aaaaaaaaaa aaaa 2984

```

<210> 336
 <211> 147
 <212> PRT
 <213> Homo sapien

```

<400> 336
Pro Ser Phe Pro Thr Leu Leu Ser Arg Arg His Leu Gly Ser Tyr Leu
1          5          10          15
Leu Asp Ser Glu Asn Thr Ser Gly Ala Leu Pro Arg Leu Pro Gln Thr
20          25          30
Pro Lys Gln Pro Gln Lys Arg Ser Arg Ala Ala Phe Ser His Thr Gln
35          40          45
Val Ile Glu Leu Glu Arg Lys Phe Ser His Gln Lys Tyr Leu Ser Ala
50          55          60
Pro Glu Arg Ala His Leu Ala Lys Asn Leu Lys Leu Thr Glu Thr Gln
65          70          75          80
Val Lys Ile Trp Phe Gln Asn Arg Arg Tyr Lys Thr Lys Arg Lys Gln
85          90          95
Leu Ser Ser Glu Leu Gly Asp Leu Glu Lys His Ser Ser Leu Pro Ala
100         105         110
Leu Lys Glu Glu Ala Phe Ser Arg Ala Ser Leu Val Ser Val Tyr Asn
115         120         125
Ser Tyr Pro Tyr Tyr Pro Tyr Leu Tyr Cys Val Gly Ser Trp Ser Pro
130         135         140
Ala Phe Trp
145

```

<210> 337
 <211> 9
 <212> PRT
 <213> Homo sapien

```

<400> 337
Ala Leu Thr Gly Phe Thr Phe Ser Ala
1          5

```

<210> 338
 <211> 9
 <212> PRT
 <213> Homo sapien

```

<400> 338
Leu Leu Ala Asn Asp Leu Met Leu Ile
1          5

```

<210> 339
 <211> 318

<212> PRT

<213> Homo sapien

<400> 339

```

Met Val Glu Leu Met Phe Pro Leu Leu Leu Leu Leu Leu Pro Phe Leu
 1          5          10          15
Leu Tyr Met Ala Ala Pro Gln Ile Arg Lys Met Leu Ser Ser Gly Val
          20          25          30
Cys Thr Ser Thr Val Gln Leu Pro Gly Lys Val Val Val Val Thr Gly
          35          40          45
Ala Asn Thr Gly Ile Gly Lys Glu Thr Ala Lys Glu Leu Ala Gln Arg
          50          55          60
Gly Ala Arg Val Tyr Leu Ala Cys Arg Asp Val Glu Lys Gly Glu Leu
65          70          75          80
Val Ala Lys Glu Ile Gln Thr Thr Thr Gly Asn Gln Gln Val Leu Val
          85          90          95
Arg Lys Leu Asp Leu Ser Asp Thr Lys Ser Ile Arg Ala Phe Ala Lys
          100          105          110
Gly Phe Leu Ala Glu Glu Lys His Leu His Val Leu Ile Asn Asn Ala
          115          120          125
Gly Val Met Met Cys Pro Tyr Ser Lys Thr Ala Asp Gly Phe Glu Met
130          135          140
His Ile Gly Val Asn His Leu Gly His Phe Leu Leu Thr His Leu Leu
145          150          155          160
Leu Glu Lys Leu Lys Glu Ser Ala Pro Ser Arg Ile Val Asn Val Ser
          165          170          175
Ser Leu Ala His His Leu Gly Arg Ile His Phe His Asn Leu Gln Gly
          180          185          190
Glu Lys Phe Tyr Asn Ala Gly Leu Ala Tyr Cys His Ser Lys Leu Ala
          195          200          205
Asn Ile Leu Phe Thr Gln Glu Leu Ala Arg Arg Leu Lys Gly Ser Gly
210          215          220
Val Thr Thr Tyr Ser Val His Pro Gly Thr Val Gln Ser Glu Leu Val
225          230          235          240
Arg His Ser Ser Phe Met Arg Trp Met Trp Trp Leu Phe Ser Phe Phe
          245          250          255
Ile Lys Thr Pro Gln Gln Gly Ala Gln Thr Ser Leu His Cys Ala Leu
          260          265          270
Thr Glu Gly Leu Glu Ile Leu Ser Gly Asn His Phe Ser Asp Cys His
          275          280          285
Val Ala Trp Val Ser Ala Gln Ala Arg Asn Glu Thr Ile Ala Arg Arg
290          295          300
Leu Trp Asp Val Ser Cys Asp Leu Leu Gly Leu Pro Ile Asp
305          310          315

```

<210> 340

<211> 483

<212> DNA

<213> Homo sapien

<400> 340

```

gccgagggtct gccttcacac ggaggacacg agactgcttc ctcaagggct cctgcctgcc      60
tggaactgg tgggagcgcg tgttagttg gctgttttca gaggggtctt tcggagggac      120
ctctgctgc aggtggagt gtctttatc ctggcgggag accgcacatt ccactgctga      180
ggttggtggg gcggtttatc aggcagtgat aaacataaga tgtcatttcc ttgactccgg      240
ccttcaattt tctctttggc tgacgacgga gtccgtggtg tcccgatgta actgaccct      300
gctccaaacg tgacatcact gatgctcttc tcgggggtgc tgatggcccg cttggtcacg      360
tgctcaatct cgccattcga ctcttgctcc aaactgtatg aagacacctg actgcacgtt      420

```

ttttctgggc ttccagaatt taaagtgaag ggcagcactc ctaagctccg actccgatgc 480
ctg 483

<210> 341
<211> 344
<212> DNA
<213> Homo sapien

<400> 341
ctgctgctga gtcacagatt tcattataaa tagcctccct aaggaaaata cactgaatgc 60
tatttttact aaccattcta tttttataga aatagctgag agtttctaaa ccaactctct 120
gctgccttac aagtattaaa tattttactt ctttccataa agagtagctc aaaatatgca 180
attaatttaa taattttctga tgatgggttt atctgcagta atatgtatat catctattag 240
aatttactta atgaaaaact gaagagaaca aaatttgtaa ccactagcac ttaagtactc 300
ctgattctta acattgtctt taatgaccac aagacaacca acag 344

<210> 342
<211> 592
<212> DNA
<213> Homo sapien

<400> 342
acagcaaaaa agaaactgag aagcccaaty tgctttcttg ttaacatcca cttatccaac 60
caatgtggaa acttcttata cttggttcca ttatgaagtt ggacaattgc tgctatcaca 120
cctggcaggt aaaccaatgc caagagagtg atggaaacca ttggcaagac tttgttgatg 180
accaggattg gaattttata aaaatattgt tgatgggaag ttgctaaagg gtgaattact 240
tccctcagaa gagtgtaaag aaaagtcaga gatgctataa tagcagctat ttttaattggc 300
aagtgccact gtggaaagag ttctgtgtg tgctgaagtt ctgaagggca gtcaaattca 360
tcagcatggg ctgtttgggtg caaatgcaaa agcacaggtc tttttagcat gctgggtctct 420
cccgtgtctt tatgcaaaata atcgtcttct tctaaatttc tcctaggctt cattttccaa 480
agttcttctt ggtttgtgat gtcttttctg ctttccatta attctataaa atagtatggc 540
ttcagccacc cactcttcgc cttagcttga ccgtgagctc cggtgccgc tg 592

<210> 343
<211> 382
<212> DNA
<213> Homo sapien

<400> 343
ttcttgacct cctcctcctt caagctcaaa caccacctcc cttattcagg accggcactt 60
cttaatgttt gtggctttct ctccagcctc tcttaggagg ggtaatggtg gaggttggcat 120
cttgaactc tctttctcc tttctctgcc cgcctttccc atcctgctgt 180
agacttcttg attgtcagtc tgtgtcacat ccagtgattg ttttggtttc tgttcccttt 240
ctgactgccc aaggggctca gaacccagc aatcccttcc tttcactacc ttcttttttg 300
ggggtagttg gaagggactg aaattgtggg gggaaggtag gaggcacatc aataaagagg 360
aaaccaccaa gctgaaaaaa aa 382

<210> 344
<211> 536
<212> DNA
<213> Homo sapien

<400> 344
ctgggcctga agctgtaggg taaatcagag gcaggcttct gagtgatgag agtcctgaga 60
caataggcca cataaacttg gctggatgga acctcacaat aagggtggtca cctcttggtt 120
gtttaggggg atgccaagga taaggccagc tcagttatat gaagagaagc agaacaaaca 180
agtctttcag agaaatggat gcaatcagag tgggatcccg gtcacatcaa ggtcacactc 240
caccttcattg tgctgaatg gttgccagggt cagaaaaatc cacccttac gaggcggtct 300

tcgaccctat atccccgcc cgcgccctt tctccataaa attcttctta gtagctatta	360
ccttcttatt atttgatcta gaaattgccc tccttttacc cctaccatga gccctacaaa	420
caactaacct gccactaata gttatgtcat ccctcttatt aatcatcatc ctagccctaa	480
gtctggccta tgagtgacta caaaaaggat tagactgagc cgaataacaa aaaaaa	536

<210> 345
 <211> 251
 <212> DNA
 <213> Homo sapien

<400> 345	
accttttgag gtctctctca ccacctccac agccaccgtc accgtgggat gtgctggatg	60
tgaatgaagc ccccatcttt gtgcctcctg aaaagagagt ggaagtgtcc gaggacttg	120
gcgtgggcca ggaaatcaca tcctacactg cccaggagcc agacacattt atggaacaga	180
aaataacata tcggatttgg agagacactg ccaactggct ggagattaat ccggacactg	240
gtgccatttc c	251

<210> 346
 <211> 282
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(282)
 <223> n = A,T,C or G

<400> 346	
cgcgctctctg acactgtgat catgacaggg gttcaaacag aaagtgcctg ggccctcctt	60
ctaagtcttg ttaccaaaaa aaggaaaaag aaaagatctt ctcagttaca aattctggga	120
agggagacta tacctggctc ttgccctaag tgagaggtct tccctccgc accaaaaaat	180
agaaaggctt tctatttcac tggcccaggt agggggaagg agagtaactt tgagtctgtg	240
ggtctcattt cccaagggtgc cttcaatgct catnaaaacc aa	282

<210> 347
 <211> 201
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(201)
 <223> n = A,T,C or G

<400> 347	
acacacataa tattataaaa tgccatctaa ttggaaggag ctttctatca ttgcaagtca	60
taaatataac ttttaaaana ntactancag cttttaccta ngctcctaaa tgcttgtaaa	120
tctgagactg actggacca cccagacca gggcaaagat acatgttacc atatcatctt	180
tataaagaat tttttttgt c	201

<210> 348
 <211> 251
 <212> DNA
 <213> Homo sapien

<400> 348	
ctgttaatca caacatttgt gcatcacttg tgccaagtga gaaaatgttc taaaatcaca	60
agagagaaca gtgccagaat gaaactgacc ctaagtccca ggtgccctg ggcaggcaga	120

aggagacact	cccagcatgg	aggagggttt	atcttttcat	cctagggtcag	gtctacaatg	180
ggggaagggt	ttattataga	actccaaca	gccacctca	ctcctgccac	ccacccgatg	240
gccctgcctc	c					251

<210> 349

<211> 251

<212> DNA

<213> Homo sapien

<400> 349

taaaaatcaa	gccatttaat	tgtatctttg	aaggtaaaca	atatatggga	gctggatcac	60
aacccctgag	gatgccagag	ctatgggtcc	agaacatggg	gtggattat	caacagagtt	120
cagaagggtc	tgaactctac	gtgttaccag	agaacataat	gcaattcatg	cattccactt	180
agcaattttg	taaaatacca	gaaacagacc	ccaagagtct	ttcaagatga	ggaaaattca	240
actcctgggt	t					251

<210> 350

<211> 908

<212> DNA

<213> Homo sapien

<400> 350

ctggacactt	tgcgagggt	tttgcctgg	gctgctgctg	ccggtcatgc	tactcatcgt	60
agcccgcccg	gtgaagctcg	ctgctttccc	tacctcctta	agtgactgcc	aaacgcccac	120
cggctggaat	tgctctgggt	atgatgacag	agaaaatgat	ctcttcctct	gtgacaccaa	180
cacctgtaaa	tttgatgggg	aatgtttaag	aattggagac	actgtgactt	gcgtctgtca	240
gttcaagtgc	aacaatgact	atgtgcctgt	gtgtgggtcc	aatggggaga	gctaccagaa	300
tgagtgttac	ctgcgacagg	ctgcatgcaa	acagcagagt	gagatacttg	tggtgtcaga	360
aggatcatgt	gccacagtcc	atgaaggctc	tgagaaaact	agtcaaaagg	agacatccac	420
ctgtgatatt	tgccagtttg	gtgcagaatg	tgacgaagat	gccgaggatg	tctgggtgtg	480
gtgtaatat	gactgtttct	aaaccaactt	caatccccct	tgcgcttctg	atgggaaatc	540
ttatgataat	gcatgccaaa	tcaaagaagc	atcgtgtcag	aaacaggaga	aaattgaagt	600
catgtctttg	ggtcgatgtc	aagataaac	aactacaact	actaagtctg	aagatgggca	660
ttatgcaaga	acagattatg	cagagaatgc	taacaaatta	gaagaaagtg	ccagagaaca	720
ccacatacct	tgcccggaac	attacaatgg	cttctgcatg	catgggaagt	gtgagcattc	780
tatcaatatg	caggagccat	cttgagggtg	tgatgctggt	tatactggac	aacactgtga	840
aaaaaaggac	tacagtgttc	tatacgttgt	tcccgggtcc	gtacgatttc	agtatgtctt	900
aatgcgcag						908

<210> 351

<211> 472

<212> DNA

<213> Homo sapien

<400> 351

ccagttatgt	gcaagtggta	agagcctatt	taccataaat	aatactaaga	accaactcaa	60
gtcaaacctt	aatgccattg	ttattgtgaa	ttaggattaa	gtagtaattt	tcaaaattca	120
cattaacttg	attttaaaat	cagwtttgyg	agtcattttac	cacaagctaa	atgtgtacac	180
tatgataaaa	acaaccattg	tattcctggt	tttctaataa	gtcctaattt	ctaactgt	240
atatatcctt	cgacatcaat	gaactttggt	ttcttttact	ccagtaataa	agtaggcaca	300
gatctgtcca	caacaaactt	gccctctcat	gccttgccct	tcaccatgct	ctgctccagg	360
tcagccccct	tttggcctgt	ttgttttgct	aaaaaacctaa	tctgcttctt	gcttttcttg	420
gtaatatata	tttagggaag	atgttgcttt	gccacacac	gaagcaaagt	aa	472

<210> 352

<211> 251

<212> DNA

<213> Homo sapien

<400> 352

ctcaaagcta	atctctcggg	aatcaaacca	gaaaagggca	aggatcttag	gcatgggtga	60
tgtggataag	gccagggtcaa	tggctgcaag	catgcagaga	aagaggtaca	tcggagcgtg	120
caggctgctg	tccgtcctta	cgatgaagac	cacgatgcag	tttccaaaca	ttgccactac	180
atacatggaa	aggaggggga	agccaaccca	gaaatgggct	ttctctaate	ctgggataacc	240
aataagcaca	a					251

<210> 353

<211> 436

<212> DNA

<213> Homo sapien

<400> 353

tttttttttt	tttttttttt	ttttttacaa	caatgcagtc	atatttttat	tgagtatgtg	60
cacattatgg	tattattact	atactgatta	tatttatcat	gtgacttcta	attaraaaat	120
gtatccaaaa	gcaaaacagc	agatatacaa	aattaaagag	acagaagata	gacattaaca	180
gataaggcaa	cttatacatt	gacaatccaa	atccaatata	tttaaacatt	tgggaaatga	240
gggggacaaa	tgggaagccar	atcaaatttg	tgtaaaacta	ttcagtatgt	ttcccttgct	300
tcatgtctga	raaggctctc	ccttcaatgg	ggatgacaaa	ctccaaatgc	cacacaaatg	360
ttaacagaat	actagattca	cactggaacg	ggggtaaaga	agaaattatt	ttctataaaa	420
gggtccttaa	tgtagt					436

<210> 354

<211> 854

<212> DNA

<213> Homo sapien

<400> 354

ccttttctag	ttcacaggtt	ttctgcaagg	atgctgggta	gggagtgtct	gcaggaggag	60
caagtctgaa	accaaatacta	ggaaacatag	gaaacgagcc	aggcacaggg	ctgggtgggcc	120
atcaggggacc	accctttggg	ttgatatttt	gcttaatctg	catcttttga	gtaagatcat	180
ctggcagtag	aagctgttct	ccagggtacat	ttctctagct	catgtacaaa	aacatcctga	240
aggactttgt	caggtgcctt	gctaaaagcc	agatgcgttc	ggcacttcct	tgggtctgag	300
ttaattgcac	acctacaggc	actggggtca	tgctttcaag	tattttgtcc	tcacttttag	360
gtgagtga	gatccccatt	ataggagcac	ttgggagaga	tcataataaa	gctgactctt	420
gagtacatgc	agtaattggg	tagatgtgtg	tgggtgtgtc	tcattcctgc	aagggtgctt	480
gttagggagt	gtttccagga	ggaacaagtc	tgaaaccaat	catgaaataa	atggtaggtg	540
tgaactggaa	aactaattca	aaagagagat	cgtgatatca	gtgtgggtga	tacaccttgg	600
caatatggaa	ggctctaatt	tgcccatatt	tgaaataata	attcagcttt	ttgtaataca	660
aaataacaaa	ggattgagaa	tcatgggtgc	taatgtataa	aagacccagg	aaacataaat	720
atatcaactg	cataaatgta	aaatgcattg	gacccaagaa	ggccccaag	tggcagacaa	780
cattgtaccc	attttccctt	ccaaaatgtg	agcggcgggc	ctgctgcttt	caaggctgtc	840
acacgggatg	tcag					854

<210> 355

<211> 676

<212> DNA

<213> Homo sapien

<400> 355

gaaattaagt	atgagctaaa	ttccctgtta	aaacctctag	gggtgacaga	tctcttcac	60
cagggtcaaa	ctgatctttc	tggaaatgtca	ccaaccaagg	gcctatattt	atcaaaagcc	120
atccacaagt	catacctgga	tgtcagcgaa	gagggcacgg	aggcagcagc	agccactggg	180
gacagcatcg	ctgtaaaaag	cctaccaatg	agagctcagt	tcaaggcgaa	ccacccttc	240
ctgttcttta	taaggcacac	tcataccaac	acgatcctat	tctgtggcaa	gcttgctct	300
ccctaatac	atgggggttg	gtaaggctca	gagttgcaga	tgaggtgcag	agacaatcct	360
gtgactttcc	cacggccaaa	aagctgttca	cacctcacgc	acctctgtgc	ctcagtttgc	420

tcactctgcaa aataggtcta ggatttcttc caaccatttc atgagttgtg aagctaaggc	480
tttgtaatac atggaaaaag gtagacttat gcagaaagcc tttctggctt tcttatctgt	540
ggtgtctcat ttgagtgtcg tccagtgcac tgatcaagtc aatgagtaaa attttaaggg	600
attagatttt cttgacttgt atgtatctgt gagatcttga ataagtgacc tgacatctct	660
gcttaaagaa aaccag	676

<210> 356
 <211> 574
 <212> DNA
 <213> Homo sapien

<400> 356	
tttttttttt tttttcagga aaacattctc ttacttttatt tgcatctcag caaaggttct	60
catgtggcac ctgactggca tcaaaccaaa gttcgtaggc caacaaagat gggccactca	120
caagcttccc atttgtagat ctcagtgcct atgagtatct gacacctgtt cctctcttca	180
gtctcttagg gaggcttaaa tctgtctcag gtgtgctaag agtgccagcc caaggkggtc	240
aaaagtccac aaaactgcag tctttgctgg gatagtaagc caagcagtgc ctggacagca	300
gagttctttt cttgggcaac agataaccag acaggactct aatcgtgctc ttattcaaca	360
ttcttctgtc tctgcctaga ctggaataaa aagccaatct ctctcgtggc acagggaagg	420
agatacaagc tcgtttacat gtgatagatc taacaaaggc atctaccgaa gtctggtctg	480
gatagacggc acaggagct cttaggtcag cgctgctggg tggaggacat tcctgagtc	540
agctttgcag cctttgtgca acagtacttt ccca	574

<210> 357
 <211> 393
 <212> DNA
 <213> Homo sapien

<400> 357	
tttttttttt tttttttttt tttttttttt tacagaatat aratgcttta tcaactgkact	60
taatatggkg kcttggtcac tatacttaaa aatgcaccac tcataaatat ttaattcagc	120
aagccacaac caaracttga ttttatcaac aaaaaccctt aaatataaac ggsaaaaaag	180
atagatataa ttattccagt ttttttaaaa cttaaaarat attccattgc cgaattaara	240
araarataag tgttatatgg aaagaagggc attcaagcac actaaaraaa cctgaggkaa	300
gcataatctg tacaaaatta aactgtcctt tttggcattt taacaaattt gcaacgktct	360
tttttttctt tttctgtttt tttttttttt tac	393

<210> 358
 <211> 630
 <212> DNA
 <213> Homo sapien

<400> 358	
acagggtaaa caggaggatc cttgctctca cggagcttac attctagcag gaggacaata	60
ttaatgttta taggaaaatg atgagtttat gacaaaggaa gtagatagtg ttttacaaga	120
gcatagagta gggaagctaa tccagcacag ggaggtcaca gagacatccc taagggaagt	180
gagtttaaac tgagagaagc aagtgcctaa actgaaggat gtgttgaaga agaagggaga	240
gtagaacaat ttgggcagag ggaaccttat agaccctaag gtgggaagggt tcaaagaact	300
gaaagagagc tagaacagct ggagccgttc tccggtgtaa agaggagtca aagagataag	360
attaaagatg tgaagattaa gatcttggtg gcattcaggg attggcactt ctacaagaaa	420
tcactgaagg gagttaatgtg acattacttt tcacttcagg atggccattc taactccagg	480
gggtagactg gactaggtaa gactggaggc aggtagacct cttctaaggc ctgcgatagt	540
gaaagacaaa aataagtggg gaaattcagg ggatagtga aatcagtagg acttaatgag	600
caagccagag gttcctccac aacaaccagt	630

<210> 359
 <211> 620
 <212> DNA

<213> Homo sapien

<400> 359

acagcattcc	aaaatataca	tctagagact	aarrgtaaat	gctctatagt	gaagaagtaa	60
taattaaaa	atgctactaa	tatagaaaat	ttataatcag	aaaaataaat	attcagggag	120
ctcaccagaa	gaataaagtg	ctctgccagt	tattaaagga	ttactgctgg	tgaattaaat	180
atggcattcc	ccaagggaaa	tagagagatt	cttctggatt	atgttcaata	tttatttcac	240
aggattaact	gttttaggaa	cagatataaa	gcttcgccac	ggaagagatg	gacaaagcac	300
aaagacaaca	tgatacctta	ggaagcaaca	ctaccctttc	aggcataaaa	tttgagagaa	360
tgcaacatta	tgcttcatga	ataatatgta	gaaagaagggt	ctgatgaaaa	tgacatcctt	420
aatgtaagat	aactttataa	gaattctggg	tcaaataaaa	ttctttgaag	aaaacatcca	480
aatgtcattg	acttatcaaa	tactatcttg	gcataatacc	tatgaaggca	aaactaaaca	540
aacaaaaagc	tcacaccaaa	caaaaccatc	aacttatttt	gtattctata	acatacgaga	600
ctgtaaagat	gtgacagtgt					620

<210> 360

<211> 431

<212> DNA

<213> Homo sapien

<400> 360

aaaaaaaa	agccagaaca	acatgtgata	gataatatga	ttggetgcac	acttcagac	60
tgatgaatga	tgaacgtgat	ggactattgt	atggagcaca	tcttcagcaa	gagggggaaa	120
tactcatcat	ttttggccag	cagttgtttg	atcaccaaac	atcatgccag	aatactcagc	180
aaaccttctt	agctcttgag	aagtcaaagt	ccgggggaat	ttattcctgg	caattttaat	240
tggtactcct	atgtgagagc	agcggctacc	cagctggggt	ggtggagcga	acccgtcact	300
agtggacatg	cagtggcaga	gctcctggta	accacctaga	ggaatacaca	ggcacatgtg	360
tgatgccaa	cgtgacacct	gtagcactca	aatttgtctt	gtttttgtct	ttcgggtgtg	420
agattcttag	t					431

<210> 361

<211> 351

<212> DNA

<213> Homo sapien

<400> 361

acactgattt	ccgatcaaaa	gaatcatcat	ctttaccttg	acttttcagg	gaattactga	60
actttcttct	cagaagatag	ggcacagcca	ttgccttggc	ctcacttgaa	gggtctgcat	120
ttgggtcctc	tggtctcttg	ccaagtttcc	cagccactcg	aggagaaaat	atcgggaggt	180
ttgacttcct	ccggggcttt	cccaggggct	tcaccgtgag	ccctgcggcc	ctcagggctg	240
caatcctgga	ttcaatgtct	gaaacctcgc	tctctgcctg	ctggacttct	gaggccgtca	300
ctgccactct	gtctccagc	tctgacagct	cctcatctgt	ggtcctgttg	t	351

<210> 362

<211> 463

<212> DNA

<213> Homo sapien

<400> 362

acttcacag	gccataatgg	gtgcctcccg	tgagaatcca	agcacctttg	gactgcgcga	60
tgtagatgag	ccggctgaag	atcttgcgca	tgccggcgtt	cagggcgaag	ttcttggcgc	120
ccccggtcac	agaaatgacc	aggttgggtg	ttttcagggtg	ccagtgtctg	gtcagcagct	180
cgtaaaggat	ttccgcgtcc	gtgtcgcagg	acagacgtat	atacttcctt	ttcttcccca	240
gtgtctcaaa	ctgaatatcc	ccaaaggcgt	cggtaggaaa	ttccttgggtg	tgtttcttgt	300
agttccattt	ctcacttttg	ttgatctggg	tgcttcccat	gtgtcggctc	tgggcatagc	360
cacacttgca	cacattctcc	ctgataagca	cgatgggtgtg	gacaggaagg	aaggatttca	420
ttgagcctgc	ttatggaaac	tggtattgtt	agcttaataa	gac		463

<210> 363
 <211> 653
 <212> DNA
 <213> Homo sapien
 <220>
 <221> misc_feature
 <222> (1)...(653)
 <223> n = A,T,C or G

<400> 363
 acccccagagt ncctgnctgg catactgnga acgaccaacg acacacccaa gctcggcctc 60
 ctcttgngga ttctgggtga catcttcattg aatggcaacc gtgccagwga ggctgtcctc 120
 tgggaggcac tacgcaagat gggactgcgt cctgggggtga gacatcctct ccttgagat 180
 ctaacgaaac ttctcaccta tgagttgtaa agcagaaata cctgnactac agacgagtgc 240
 ccaacagcaa ccccccgaa gtatgagttc ctctrgggcc tccgttccta ccatgagasc 300
 tagcaagatg naagtgttga gantcattgc agaggttcag aaaagagacc cntcgtgact 360
 ggtctgcaca gttcatggag gctgcagatg aggccttgga tgctctggat gctgctgcag 420
 ctgaggccga agcccgggct gaagcaagaa cccgcattgg aattggagat gaggctgtgt 480
 ntgggccctg gagctgggat gacattgagt ttgagctgct gacctgggat gaggaaggag 540
 attttgagaga tccntgggtcc agaattccat ttaccttctg ggccagatac caccagaatg 600
 cccgctccag attccctcag acctttgccg gtoccatat tggtcstggt ggt 653

<210> 364
 <211> 401
 <212> DNA
 <213> Homo sapien

<400> 364
 actagaggaa agacgttaaa ccactctact accacttgtg gaactctcaa agggtaaagt 60
 acaaagccaa tgaatgactc taaaaacaat atttacattt aatggtttgt agacaataaa 120
 aaaacaaggt ggatagatct agaattgtaa cattttaaga aaaccatagc atttgacaga 180
 tgagaaagct caattataga tgcaaagtta taactaaact actatagtag taaagaaata 240
 catttcacac ccttcatata aattcactat cttggcttga ggcactccat aaaatgtatc 300
 acgtgcatag taaatcttta tatttgctat ggcgttgcac tagaggactt ggactgcaac 360
 aagtggatgc gcggaaaatg aaatcttctt caatagccca g 401

<210> 365
 <211> 356
 <212> DNA
 <213> Homo sapien

<400> 365
 ccagtgtcat atttgggctt aaaatttcaa gaagggcact tcaaattggct ttgcatttgc 60
 atgtttcagt gctagagcgt aggaatagac cctggcgctc actgtgagat gttcttcagc 120
 taccagagca tcaagtctct gcagcaggtc attcttgggt aaagaaatga cttccacaaa 180
 ctctccatcc cctggccttg gcttcggcct tgcgttttcg gcatcatctc cgttaatggt 240
 gactgtcacg atgtgtatag tacagtttga caagcctggg tccatacaga ccgctggaga 300
 acattcggca atgtcccctt tgtagccagt ttcttcttcg agtccccgga gagcag 356

<210> 366
 <211> 1851
 <212> DNA
 <213> Homo sapien

<400> 366
 tcatacccat tgccagcagc ggcaccgtta gtcaggtttt ctgggaatcc cacatgagta 60
 cttccgtgtt cttcattctt cttcaatagc cataaatctt ctagctctgg ctggctgttt 120

tcacttcctt	taagcctttg	tgactcttcc	tctgatgtca	gctttaagtc	ttgttctgga	180
ttgctgtttt	cagaagagat	ttttaacatc	tgtttttctt	tgtagtcaga	aagtaactgg	240
caaattacat	gatgatgact	agaaacagca	tactctctgg	ccgtctttcc	agatcttgag	300
aagatacatc	aacattttgc	tcaagtagag	ggctgactat	acttgctgat	ccacaacata	360
cagcaagtat	gagagcagtt	cttccatata	tatccagcgc	atttaaattc	gcttttttct	420
tgattaaaaa	tttcaccact	tgctgttttt	gctcatgtat	accaagtagc	agtgggtgga	480
ggccatgctt	gttttttgat	tcgatatacag	caccgtataa	gagcagtgtc	ttggccatta	540
atttatcttc	attgtagaca	gcatagtgta	gagtggtatt	tccatactca	tctgggaatat	600
ttggatcagt	gccatgttcc	agcaacatta	acgcacattc	atcttctctg	cattgtacgg	660
cctttgtcag	agctgtcctc	tttttgttgt	caaggacatt	aagttgacat	cgtctgtcca	720
gcacgagttt	tactacttct	gaattcccat	tggcagaggc	cagatgtaga	gcagtcctct	780
tttgcttgtc	cctcttggtc	acatccgtgt	ccctgagcat	gacgatgaga	tcctttctgg	840
ggactttacc	ccaccaggca	gctctgtgga	gcttggtccag	atcttctcca	tggacgtggg	900
acctgggata	catgaaggcg	ctgtcatcgt	agtctcccca	agcgaccacg	ttgctcttgc	960
cgtctccctg	cagcagggga	agcagtggca	gcaccacttg	cacctcttgc	tccaagcgt	1020
cttcacagag	gagtcgttgt	ggtctgcaga	agtgccacg	ttgctcttgc	cgtctccct	1080
gtccatccag	ggaggaagaa	atgcaggaaa	tgaaagatgc	atgcacgatg	gtatactcct	1140
cagccatcaa	acttctggac	agcagggtcac	ttccagcaag	gtggagaaaag	ctgtccaccc	1200
acagaggatg	agatccagaa	accacaatat	ccattcacaa	acaaacactt	ttcagccaga	1260
cacaggtact	gaaatcatgt	catctgcggc	aacatgggtg	aacctaccga	atcacacatc	1320
aagagatgaa	gacactgcag	tatatctgca	caacgtaata	ctcttcatcc	ataacaaaat	1380
aatataattt	tcctctggag	ccatatggat	gaactatgaa	ggaagaactc	cccgaagaag	1440
ccagtcgcag	agaagccaca	ctgaagctct	gtcctcagcc	atcagcgcca	cggacaggag	1500
tgtgtttctt	ccccagtgat	gcagcctcaa	gttatcccga	agctgccgca	gcacacggtg	1560
gctcctgaga	aacaccccag	ctcttccggt	ctaacacagg	caagtcaata	aatgtgataa	1620
tcacataaaa	agaattaaaa	gcaaagtcac	ataagcatct	caacagacac	agaaaaggca	1680
tttgacaaaa	tccagcatcc	ttgtatttat	tgttgaggtt	ctcagaggaa	atgcttctaa	1740
cttttcccca	tttagtatta	tggttggtgt	gggttggtca	taggtgggtt	ttattacttt	1800
aaggatgtgc	ccttctatgc	ctgttttgct	gaggggttta	attctcgtgc	c	1851

<210> 367

<211> 668

<212> DNA

<213> Homo sapien

<400> 367

cttgagcttc	caaataygga	agactggccc	ttacacasgt	caatgttaaa	atgaatgcat	60
ttcagtat	tgaagataaa	attttagat	ctataccttg	ttttttgatt	cgatatcagc	120
accrtataag	agcagtgtt	tggccattaa	tttatctttc	attttagaca	gcrtagtgya	180
gagtggtatt	tccatactca	tctggaatat	ttggatcagt	gccatgttcc	agcaacatta	240
acgcacattc	atcttctctg	cattgtacgg	cctgtcagta	ttagacccaa	aaacaaatta	300
catatcttag	gaattcaaaa	taacattcca	cagctttcac	caactagtta	tatttaaagg	360
agaaaactca	tttttatgcc	atgtattgaa	atcaaaccca	cctcatgctg	atatagtggg	420
ctactgcata	cctttatcag	agctgtcctc	tttttgttgt	caaggacatt	aagttgacat	480
cgtctgtcca	gcaggagttt	tactacttct	gaattcccat	tggcagaggc	cagatgtaga	540
gcagtcctat	gagagtgaga	agacttttta	ggaaattgta	gtgcactagc	tacagccata	600
gcaatgattc	atgtaactgc	aaacactgaa	tagcctgcta	ttactctgcc	ttcaaaaaaa	660
aaaaaaa						668

<210> 368

<211> 1512

<212> DNA

<213> Homo sapien

<400> 368

gggtgcacca	ggggsgcgt	gggttttctt	cgggtgggtg	tgggttttcc	ctgggtgggg	60
tgggtggggc	trgaatcccc	tgctgggggt	ggcaggtttt	ggctgggatt	gacttttytc	120
ttcaaacaga	ttggaaaccc	ggagttacct	gctagtttgt	gaaactggtt	ggtagacgcg	180

atctgttggc	tactactggc	ttctcctggc	tgttaaaagc	agatgggtgt	tgagggtgat	240
tccatgccgg	ctgcttcttc	tgtgaagaag	ccatttggtc	tcaggagcaa	gatgggcaag	300
tggtgctgcc	gttgcttccc	ctgctgcagg	gagagcggca	agagcaacgt	gggcacttct	360
ggagaccacg	acgactctgc	tatgaagaca	ctcaggagca	agatgggcaa	gtggtgccgc	420
cactgcttcc	cctgctgcag	ggggagtggc	aagagcaacg	tgggcgcttc	tggagaccac	480
gacgaytctg	ctatgaagac	actcaggaac	aagatgggca	agtgggtgctg	ccactgcttc	540
ccctgctgca	gggggagcrg	caagagcaag	gtgggcgctt	ggggagacta	cgatgacagt	600
gccttcatgg	agcccaggta	ccacgtccgt	ggagaagatc	tggacaagct	ccacagagct	660
gcctggtggg	gtaaagtccc	cagaaaggat	ctcatcgtca	tgctcaggga	cactgacgtg	720
aacaagaagg	acaagcaaaa	gaggactgct	ctacatctgg	cctctgccaa	tggaattca	780
gaagtagtaa	aactcstgct	ggacagacga	tgtcaactta	atgtccttga	caacaaaaag	840
aggacagctc	tgayaaaggc	cgtacaatgc	caggaagatg	aatgtgcgtt	aatggtgctg	900
gaacatggca	ctgatccaaa	tattccagat	gagtatggaa	ataccactct	rcactaygct	960
rtctayaatg	aagataaatt	aatggccaaa	gcactgctct	tatayggtgc	tgatatcgaa	1020
tcaaaaaaca	aggtatagat	ctactaattt	tatcttcaaa	atactgaaat	gcattcattt	1080
taacattgac	gtgtgtaagg	gccagtcttc	cgtatttggg	agctcaagca	taacttgaat	1140
gaaaatattt	tgaatgacc	taattatctm	agactttatt	ttaaattattg	ttattttcaa	1200
agaagcatta	gagggtacag	tttttttttt	ttaaattgcac	ttctggtaaa	tacttttgtt	1260
gaaaacactg	aatttgtaaa	aggtaatatc	tactattttt	caatttttcc	ctcctaggat	1320
ttttttcccc	taattgaatgt	aagatggcaa	aatttgcctt	gaaataggtt	ttacatgaaa	1380
actccaagaa	aagttaaaca	tgtttcagtg	aatagagatc	ctgctccttt	ggcaagtccc	1440
taaaaaacag	taatagatac	gaggtgatgc	gcctgtcagt	ggcaagggtt	aagatatttc	1500
tgatctcgtg	cc					1512

<210> 369

<211> 1853

<212> DNA

<213> Homo sapien

<400> 369

gggtcgccca	ggggsgcgt	ggcctttcct	cgggtgggtg	tgggttttcc	ctgggtgggg	60
tgggctgggc	trgaatcccc	tgctgggggt	ggcagggttt	ggctgggatt	gacttttytc	120
ttcaaacaga	tggaaacccc	ggagttacct	tgtagttggt	gaaactgggt	ggtagacgcg	180
atctgttggc	tactactggc	ttctcctggc	tgttaaaagc	agatgggtgt	tgagggtgat	240
tccatgccgg	ctgcttcttc	tgtgaagaag	ccatttggtc	tcaggagcaa	gatgggcaag	300
tggtgctgcc	gttgcttccc	ctgctgcagg	gagagcggca	agagcaacgt	gggcacttct	360
ggagaccacg	acgactctgc	tatgaagaca	ctcaggagca	agatgggcaa	gtggtgccgc	420
cactgcttcc	cctgctgcag	ggggagtggc	aagagcaacg	tgggcgcttc	tggagaccac	480
gacgaytctg	ctatgaagac	actcaggaac	aagatgggca	agtgggtgctg	ccactgcttc	540
ccctgctgca	gggggagcrg	caagagcaag	gtgggcgctt	ggggagacta	cgatgacagy	600
gccttcatgg	akcccaggta	ccacgtccrt	ggagaagatc	tggacaagct	ccacagagct	660
gcctggtggg	gtaaagtccc	cagaaaggat	ctcatcgtca	tgctcaggga	cackgaygtg	720
aacaagargg	acaagcaaaa	gaggactgct	ctacatctgg	cctctgccaa	tggaattca	780
gaagtagtaa	aactcstgct	ggacagacga	tgtcaactta	atgtccttga	caacaaaaag	840
aggacagctc	tgayaaaggc	cgtacaatgc	caggaagatg	aatgtgcgtt	aatggtgctg	900
gaacatggca	ctgatccaaa	tattccagat	gagtatggaa	ataccactct	rcactaygct	960
rtctayaatg	aagataaatt	aatggccaaa	gcactgctct	tatayggtgc	tgatatcgaa	1020
tcaaaaaaca	agcatggcct	cacaccactg	ytacttggtr	tacatgagca	aaaacagcaa	1080
gtsgtgaaat	ttttaatyaa	gaaaaaagcg	aatttaaaat	gcrctggata	gatatggaa	1140
ractgctctc	atacttgctg	tatgttgttg	atcagcaagt	atagtcagcc	ytctacttga	1200
gcaaaatrtr	gatgtatctt	ctcaagatct	ggaaagacgg	ccagagagta	tgctgtttct	1260
agtcacatc	atgtaatttg	ccagttactt	tctgactaca	aagaaaaaca	gatgttaaaa	1320
atctcttctg	aaaacagcaa	tccagaacaa	gacttaaagc	tgacatcaga	ggaagagtca	1380
caaaggctta	aaggaagtga	aaacagccag	ccagaggcat	ggaaactttt	aaatttaaac	1440
ttttggttta	atgttttttt	tttttgcctt	ataataatta	gatagtccca	aatgaaatwa	1500
cctatgagac	taggctttga	gaatcaatag	attctttttt	taagaatctt	ttggctagga	1560
gcggtgtctc	acgcctgtaa	ttccagcacc	ttgagaggct	gaggtgggca	gatcacgaga	1620
tcaggagatc	gagaccatcc	tggctaacac	ggtgaaaccc	catctctact	aaaaatacaa	1680

aaacttagct	gggtgtggtg	gcgggtgcct	gtagtcccag	ctactcagga	rgctgaggca	1740
ggagaatggc	atgaaccccg	gaggtggagg	ttgcagtgag	ccgagatccg	ccactacact	1800
ccagcctggg	tgacagagca	agactctgtc	tcaaaaaaaaa	aaaaaaaaaa	aaa	1853

<210> 370
 <211> 2184
 <212> DNA
 <213> Homo sapien

<400> 370						
ggcagcagaa	ttaaaaccct	cagcaaaaaca	ggcatagaag	ggacatacct	ttaaagtaata	60
aaaaccacct	atgacaagcc	cacagccaac	ataatactaa	atggggaaaa	gttagaagca	120
tttctcttga	gaactgcaac	aataaataca	aggatgctgg	attttgtcaa	atgccttttc	180
tgtgtctgtt	gagatgctta	tgtgactttg	cttttaattc	tgtttatgtg	attatcacat	240
ttattgactt	gcctgtgtta	gaccggaaga	gctggggtgt	ttctcaggag	ccaccgtgtg	300
ctgcggcagc	ttcgggataa	cttgaggctg	catcactggg	gaagaaacac	aytcctgtcc	360
gtggcgctga	tggctgagga	cagagcttca	gtgtggcttc	tctgcgactg	gcttcttcgg	420
ggagttcttc	cttcatagtt	catccatatg	gctccagagg	aaaattatat	tattttgtta	480
tggatgaaga	gtattacgtt	gtgcagatat	actgcagtgt	cttcactctc	tgatgtgtga	540
ttgggtagg	tccaccatgt	tgccgcagat	gacatgattt	cagtacctgt	gtctggctga	600
aaagtgtttg	tttgtgaatg	gatattgttg	tttctggatc	tcactcctctg	tgggtggaca	660
gctttctcca	ccttgctgga	agtgacctgc	tgtccagaag	tttgatggct	gaggagtata	720
ccatcgtgca	tgcatctttc	atttcctgca	tttcttcctc	cctggatgga	cagggggagc	780
ggcaagagca	acgtgggcac	ttctggagac	cacaacgact	cctctgtgaa	gacgcttggg	840
agcaagaggt	gcaagtgtgtg	ctgccactgc	ttcccctgct	gcaggggagc	ggcaagagca	900
acgtggtcgc	ttggggagac	tacgatgaca	gcgccttcat	ggatcccagg	taccacgtcc	960
atggagaaga	tctggacaag	ctccacagag	ctgcctggtg	gggtaaaagtc	cccagaaagg	1020
atctcatcgt	catgctcagg	gacacggatg	tgaaacaagag	ggacaagcaa	aagaggactg	1080
ctctacatct	ggcctctgcc	aatgggaatt	cagaagtagt	aaaactcgtg	ctggacagac	1140
gatgtcaact	taatgtcctt	gacaacaaaa	agaggacagc	tctgacaaaag	gccgtacaat	1200
gccaggaaga	tgaatgtgcg	ttaatgttgc	tggaaacatgg	cactgatcca	aatattccag	1260
atgagtatgg	aaataccact	ctacactatg	ctgtctacaa	tgaagataaa	ttaatggcca	1320
aagcactgct	cttatacgg	gctgatatcg	aatcaaaaaa	caagcatggc	ctcacaccac	1380
tgctactttg	tatacatgag	caaaaacagc	aagtggtgaa	atttttaatc	aagaaaaaag	1440
cgaattttaa	tgcgctggat	agatatggaa	gaactgctct	catacttgct	gtatgttgtg	1500
gatcagcaag	tatagtcagc	cctctacttg	agcaaaatgt	tgatgtatct	tctcaagatc	1560
tggaaagacg	gccagagagt	atgctgtttc	tagtcatcat	catgtaattt	gccagttact	1620
ttctgactac	aaagaaaaac	agatgttaaa	aatctcttct	gaaaacagca	atccagaaca	1680
agacttaaag	ctgacatcag	aggaagagtc	acaaaggcct	aaaggaagtg	aaaacagcca	1740
gccagaggca	tggaaacttt	taaatttaaa	cttttggttt	aatgtttttt	ttttttgcct	1800
taataatatt	agatagtccc	aaatgaaatw	acctatgaga	ctaggccttg	agaatcaata	1860
gattcttttt	ttaagaatct	tttggttagg	agcgggtgtc	cacgcctgta	attccagcac	1920
cttgagaggc	tgaggtgggc	agatcacgag	atcaggagat	cgagaccatc	ctggctaaca	1980
cgggtgaaac	ccatctctac	taaaaataca	aaaacttagc	tgggtgtggt	ggcgggtgcc	2040
tgtagtccca	gctactcagg	argctgaggc	aggagaatgg	catgaacccg	ggaggtggag	2100
gttgacagtga	gccgagatcc	gccactacac	tccagcctgg	gtgacagagc	aagactctgt	2160
ctcaaaaaaa	aaaaaaaaaa	aaaa				2184

<210> 371
 <211> 1855
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(1855)
 <223> n = A,T,C or G

<400> 371

tgacgcac	ggccagtg	tgtgccacgt	acactgacgc	cccctgagat	gtgcacgccg	60
cacgcgcacg	ttgcacgcgc	ggcagcggct	tggctggctt	gtaacggctt	gcacgcgcac	120
gccgcccccg	cataaccgtc	agactggcct	gtaacggctt	gcaggcgac	gccgcacgcg	180
cgtaacggct	tggtgccct	gtaacggctt	gcacgtgcat	gctgcacgcg	cgtaacggc	240
ttggctggca	tgtagccgt	tggttggct	ttgcattt	tgtkggctk	ggcgttgkty	300
tcttggattg	acgttctc	cttggatkga	cgttctctcc	ttggatkga	gttctytyty	360
tcgcgttct	ttgctggact	tgacctt	tctgctgggt	ttggcattcc	tttggggtg	420
gctgggtgtt	ttctccgggg	gggkkgccc	ttctgggggt	gggctgggk	cgcccccagg	480
gggctgggc	tttccccggg	tgggtgtggg	tttctctggg	gtggggtggg	ctgtgctggg	540
atccccctgc	tggggttggc	agggattgac	tttttcttc	aaacagattg	gaaaccggga	600
gtaacntgct	agttggtgaa	actggttggg	agacgcgac	tgtgtgtact	actgttctc	660
ctggctgtta	aaagcagatg	gtggctgagg	ttgattcaat	gccggctgct	tcttctgtga	720
agaagccatt	tggctctcagg	agcaagatgg	gcaagtgggt	cgccactgct	tccccctgctg	780
cagggggagc	ggcaagagca	acgtgggcac	ttctggagac	cacaacgact	cctctgtgaa	840
gacgcttggg	agcaagaggt	gcaagtgggt	ctgccactg	cttccccctgc	tgcaggggag	900
cggaagagc	aacgtggkcg	cttggggaga	ctacgatgac	agcgccttca	tggakccag	960
gtaccacgtc	crtggagaag	atctggacaa	gctccacaga	gctgcctgggt	ggggtaaagt	1020
ccccagaaaag	gatctcatcg	tcatgctcag	ggacactgay	gtgaacaaga	rggacaagca	1080
aaagaggact	gctctacatc	tggcctctgc	caatgggaat	tcagaagtag	taaaactcgt	1140
gctggacaga	cgatgtcaac	ttaatgtcct	tgacaacaaa	aagaggacag	ctctgacaaa	1200
ggcgtacaa	tgccaggaag	atgaatgtgc	gttaatgttg	ctggaacatg	gcactgatcc	1260
aaatattcca	gatgagtatg	gaaataccac	tctacactat	gctgtctaca	atgaagataa	1320
attaatggcc	aaagcactgc	tcttatacgg	tgtgtatc	gaatcaaaaa	acaaggtata	1380
gatctactaa	ttttatcttc	aaaatactga	aatgcattca	ttttaacatt	gacgtgtgta	1440
agggccagtc	ttccgtattt	ggaagctcaa	gcataacttg	aatgaaaata	ttttgaaatg	1500
acctaattat	ctaagacttt	attttaaata	tgtttattt	caaagaagca	ttagagggtg	1560
cagttttttt	tttttaaatg	cacttctggt	aaatactttt	gttgaaaaca	ctgaatttgt	1620
aaaaggtaat	acttactatt	tttcaatttt	tccctcctag	gatttttttc	ccctaatagaa	1680
tgtgaagtgg	caaaatttgc	cctgaaatag	gttttacatg	aaaactccaa	gaaaagttaa	1740
acatgtttca	gtgaatagag	atcctgctcc	tttggaagt	tcttaaaaaa	cagtaataga	1800
tacgaggtga	tgcgcctgtc	agtggcaagg	tttaagatat	ttctgatctc	gtgcc	1855

<210> 372

<211> 1059

<212> DNA

<213> Homo sapien

<400> 372

gcaacgtggg	cacttctgga	gaccacaacg	actcctctgt	gaagacgctt	gggagcaaga	60
ggtgcaagtg	gtgctgccca	ctgcttcccc	tgtctgaggg	gagcggaag	agcaacgtgg	120
gcgcttgrgg	agactmcgat	gacagygcct	tcatggagcc	caggtaccac	gtccgtggag	180
aagatctgga	caagctccac	agagctgccc	tgggtgggta	aagtccccag	aaaggatctc	240
atcgatcatg	tcaggagacac	tgaygtgaac	aagarggaca	agcaaaagag	gactgctcta	300
catctggcct	ctgccaatgg	gaattcagaa	gtagtaaaac	tctgtctgga	cagacgatgt	360
caacttaatg	tccttgacaa	caaaaagagg	acagctctga	yaaaggccgt	acaatgccag	420
gaagatgaat	gtgcgttaat	gttgtctgga	catggcactg	atccaaatat	tccagatgag	480
tatggaaata	ccactctrca	ctaygctrct	tayaatgaag	ataaattaat	ggccaaagca	540
ctgctcttat	ayygtgctga	tatcgatatca	aaaaacaagg	tatagatcta	ctaattttat	600
cttcaaaata	ctgaaatgca	ttcattttta	cattgacgtg	tgtgaaggcc	agtcttccgt	660
atttggagc	tcaagcataa	cttgaatgaa	aataatttga	aatgacctaa	ttatctaaga	720
ctttatttta	aatattgtta	ttttcaaaga	agcattagag	ggtacagttt	ttttttttta	780
aatgcacttc	tggtaaatac	ttttgttgaa	aacactgaat	ttgtaaaagg	taatacttac	840
tatttttcaa	tttttccctc	ctaggatttt	tttcccctaa	tgaatgtaag	atggcaaat	900
ttggccctgaa	ataggtttta	catgaaaact	ccaagaaaag	ttaaacatgt	ttcagtgaat	960
agagatcctg	ctcctttggc	aagttcctaa	aaaacagtaa	tagatacgag	gtgatgcgcc	1020
tgtcagtggc	aaggtttaag	atatttctga	tctcgtgcc			1059

<210> 373
 <211> 1155
 <212> DNA
 <213> Homo sapien

<400> 373
 atggtggttg aggttgattc catgccggct gcctcttctg tgaagaagcc atttggtctc 60
 aggagcaaga tgggcaagtg gtgctgccgt tgcttcccct gctgcaggga gagcggcaag 120
 agcaacgttg gcacttcttg agaccacgac gactctgcta tgaagacact caggagcaag 180
 atgggcaagt ggtgccgcca ctgcttcccc tgctgcaggg ggagtggcaa gagcaacgtg 240
 ggcgcttctg gagaccacga cgactctgct atgaagacac tcaggaacaa gatgggcaag 300
 tgggtgctgcc actgcttccc ctgctgcagg gggagcggca agagcaagggt gggcgcttgg 360
 ggagactacg atgacagtgc cttcatggag ccaggtacc acgtccgtgg agaagatctg 420
 gacaagctcc acagagctgc ctggtggggt aaagtcccca gaaaggatct catcgtcatg 480
 ctcagggaca ctgacgtgaa caagaaggac aagcaaaaga ggactgctct acatctggcc 540
 tctgccaatg ggaattcaga agtagtaaaa ctctgctgg acagacgatg tcaacttaat 600
 gtcttgaca acaaaaagag gacagctctg ataaaggccg tacaatgcca ggaagatgaa 660
 tgtgcgttaa tgttgctgga acatggcact gatccaaata ttccagatga gtatggaat 720
 accactctgc actacgctat ctataatgaa gataaattaa tggccaaagc actgctctta 780
 tatggtgctg atatcgaatc aaaaaacaag catggcctca caccactgtt acttggtgta 840
 catgagcaaa aacagcaagt cgtgaaatct ttaatcaaga aaaaagcgaa tttaaatgca 900
 ctggatagat atggaaggac tgctctcata cttgctgtat gttgtggatc agcaagtata 960
 gtcagccttc tacttgagca aaatattgat gtatcttctc aagatctatc tggacagacg 1020
 gccagagagt atgctgtttc tagtcatcat catgtaattt gccagttact ttctgactac 1080
 aaagaaaaac agatgctaaa aatctcttct gaaaacagca atccagaaaa tgtctcaaga 1140
 accagaata aataa 1155

<210> 374
 <211> 2000
 <212> DNA
 <213> Homo sapien

<400> 374
 atggtggttg aggttgattc catgccggct gcctcttctg tgaagaagcc atttggtctc 60
 aggagcaaga tgggcaagtg gtgctgccgt tgcttcccct gctgcaggga gagcggcaag 120
 agcaacgttg gcacttcttg agaccacgac gactctgcta tgaagacact caggagcaag 180
 atgggcaagt ggtgccgcca ctgcttcccc tgctgcaggg ggagtggcaa gagcaacgtg 240
 ggcgcttctg gagaccacga cgactctgct atgaagacac tcaggaacaa gatgggcaag 300
 tgggtgctgcc actgcttccc ctgctgcagg gggagcggca agagcaagggt gggcgcttgg 360
 ggagactacg atgacagtgc cttcatggag ccaggtacc acgtccgtgg agaagatctg 420
 gacaagctcc acagagctgc ctggtggggt aaagtcccca gaaaggatct catcgtcatg 480
 ctcagggaca ctgacgtgaa caagaaggac aagcaaaaga ggactgctct acatctggcc 540
 tctgccaatg ggaattcaga agtagtaaaa ctctgctgg acagacgatg tcaacttaat 600
 gtccttgaca acaaaaagag gacagctctg ataaaggccg tacaatgcca ggaagatgaa 660
 tgtgcgttaa tgttgctgga acatggcact gatccaaata ttccagatga gtatggaat 720
 accactctgc actacgctat ctataatgaa gataaattaa tggccaaagc actgctctta 780
 tatggtgctg atatcgaatc aaaaaacaag catggcctca caccactgtt acttggtgta 840
 catgagcaaa aacagcaagt cgtgaaatct ttaatcaaga aaaaagcgaa tttaaatgca 900
 ctggatagat atggaaggac tgctctcata cttgctgtat gttgtggatc agcaagtata 960
 gtcagccttc tacttgagca aaatattgat gtatcttctc aagatctatc tggacagacg 1020
 gccagagagt atgctgtttc tagtcatcat catgtaattt gccagttact ttctgactac 1080
 aaagaaaaac agatgctaaa aatctcttct gaaaacagca atccagaaaa agacttaaaag 1140
 ctgacatcag aggaagagtc acaaagggtc aaaggcagtg aaaatagcca gccagagaaa 1200
 atgtctcaag aaccagaaat aaataaggat ggtgatagag aggttgaaga agaaatgaag 1260
 aagcatgaaa gtataaatgt gggattacta gaaaacctga ctaatggtgt cactgctggc 1320
 aatggtgata atggattaat tcctcaaagg aagagcagaa cacctgaaaa tcagcaattt 1380
 cctgacaacg aaagtgaaga gtatcacaga atttgcgaat tagtttctga ctacaaagaa 1440
 aaacagatgc caaaatactc ttctgaaaac agcaaccag aacaagactt aaagctgaca 1500

tcagaggaag	agtcacaaaag	gcttgagggc	agtgaaaatg	gccagccaga	gctagaaaat	1560
tttatggcta	tcgaagaaat	gaagaagcac	ggaagtactc	atgtcggatt	cccagaaaac	1620
ctgactaatg	gtgccactgc	tggcaatggt	gatgatggat	taattcctcc	aaggaagagc	1680
agaacacctg	aaagccagca	atctcctgac	actgagaatg	aagagtatca	cagtgacgaa	1740
caaatgata	ctcagaagca	atcttgtaa	gaacagaaca	ctggaatatt	acacgatgag	1800
attctgattc	atgaagaaaa	gcagatagaa	gtggttgaaa	aaatgaattc	tgagctttct	1860
cttagttgta	agaaagaaaa	agacatcttg	catgaaaata	gtacgttgcg	ggaagaaatt	1920
gccatgctaa	gactggagct	agacacaatg	aaacatcaga	gccagctaaa	aaaaaaaaaa	1980
aaaaaaaaaa	aaaaaaaaaa					2000

<210> 375

<211> 2040

<212> DNA

<213> Homo sapien

<400> 375

atggtggttg	aggttgattc	catgccggct	gcctcttctg	tgaagaagcc	atttggctct	60
aggagcaaga	tgggcaagtg	gtgctgccgt	tgcttcccct	gctgcaggga	gagcggcaag	120
agcaacgtgg	gcatttctgg	agaccacgac	gactctgcta	tgaagacact	caggagcaag	180
atgggcaagt	gggtccgcca	ctgcttcccc	tgctgcaggg	ggagtggcaa	gagcaacgtg	240
ggcgcttctg	gagaccacga	cgactctgct	atgaagacac	tcaggaacaa	gatgggcaag	300
tggtgctgcc	actgcttccc	ctgctgcagg	gggagcggca	agagcaagggt	ggcgcttgg	360
ggagactacg	atgacagtgc	cttcatggag	cccaggtacc	acgtccgtgg	agaagatctg	420
gacaagctcc	acagagctgc	ctggtggggg	aaagtcccca	gaaaggatct	catcgatcatg	480
ctcagggaca	ctgacgtgaa	caagaaggac	aagcaaaaga	ggactgctct	acatctggcc	540
tctgccaatg	ggaattcaga	agtagtaaaa	ctcctgctgg	acagacgatg	tcaacttaat	600
gtccttgaca	acaaaaagag	gacagctctg	ataaaggccg	tacaatgcc	ggaagatgaa	660
tgtgcgttaa	tggtgctgga	acatggcact	gatccaaata	ttccagatga	gtatggaaat	720
accactctgc	actacgctat	ctataatgaa	gataaattaa	tggccaaagc	actgctctta	780
tatggtgctg	atatcgaatc	aaaaaacaag	catggcctca	caccactggt	acttgggtgta	840
catgagcaaa	aacagcaagt	cgtgaaattt	ttaatcaaga	aaaaagcgaa	tttaaatgca	900
ctggatagat	atggaaggac	tgctctcata	cttgctgtat	gttgtggatc	agcaagtata	960
gtcagccttc	tacttgagca	aaatattgat	gtatcttctc	aagatctatc	tggacagacg	1020
gccagagagt	atgctgtttc	tagtcatcat	catgtaattt	gccagttact	ttctgactac	1080
aaagaaaaac	agatgctaaa	aatctcttct	gaaaacagca	atccagaaca	agacttaaag	1140
ctgacatcag	aggaagagtc	acaaagggtc	aaaggcagtg	aaaatagcca	gccagagaaa	1200
atgtctcaag	aaccagaaat	aaataaggat	ggtgatagag	aggttgaaga	agaaatgaag	1260
aagcatgaaa	gtaataatgt	gggattacta	gaaaacctga	ctaattggtg	cactgctggc	1320
aatggtgata	atggattaat	tcctcaaagg	aagagcagaa	cacctgaaaa	tcagcaattt	1380
cctgacaacg	aaagtgaaga	gtatcacaga	atcttcgaa	tagtttctga	ctacaagaa	1440
aaacagatgc	caaaataactc	ttctgaaaac	agcaaccag	aacaagactt	aaagctgaca	1500
tcagaggaag	agtcacaaaag	gcttgagggc	agtgaaaatg	gccagccaga	gaaaagatct	1560
caagaaccag	aaataaataa	ggatggtgat	agagagctag	aaaattttat	ggctatcgaa	1620
gaaatgaaga	agcacggaag	tactcatgtc	ggattcccag	aaaacctgac	taatggtgcc	1680
actgctggca	atggtgatga	tggattaatt	cctccaagga	agagcagaac	acctgaaagc	1740
cagcaatttc	ctgacactga	gaatgaagag	tatcacagt	acgaacaaaa	tgatactcag	1800
aagcaatttt	gtgaagaaca	gaacactgga	atattacacg	atgagattct	gattcatgaa	1860
gaaaagcaga	tagaagtggt	tgaaaaaatg	aattctgagc	tttctcttag	ttgtaagaaa	1920
gaaaagaca	tcttgcatga	aaatagtacg	ttgcgggaag	aaattgccat	gctaagactg	1980
gagctagaca	caatgaaaca	tcagagccag	ctaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	2040

<210> 376

<211> 329

<212> PRT

<213> Homo sapien

<400> 376

Met Asp Ile Val Val Ser Gly Ser His Pro Leu Trp Val Asp Ser Phe


```

1           5           10           15
Leu His Leu Ala Gly Ser Asp Leu Leu Ser Arg Ser Leu Met Ala Glu
20           25           30
Glu Tyr Thr Ile Val His Ala Ser Phe Ile Ser Cys Ile Ser Ser Ser
35           40           45
Leu Asp Gly Gln Gly Glu Arg Gln Glu Gln Arg Gly His Phe Trp Arg
50           55           60
Pro Gln Arg Leu Leu Cys Glu Asp Ala Trp Glu Gln Glu Val Gln Val
65           70           75           80
Val Leu Pro Leu Leu Pro Leu Leu Gln Gly Ser Gly Lys Ser Asn Val
85           90           95
Val Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe Met Asp Pro Arg Tyr
100          105          110
His Val His Gly Glu Asp Leu Asp Lys Leu His Arg Ala Ala Trp Trp
115          120          125
Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met Leu Arg Asp Thr Asp
130          135          140
Val Asn Lys Arg Asp Lys Gln Lys Arg Thr Ala Leu His Leu Ala Ser
145          150          155          160
Ala Asn Gly Asn Ser Glu Val Val Lys Leu Val Leu Asp Arg Arg Cys
165          170          175
Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr Ala Leu Thr Lys Ala
180          185          190
Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met Leu Leu Glu His Gly
195          200          205
Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn Thr Thr Leu His Tyr
210          215          220
Ala Val Tyr Asn Glu Asp Lys Leu Met Ala Lys Ala Leu Leu Leu Tyr
225          230          235          240
Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly Leu Thr Pro Leu Leu
245          250          255
Leu Gly Ile His Glu Gln Lys Gln Gln Val Val Lys Phe Leu Ile Lys
260          265          270
Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr Gly Arg Thr Ala Leu
275          280          285
Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile Val Ser Pro Leu Leu
290          295          300
Glu Gln Asn Val Asp Val Ser Ser Gln Asp Leu Glu Arg Arg Pro Glu
305          310          315          320
Ser Met Leu Phe Leu Val Ile Ile Met
325

```

<210> 377

<211> 148

<212> PRT

<213> Homo sapien

<220>

<221> VARIANT

<222> (1)...(148)

<223> Xaa = Any Amino Acid

<400> 377

```

Met Thr Xaa Pro Ser Trp Ser Pro Gly Thr Thr Ser Val Glu Lys Ile
1           5           10           15
Trp Thr Ser Ser Thr Glu Leu Pro Trp Trp Gly Lys Val Pro Arg Lys
20           25           30
Asp Leu Ile Val Met Leu Arg Asp Thr Asp Val Asn Lys Xaa Asp Lys

```

35 40 45
 Gln Lys Arg Thr Ala Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu
 50 55 60
 Val Val Lys Leu Xaa Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp
 65 70 75 80
 Asn Lys Lys Arg Thr Ala Leu Xaa Lys Ala Val Gln Cys Gln Glu Asp
 85 90 95
 Glu Cys Ala Leu Met Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro
 100 105 110
 Asp Glu Tyr Gly Asn Thr Thr Leu His Tyr Ala Xaa Tyr Asn Glu Asp
 115 120 125
 Lys Leu Met Ala Lys Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser
 130 135 140
 Lys Asn Lys Val
 145

<210> 378
 <211> 1719
 <212> PRT
 <213> Homo sapien

<400> 378
 Met Val Val Glu Val Asp Ser Met Pro Ala Ala Ser Ser Val Lys Lys
 1 5 10 15
 Pro Phe Gly Leu Arg Ser Lys Met Gly Lys Trp Cys Cys Arg Cys Phe
 20 25 30
 Pro Cys Cys Arg Glu Ser Gly Lys Ser Asn Val Gly Thr Ser Gly Asp
 35 40 45
 His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys Met Gly Lys Trp
 50 55 60
 Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Val
 65 70 75 80
 Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Asn
 85 90 95
 Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys Cys Arg Gly Ser
 100 105 110
 Gly Lys Ser Lys Val Gly Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe
 115 120 125
 Met Glu Pro Arg Tyr His Val Arg Gly Glu Asp Leu Asp Lys Leu His
 130 135 140
 Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met
 145 150 155 160
 Leu Arg Asp Thr Asp Val Asn Lys Lys Asp Lys Gln Lys Arg Thr Ala
 165 170 175
 Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val Val Lys Leu Leu
 180 185 190
 Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr
 195 200 205
 Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met
 210 215 220
 Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn
 225 230 235 240
 Thr Thr Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys Leu Met Ala Lys
 245 250 255
 Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly
 260 265 270
 Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys Gln Gln Val Val
 275 280 285

Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr
 290 295 300
 Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile
 305 310 315 320
 Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser Ser Gln Asp Leu
 325 330 335
 Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser His His His Val
 340 345 350
 Ile Cys Gln Leu Leu Ser Asp Tyr Lys Glu Lys Gln Met Leu Lys Ile
 355 360 365
 Ser Ser Glu Asn Ser Asn Pro Glu Asn Val Ser Arg Thr Arg Asn Lys
 370 375 380
 Pro Arg Thr His Met Val Val Glu Val Asp Ser Met Pro Ala Ala Ser
 385 390 395 400
 Ser Val Lys Lys Pro Phe Gly Leu Arg Ser Lys Met Gly Lys Trp Cys
 405 410 415
 Cys Arg Cys Phe Pro Cys Cys Arg Glu Ser Gly Lys Ser Asn Val Gly
 420 425 430
 Thr Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys
 435 440 445
 Met Gly Lys Trp Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly
 450 455 460
 Lys Ser Asn Val Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys
 465 470 475 480
 Thr Leu Arg Asn Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys
 485 490 495
 Cys Arg Gly Ser Gly Lys Ser Lys Val Gly Ala Trp Gly Asp Tyr Asp
 500 505 510
 Asp Ser Ala Phe Met Glu Pro Arg Tyr His Val Arg Gly Glu Asp Leu
 515 520 525
 Asp Lys Leu His Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp
 530 535 540
 Leu Ile Val Met Leu Arg Asp Thr Asp Val Asn Lys Lys Asp Lys Gln
 545 550 555 560
 Lys Arg Thr Ala Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val
 565 570 575
 Val Lys Leu Leu Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn
 580 585 590
 Lys Lys Arg Thr Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu
 595 600 605
 Cys Ala Leu Met Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro Asp
 610 615 620
 Glu Tyr Gly Asn Thr Thr Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys
 625 630 635 640
 Leu Met Ala Lys Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys
 645 650 655
 Asn Lys His Gly Leu Thr Pro Leu Leu Gly Val His Glu Gln Lys
 660 665 670
 Gln Gln Val Val Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala
 675 680 685
 Leu Asp Arg Tyr Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly
 690 695 700
 Ser Ala Ser Ile Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser
 705 710 715 720
 Ser Gln Asp Leu Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser
 725 730 735
 His His His Val Ile Cys Gln Leu Leu Ser Asp Tyr Lys Glu Lys Gln
 740 745 750

Met Leu Lys Ile Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp Leu Lys
 755 760 765
 Leu Thr Ser Glu Glu Glu Ser Gln Arg Phe Lys Gly Ser Glu Asn Ser
 770 775 780
 Gln Pro Glu Lys Met Ser Gln Glu Pro Glu Ile Asn Lys Asp Gly Asp
 785 790 795 800
 Arg Glu Val Glu Glu Glu Met Lys Lys His Glu Ser Asn Asn Val Gly
 805 810 815
 Leu Leu Glu Asn Leu Thr Asn Gly Val Thr Ala Gly Asn Gly Asp Asn
 820 825 830
 Gly Leu Ile Pro Gln Arg Lys Ser Arg Thr Pro Glu Asn Gln Gln Phe
 835 840 845
 Pro Asp Asn Glu Ser Glu Glu Tyr His Arg Ile Cys Glu Leu Val Ser
 850 855 860
 Asp Tyr Lys Glu Lys Gln Met Pro Lys Tyr Ser Ser Glu Asn Ser Asn
 865 870 875 880
 Pro Glu Gln Asp Leu Lys Leu Thr Ser Glu Glu Ser Gln Arg Leu
 885 890 895
 Glu Gly Ser Glu Asn Gly Gln Pro Glu Leu Glu Asn Phe Met Ala Ile
 900 905 910
 Glu Glu Met Lys Lys His Gly Ser Thr His Val Gly Phe Pro Glu Asn
 915 920 925
 Leu Thr Asn Gly Ala Thr Ala Gly Asn Gly Asp Asp Gly Leu Ile Pro
 930 935 940
 Pro Arg Lys Ser Arg Thr Pro Glu Ser Gln Gln Phe Pro Asp Thr Glu
 945 950 955 960
 Asn Glu Glu Tyr His Ser Asp Glu Gln Asn Asp Thr Gln Lys Gln Phe
 965 970 975
 Cys Glu Glu Gln Asn Thr Gly Ile Leu His Asp Glu Ile Leu Ile His
 980 985 990
 Glu Glu Lys Gln Ile Glu Val Val Glu Lys Met Asn Ser Glu Leu Ser
 995 1000 1005
 Leu Ser Cys Lys Lys Glu Lys Asp Ile Leu His Glu Asn Ser Thr Leu
 1010 1015 1020
 Arg Glu Glu Ile Ala Met Leu Arg Leu Glu Leu Asp Thr Met Lys His
 1025 1030 1035 1040
 Gln Ser Gln Leu Pro Arg Thr His Met Val Val Glu Val Asp Ser Met
 1045 1050 1055
 Pro Ala Ala Ser Ser Val Lys Lys Pro Phe Gly Leu Arg Ser Lys Met
 1060 1065 1070
 Gly Lys Trp Cys Cys Arg Cys Phe Pro Cys Cys Arg Glu Ser Gly Lys
 1075 1080 1085
 Ser Asn Val Gly Thr Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr
 1090 1095 1100
 Leu Arg Ser Lys Met Gly Lys Trp Cys Arg His Cys Phe Pro Cys Cys
 1105 1110 1115 1120
 Arg Gly Ser Gly Lys Ser Asn Val Gly Ala Ser Gly Asp His Asp Asp
 1125 1130 1135
 Ser Ala Met Lys Thr Leu Arg Asn Lys Met Gly Lys Trp Cys Cys His
 1140 1145 1150
 Cys Phe Pro Cys Cys Arg Gly Ser Gly Lys Ser Lys Val Gly Ala Trp
 1155 1160 1165
 Gly Asp Tyr Asp Asp Ser Ala Phe Met Glu Pro Arg Tyr His Val Arg
 1170 1175 1180
 Gly Glu Asp Leu Asp Lys Leu His Arg Ala Ala Trp Trp Gly Lys Val
 1185 1190 1195 1200
 Pro Arg Lys Asp Leu Ile Val Met Leu Arg Asp Thr Asp Val Asn Lys
 1205 1210 1215

Lys Asp Lys Gln Lys Arg Thr Ala Leu His Leu Ala Ser Ala Asn Gly
 1220 1225 1230
 Asn Ser Glu Val Val Lys Leu Leu Asp Arg Arg Cys Gln Leu Asn
 1235 1240 1245
 Val Leu Asp Asn Lys Lys Arg Thr Ala Leu Ile Lys Ala Val Gln Cys
 1250 1255 1260
 Gln Glu Asp Glu Cys Ala Leu Met Leu Leu Glu His Gly Thr Asp Pro
 1265 1270 1275 1280
 Asn Ile Pro Asp Glu Tyr Gly Asn Thr Thr Leu His Tyr Ala Ile Tyr
 1285 1290 1295
 Asn Glu Asp Lys Leu Met Ala Lys Ala Leu Leu Leu Tyr Gly Ala Asp
 1300 1305 1310
 Ile Glu Ser Lys Asn Lys His Gly Leu Thr Pro Leu Leu Leu Gly Val
 1315 1320 1325
 His Glu Gln Lys Gln Gln Val Val Lys Phe Leu Ile Lys Lys Lys Ala
 1330 1335 1340
 Asn Leu Asn Ala Leu Asp Arg Tyr Gly Arg Thr Ala Leu Ile Leu Ala
 1345 1350 1355 1360
 Val Cys Cys Gly Ser Ala Ser Ile Val Ser Leu Leu Leu Glu Gln Asn
 1365 1370 1375
 Ile Asp Val Ser Ser Gln Asp Leu Ser Gly Gln Thr Ala Arg Glu Tyr
 1380 1385 1390
 Ala Val Ser Ser His His His Val Ile Cys Gln Leu Leu Ser Asp Tyr
 1395 1400 1405
 Lys Glu Lys Gln Met Leu Lys Ile Ser Ser Glu Asn Ser Asn Pro Glu
 1410 1415 1420
 Gln Asp Leu Lys Leu Thr Ser Glu Glu Glu Ser Gln Arg Phe Lys Gly
 1425 1430 1435 1440
 Ser Glu Asn Ser Gln Pro Glu Lys Met Ser Gln Glu Pro Glu Ile Asn
 1445 1450 1455
 Lys Asp Gly Asp Arg Glu Val Glu Glu Glu Met Lys Lys His Glu Ser
 1460 1465 1470
 Asn Asn Val Gly Leu Leu Glu Asn Leu Thr Asn Gly Val Thr Ala Gly
 1475 1480 1485
 Asn Gly Asp Asn Gly Leu Ile Pro Gln Arg Lys Ser Arg Thr Pro Glu
 1490 1495 1500
 Asn Gln Gln Phe Pro Asp Asn Glu Ser Glu Glu Tyr His Arg Ile Cys
 1505 1510 1515 1520
 Glu Leu Val Ser Asp Tyr Lys Glu Lys Gln Met Pro Lys Tyr Ser Ser
 1525 1530 1535
 Glu Asn Ser Asn Pro Glu Gln Asp Leu Lys Leu Thr Ser Glu Glu Glu
 1540 1545 1550
 Ser Gln Arg Leu Glu Gly Ser Glu Asn Gly Gln Pro Glu Lys Arg Ser
 1555 1560 1565
 Gln Glu Pro Glu Ile Asn Lys Asp Gly Asp Arg Glu Leu Glu Asn Phe
 1570 1575 1580
 Met Ala Ile Glu Glu Met Lys Lys His Gly Ser Thr His Val Gly Phe
 1585 1590 1595 1600
 Pro Glu Asn Leu Thr Asn Gly Ala Thr Ala Gly Asn Gly Asp Asp Gly
 1605 1610 1615
 Leu Ile Pro Pro Arg Lys Ser Arg Thr Pro Glu Ser Gln Gln Phe Pro
 1620 1625 1630
 Asp Thr Glu Asn Glu Glu Tyr His Ser Asp Glu Gln Asn Asp Thr Gln
 1635 1640 1645
 Lys Gln Phe Cys Glu Glu Gln Asn Thr Gly Ile Leu His Asp Glu Ile
 1650 1655 1660
 Leu Ile His Glu Glu Lys Gln Ile Glu Val Val Glu Lys Met Asn Ser
 1665 1670 1675 1680

Glu Leu Ser Leu Ser Cys Lys Lys Glu Lys Asp Ile Leu His Glu Asn
 1685 1690 1695
 Ser Thr Leu Arg Glu Glu Ile Ala Met Leu Arg Leu Glu Leu Asp Thr
 1700 1705 1710
 Met Lys His Gln Ser Gln Leu
 1715

<210> 379
 <211> 656
 <212> PRT
 <213> Homo sapien

<400> 379
 Met Val Val Glu Val Asp Ser Met Pro Ala Ala Ser Ser Val Lys Lys
 1 5 10 15
 Pro Phe Gly Leu Arg Ser Lys Met Gly Lys Trp Cys Cys Arg Cys Phe
 20 25 30
 Pro Cys Cys Arg Glu Ser Gly Lys Ser Asn Val Gly Thr Ser Gly Asp
 35 40 45
 His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys Met Gly Lys Trp
 50 55 60
 Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Val
 65 70 75 80
 Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Asn
 85 90 95
 Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys Cys Arg Gly Ser
 100 105 110
 Gly Lys Ser Lys Val Gly Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe
 115 120 125
 Met Glu Pro Arg Tyr His Val Arg Gly Glu Asp Leu Asp Lys Leu His
 130 135 140
 Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met
 145 150 155 160
 Leu Arg Asp Thr Asp Val Asn Lys Lys Asp Lys Gln Lys Arg Thr Ala
 165 170 175
 Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val Val Lys Leu Leu
 180 185 190
 Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr
 195 200 205
 Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met
 210 215 220
 Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn
 225 230 235 240
 Thr Thr Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys Leu Met Ala Lys
 245 250 255
 Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly
 260 265 270
 Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys Gln Gln Val Val
 275 280 285
 Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr
 290 295 300
 Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile
 305 310 315 320
 Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser Ser Gln Asp Leu
 325 330 335
 Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser His His His Val
 340 345 350
 Ile Cys Gln Leu Leu Ser Asp Tyr Lys Glu Lys Gln Met Leu Lys Ile

355	360	365
Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp Leu Lys Leu Thr Ser Glu		
370	375	380
Glu Glu Ser Gln Arg Phe Lys Gly Ser Glu Asn Ser Gln Pro Glu Lys		
385	390	395
Met Ser Gln Glu Pro Glu Ile Asn Lys Asp Gly Asp Arg Glu Val Glu		
405	410	415
Glu Glu Met Lys Lys His Glu Ser Asn Asn Val Gly Leu Leu Glu Asn		
420	425	430
Leu Thr Asn Gly Val Thr Ala Gly Asn Gly Asp Asn Gly Leu Ile Pro		
435	440	445
Gln Arg Lys Ser Arg Thr Pro Glu Asn Gln Gln Phe Pro Asp Asn Glu		
450	455	460
Ser Glu Glu Tyr His Arg Ile Cys Glu Leu Val Ser Asp Tyr Lys Glu		
465	470	475
Lys Gln Met Pro Lys Tyr Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp		
485	490	495
Leu Lys Leu Thr Ser Glu Glu Glu Ser Gln Arg Leu Glu Gly Ser Glu		
500	505	510
Asn Gly Gln Pro Glu Leu Glu Asn Phe Met Ala Ile Glu Glu Met Lys		
515	520	525
Lys His Gly Ser Thr His Val Gly Phe Pro Glu Asn Leu Thr Asn Gly		
530	535	540
Ala Thr Ala Gly Asn Gly Asp Asp Gly Leu Ile Pro Pro Arg Lys Ser		
545	550	555
Arg Thr Pro Glu Ser Gln Gln Phe Pro Asp Thr Glu Asn Glu Glu Tyr		
565	570	575
His Ser Asp Glu Gln Asn Asp Thr Gln Lys Gln Phe Cys Glu Glu Gln		
580	585	590
Asn Thr Gly Ile Leu His Asp Glu Ile Leu Ile His Glu Glu Lys Gln		
595	600	605
Ile Glu Val Val Glu Lys Met Asn Ser Glu Leu Ser Leu Ser Cys Lys		
610	615	620
Lys Glu Lys Asp Ile Leu His Glu Asn Ser Thr Leu Arg Glu Glu Ile		
625	630	635
Ala Met Leu Arg Leu Glu Leu Asp Thr Met Lys His Gln Ser Gln Leu		
645	650	655

<210> 380

<211> 671

<212> PRT

<213> Homo sapien

<400> 380

Met Val Val Glu Val Asp Ser Met Pro Ala Ala Ser Ser Val Lys Lys	
1	5
Pro Phe Gly Leu Arg Ser Lys Met Gly Lys Trp Cys Cys Arg Cys Phe	
20	25
Pro Cys Cys Arg Glu Ser Gly Lys Ser Asn Val Gly Thr Ser Gly Asp	
35	40
His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys Met Gly Lys Trp	
50	55
Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Val	
65	70
Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Asn	
85	90
Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys Cys Arg Gly Ser	
100	105
	110

Gly Lys Ser Lys Val Gly Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe
 115 120 125
 Met Glu Pro Arg Tyr His Val Arg Gly Glu Asp Leu Asp Lys Leu His
 130 135 140
 Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met
 145 150 155 160
 Leu Arg Asp Thr Asp Val Asn Lys Lys Asp Lys Gln Lys Arg Thr Ala
 165 170 175
 Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val Val Lys Leu Leu
 180 185 190
 Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr
 195 200 205
 Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met
 210 215 220
 Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn
 225 230 235 240
 Thr Thr Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys Leu Met Ala Lys
 245 250 255
 Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly
 260 265 270
 Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys Gln Gln Val Val
 275 280 285
 Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr
 290 295 300
 Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile
 305 310 315 320
 Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser Ser Gln Asp Leu
 325 330 335
 Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser His His His Val
 340 345 350
 Ile Cys Gln Leu Leu Ser Asp Tyr Lys Glu Lys Gln Met Leu Lys Ile
 355 360 365
 Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp Leu Lys Leu Thr Ser Glu
 370 375 380
 Glu Glu Ser Gln Arg Phe Lys Gly Ser Glu Asn Ser Gln Pro Glu Lys
 385 390 395 400
 Met Ser Gln Glu Pro Glu Ile Asn Lys Asp Gly Asp Arg Glu Val Glu
 405 410 415
 Glu Glu Met Lys Lys His Glu Ser Asn Asn Val Gly Leu Leu Glu Asn
 420 425 430
 Leu Thr Asn Gly Val Thr Ala Gly Asn Gly Asp Asn Gly Leu Ile Pro
 435 440 445
 Gln Arg Lys Ser Arg Thr Pro Glu Asn Gln Gln Phe Pro Asp Asn Glu
 450 455 460
 Ser Glu Glu Tyr His Arg Ile Cys Glu Leu Val Ser Asp Tyr Lys Glu
 465 470 475 480
 Lys Gln Met Pro Lys Tyr Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp
 485 490 495
 Leu Lys Leu Thr Ser Glu Glu Glu Ser Gln Arg Leu Glu Gly Ser Glu
 500 505 510
 Asn Gly Gln Pro Glu Lys Arg Ser Gln Glu Pro Glu Ile Asn Lys Asp
 515 520 525
 Gly Asp Arg Glu Leu Glu Asn Phe Met Ala Ile Glu Glu Met Lys Lys
 530 535 540
 His Gly Ser Thr His Val Gly Phe Pro Glu Asn Leu Thr Asn Gly Ala
 545 550 555 560
 Thr Ala Gly Asn Gly Asp Asp Gly Leu Ile Pro Pro Arg Lys Ser Arg
 565 570 575

Thr Pro Glu Ser Gln Gln Phe Pro Asp Thr Glu Asn Glu Glu Tyr His
 580 585 590
 Ser Asp Glu Gln Asn Asp Thr Gln Lys Gln Phe Cys Glu Glu Gln Asn
 595 600 605
 Thr Gly Ile Leu His Asp Glu Ile Leu Ile His Glu Glu Lys Gln Ile
 610 615 620
 Glu Val Val Glu Lys Met Asn Ser Glu Leu Ser Leu Ser Cys Lys Lys
 625 630 635 640
 Glu Lys Asp Ile Leu His Glu Asn Ser Thr Leu Arg Glu Glu Ile Ala
 645 650 655
 Met Leu Arg Leu Glu Leu Asp Thr Met Lys His Gln Ser Gln Leu
 660 665 670

<210> 381
 <211> 251
 <212> DNA
 <213> Homo sapien

<400> 381
 ggagaagcgt ctgctggggc aggaaggggt ttccctgccc tctcacctgt ccctcaccaa 60
 ggtaacatgc ttcccctaag ggtatcccaa ccagggggcc tcaccatgac ctctgagggg 120
 ccaatatccc aggagaagca ttggggaggt gggggcaggt gaaggacca ggactcacac 180
 atctggggcc tccaaggcag aggagaggggt cctcaagaag gtcaggagga aaatccgtaa 240
 caagcagtca g 251

<210> 382
 <211> 3279
 <212> DNA
 <213> Homo sapiens

<400> 382
 ctctctgcag ccccatgct ggtgaggggc acggggcagga acagtggacc caacatggaa 60
 atgctggagg gtgtcaggaa gtgatcgggc tctggggcag ggaggagggg tggggagtg 120
 cactgggagg ggacatcctg cagaaggtag gaggtagcaa acacccgctg caggggaggg 180
 gagagccctg cggcacctgg gggagcagag ggagcagcac ctgcccaggc ctgggaggag 240
 gggcctggag ggcgtgagga ggagcgaggg ggtcgcattg ctggagtgag ggatcagggg 300
 cagggcgcgga gatggcctca cacaggggaag agagggcccc tctgcaggg cctcacctgg 360
 gccacaggag gacactgctt ttctcttgag gaggcaggag ctgtggatgg tgctggacag 420
 aagaaggaca gggcctggct caggtgtcca gaggtgtcg ctggcttccc ttggggatca 480
 gactgcaggg agggagggcg gcagggttgg ggggggagtg acgatgagga tgacctgggg 540
 gtggctccag gccttgcccc tgcttgggcc ctacccagc ctccctcaca gtctcctggc 600
 cctcagtctc tccccccac tccatcctcc atctggcctc agtgggtcat tctgatcact 660
 gaactgacca taccagccc tgcccacggc cctccatggc tccccaatgc cctggagagg 720
 ggacatctag tcagagagta gtccatgaaga ggtggcctct gcgatgtgcc tgtgggggca 780
 gcatcctgca gatggtcccg gccctcatcc tgtgcacctg tctgcaggga ctgtcctcct 840
 ggaccttgcc ccttggtcag gactgggacc ctgaagtccc ctccccatag gccaagactg 900
 gaggcttgtt ccctctgttg gactccctgc ccatattctt gtgggagtg gttctggaga 960
 catttctgtc tgttcttgag agctgggaat tgcctcagc catctgcctg cgcggttctg 1020
 agagatggag ttgcctaggc agttattggg gccaatcttt ctactgtgt ctctcctcct 1080
 ttacccttag ggtgattctg ggggtocact tgtctgtaat ggtgtgcttc aaggtatcac 1140
 atcatggggc cctgagccat gtgcctgcc tgaagaagcct gctgtgtaca ccaaggtggt 1200
 gcattaccgg aagtggatca aggacaccat cgcagccaac ccctgagtg ccctgtccca 1260
 cccctacctc tagtaaatat aagtccacct cacgttctgg catcacttgg cctttctgga 1320
 tgctggacac ctgaagcttg gaactcacct gcccgagct cgagcctcct gactcctact 1380
 gacctgtgct ttctggtgtg gattccaggg ctgctaggaa aaggaatggg cagacacagg 1440
 tgtatgccaa tgtttctgaa atgggtataa ttctgcctc tccttcggaa cactggctgt 1500
 ctctgaagac ttctcgtca gtttcagtga ggacacacac aaagacgtgg gtgacctagt 1560
 tgtttgtggg gtgcagagat gggaggggtg gggccaccc tggagagagt gacagtgaca 1620

```

caaggtggac actctctaca gatcactgag gataagctgg agccacaatg catgaggcac 1680
acacacagca aggttgacgc tgtaaacata gccacgctg tcctgggggc actgggaagc 1740
ctagataagg ccgtgagcag aaagaagggg aggatcctcc tatgttggtg aaggagggac 1800
tagggggaga aactgaaagc tgattaatta caggagggtt gttaggtcc cccaaaccac 1860
cgtcagattt gatgatttcc tagcaggact tacagaaata aagagctatc atgctgtggt 1920
ttattatggt ttgttacatt gataggatac atactgaaat cagcaaaca aacagatgta 1980
tagattagag tgtggagaaa acagagggaaa acttgcagtt acgaagactg gcaacttggc 2040
tttactaagt tttcagactg gcaggaagtc aaacctatta ggctgaggac cttgtggagt 2100
gtagctgatc cagctgatag aggaactagc caggtggggg cctttccctt tggatggggg 2160
gcatatccga cagttattct ctccaagtgg agacttacgg acagcatata attctccctg 2220
caaggatgta tgataatatg tacaagtaaa ttccaactga ggaagctcac ctgatcctta 2280
gtgtccaggg tttttactgg gggctctgtag gacgagtatg gagtacttga ataattgacc 2340
tgaagtcctc agacctgagg ttccctagag ttcaaacaga tacagcatgg tccagagtcc 2400
cagatgtaca aaaacaggga ttcacacaa atcccatctt tagcatgaag ggtctggcat 2460
ggccaaggc cccaagtata tcaaggcact tgggcagaac atgccaagga atcaaagtgc 2520
atctcccagg agttattcaa gggtagagccc tttacttggg atgtacaggc tttgagcagt 2580
gcagggtgc tgagtcaacc ttttattgta caggggatga gggaaaggga gaggatgagg 2640
aagccccctt ggggatttgg tttggtcttg tgatcaggtg gtctatgggg ctatccctac 2700
aaagaagaat ccagaaatag gggcacattg aggaatgata ctgagcccaa agagcattca 2760
atcattgttt tatttgcctt cttttcacac cattggtgag ggagggatta ccaccctggg 2820
gttatgaaga tggttgaaca cccacacat agcacoggag atatgagatc aacagtttct 2880
tagccataga gattcacagc ccagagcagg aggacgctgc acaccatgca ggatgacatg 2940
ggggatgcgc tcgggatttg tgtgaagaag caaggactgt tagaggcagg ctttatagta 3000
acaagacggt ggggcaaact ctgatttccg tgggggaatg tcatggtctt gctttactaa 3060
gttttgagac tggcaggtag tgaaactcat taggctgaga accttgtgga atgcagctga 3120
cccagctgat agaggaagta gccaggtggg agcctttccc agtgggtgtg ggacatatct 3180
ggcaagattt tgtggcactc ctggttacag atactggggc agcaaataaa actgaatctt 3240
gttttcagac cttaaaaaaa aaaaaaaaaa aaaagtitt 3279

```

<210> 383

<211> 154

<212> PRT

<213> Homo sapiens

<400> 383

```

Met Ala Gly Val Arg Asp Gln Gly Gln Gly Ala Arg Trp Pro His Thr
          5                      10                      15

```

```

Gly Lys Arg Gly Pro Leu Leu Gln Gly Leu Thr Trp Ala Thr Gly Gly
          20                      25                      30

```

```

His Cys Phe Ser Ser Glu Glu Ser Gly Ala Val Asp Gly Ala Gly Gln
          35                      40                      45

```

```

Lys Lys Asp Arg Ala Trp Leu Arg Cys Pro Glu Ala Val Ala Gly Phe
          50                      55                      60

```

```

Pro Leu Gly Ser Asp Cys Arg Glu Gly Gly Arg Gln Gly Cys Gly Gly
          65                      70                      75                      80

```

```

Ser Asp Asp Glu Asp Asp Leu Gly Val Ala Pro Gly Leu Ala Pro Ala
          85                      90                      95

```

```

Trp Ala Leu Thr Gln Pro Pro Ser Gln Ser Pro Gly Pro Gln Ser Leu
          100                     105                     110

```

```

Pro Ser Thr Pro Ser Ser Ile Trp Pro Gln Trp Val Ile Leu Ile Thr
          115                     120                     125

```

Glu Leu Thr Ile Pro Ser Pro Ala His Gly Pro Pro Trp Leu Pro Asn
 130 135 140

Ala Leu Glu Arg Gly His Leu Val Arg Glu
 145 150

<210> 384

<211> 557

<212> DNA

<213> Homo sapiens

<400> 384

```

ggatcctcta gagcgccgc ctactactac taaattcgcg gccgcgtcga cgaagaagag 60
aaagatgtgt tttgttttg actctctgtg gtcccttcca atgctgtggg tttccaacca 120
ggggaagggt cccttttgca ttgccaagtg ccataacat gagcactact ctaccatggt 180
tctgcctcct ggccaagcag gctggtttg aagaatgaaa tgaatgattc tacagctagg 240
acttaacctt gaaatggaaa gtcttgcaat cccatttgca ggatccgtct gtgcacatgc 300
ctctgtagag agcagcattc ccagggacct tggaaacagt tggcactgta aggtgcttgc 360
tccccaagac acatcctaaa aggtgttgta atggtgaaaa cgtcttcctt ctttattgcc 420
ccttcttatt tatgtgaaca actgtttgtc tttttttgta tcttttttaa actgtaaaag 480
tcaattgtga aaatgaatat catgcaata aattatgcga ttttttttcc aaagtaaaaa 540
aaaaaaaaa aaaaaaa 557

```

<210> 385

<211> 337

<212> DNA

<213> Homo sapiens

<400> 385

```

ttcccagggt atgtgcgagg gaagacacat ttactatcct tgatggggct gattccttta 60
gtttctctag cagcagatgg gttaggagga agtgaccaa gtggttgact cctatgtgca 120
tctcaaagcc atctgtgtc ttcgagtacg gacacatcat cactcctgca ttgttgatca 180
aaacgtggag gtgcttttcc tcagctaaga agcccttagc aaaagctcga atagacttag 240
tatcagacag gtccagtttc cgcaccaaca cctgtgggtt ccctgtcgtg gtctggatct 300
ctttggccac caattcccc tttccacat cccgca 337

```

<210> 386

<211> 300

<212> DNA

<213> Homo sapiens

<400> 386

```

gggcccgccta cggccccagg cccgcctcg cgagtcctcc tccccgggtg cctgcccga 60
gcccgtcgg cccagaggggt gggcggggg ctgcctctac cggctggcgg ctgtaactca 120
gcgaccttgg cccgaaggct ctagcaagga cccaccgacc ccagccgagg cggcggcggc 180
gcggaacttg cccggtgtgt ggggcggagc ggactgcgtg tccgcggacg ggcagcgaag 240
atgttagcct tcgctgccag gaccgtggac cgatcccagg gctgtggtgt aacctcagcc 300

```

<210> 387

<211> 537

<212> DNA

<213> Homo sapiens

<400> 387

```

gggccgagtc gggcaccaag ggactctttg caggcttctt tcctcggatc atcaaggctg 60
ccccctcctg tgccatcatg atcagacct atgagttcgg caaaagcttc ttccagaggc 120

```

```

tgaaccagga ccggttctg ggcggctgaa aggggcaagg aggcaaggac cccgtctctc 180
ccacggatgg ggagagggca ggaggagacc cagccaagtg ccttttctc agcactgagg 240
gagggggctt gtttcccttc cctcccggcg acaagctcca gggcagggct gtccctctgg 300
gcggcccagc acttcctcag acacaacttc ttctgctgc tccagtcgtg gggatcatca 360
cttaccaccc cccaagttc aagaccaa atctccagctg ccccttcgt gtttccctgt 420
gtttgctgta gctgggcatg tctccaggaa ccaagaagcc ctgagcctgg tgtagtctcc 480
ctgacccttg ttaattcctt aagtctaaag atgatgaact tcaaaaaaaa aaaaaa 537

```

<210> 388

<211> 520

<212> DNA

<213> Homo sapiens

<400> 388

```

aggataatTT ttaaaccaat caaatgaaaa aaacaaacaa acaaaaaagg aaatgtcatg 60
tgaggTTaaa ccagtttTgca ttccccta atgtgaaaaag taagaggact actcagcact 120
gtttgaagat tgctcttTct acagcttTct agaattTgtt tatttTcactt gccaagtTgaa 180
ggacccccct cccaacatgc cccagcccac ccctaagcat ggtccctTgt caccaggTcaa 240
ccaggaaaact gctactTgtg gacctcacca gagaccagga gggttTgtt agctcacagg 300
acttccccca cccagaaga ttagcatccc atactagact catactcaac tcaactaggc 360
tcatactcaa ttgatggTta ttagacaatt ccatttcttt ctggttatta taaacagaaa 420
atctttctct ttctcattac cagtaaaggc tcttggtatc tttctgtTgg aatgattTct 480
atgaactTgt cttattttta tggTgggtt ttttctgtt 520

```

<210> 389

<211> 365

<212> DNA

<213> Homo sapiens

<400> 389

```

cgTTgcccc gtttgacaga aggaaaggcg gagcttattc aaagtctaga gggagtggag 60
gagTTaaggc tggatttTcag atctgctTg ttccagccgc agtTgtccct ctgctcccc 120
aacgactTtc caaataatct caccagegcc ttccagctca ggcgtcctag aagcgtcttg 180
aagcctatgg ccagctgtct ttgtgttccc tctcaccgc ctgtcctcac agctgagact 240
cccaggaaac cttcagacta ccttctctg ccttcagcaa ggggcgtTgc ccacattctc 300
tgagggtcag tggagaacc tagactccca ttgctagagg tagaaagggg aagggtgctg 360
gggag 365

```

<210> 390

<211> 221

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(221)

<223> n = A,T,C or G

<400> 390

```

tgctctcca tcctggcccc gacttctctg tcaggaaagt ggggatggac cccatctgca 60
tacacgntt ctcattgggtg tggacatct ctgcttgcgg ttccaggaag gcctctggct 120
gctctangag tctgancnga ntcgttgccc cantntgaca naaggaaagg cggagcttat 180
tcaaagtcta gagggagtgg aggagttaag gctggatttc a 221

```

<210> 391

<211> 325

<212> DNA

<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(325)
<223> n = A,T,C or G

<400> 391
tggagcaggt cccgaggcct ccctagagcc tggggccgac tctgtgncga tgcangcttt 60
ctctcgcgcc cagcctggag ctgctcctgg catctaccaa caatcagncg aggcgagcag 120
tagccagggc actgctgcca acagccagtc cnnataccat catgtnaccc ggtgngctct 180
naantngat ntccanagcc ctacccatcn tagttctgct ctcccaccgg ntaccagccc 240
cactgcccag gaatcctaca gccagtaccc tgtcccgacg tctctaccta ccagtacgat 300
gagacctccg gctactacta tgacc 325

<210> 392
<211> 277
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(277)
<223> n = A,T,C or G

<400> 392
atattgttta actccttcct ttatatcttt taacattttc atggngaaaag gttcacatct 60
agtctcactt nggcnagnn ctccacttg agtctcttcc ccggcctggn ccagtngnaa 120
antaccanga accgncatgn cttaanaacn ncttggttn tgggttnntc aatgactgca 180
tgacgtgcac caccctgtcc actacgtgat gctgtaggat taaagtctca cagtgggcgg 240
ctgaggatac agcgccgcgt cctgtgttgc tggggaa 277

<210> 393
<211> 566
<212> DNA
<213> Homo sapiens

<400> 393
actagtccag tgtggtggaa ttcgcgcccg cgtcgacgga caggtcagct gtctggctca 60
gtgatctaca ttctgaagtt gtctgaaaat gtcttcatga ttaaattcag cctaaacggt 120
ttgccgggaa cactgcagag acaatgctgt gagtttccaa ccttagccca tctgcgggca 180
gagaaggctct agtttgtcca tcagcattat catgatatca ggactggta cttggttaag 240
gaggggtcta ggagatctgt cccttttaga gacaccttac ttataatgaa gtatttgga 300
gggtgggttt caaaagtaga aatgtcctgt attccgatga tcatcctgta aacattttat 360
catttattaa tcatccctgc ctgtgtctat tattatattc atatctctac gctggaaact 420
ttctgcctca atgtttactg tgcctttggt tttgctagtt tgtgttggtg aaaaaaaaaa 480
cattctctgc ctgagtttta atttttgtcc aaagttattt taatctatac aattaaaagc 540
ttttgcctat caaaaaaaaa aaaaaa 566

<210> 394
<211> 384
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(384)
<223> n = A,T,C or G

<400> 394

```

gaacatacat gtcccgccac ctgagctgca gtctgacatc atcgccatca cgggcctcgc 60
tgcaaatng gaccgggcca aggctggact gctggagcgt gtgaaggagc tacaggccna 120
gcaggaggac cgggctttaa ggagttttaa gctgagtgtc actgtagacc ccaaatacca 180
tcccaagatt atcgggagaa agggggcagt aattacccaa atccggttgg agcatgacgt 240
gaacatccag tttcctgata aggacgatgg gaaccagccc caggaccaa ttaccatcac 300
agggtacgaa aagaacacag aagctgccag ggatgctata ctgagaattg tgggtgaact 360
tgagcagatg gtttctgagg acgt 384

```

<210> 395

<211> 399

<212> DNA

<213> Homo sapiens

<400> 395

```

ggcaaaactg tgtgacctca ataagacctc gcagatccaa ggtcaagtat cagaagtgc 60
tctgaccttg gactccaaga cctacatcaa cagcctggct atattagatg atgagccagt 120
tatcagaggt ttcatcattg cggaaattgt ggagtctaag gaaatcatgg cctctgaagt 180
attcagctct ttcagttacc ctgagttctc tatagagttg cctaacacag gcagaattgg 240
ccagctactt gtctgcaatt gtatcttcaa gaataacctg gccatccctt tgactgacgt 300
caagttctct ttgaaagcc tgggcatctc ctactacag acctctgacc atgggacggt 360
gcagcctggt gagaccatcc aatcccaaat aaaatgcac 399

```

<210> 396

<211> 403

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(403)

<223> n = A,T,C or G

<400> 396

```

tggagtntc agtgcaaca agccataaag cttcagtagc aaattactgt ctcacagaaa 60
gacattttca acttctgctc cagctgctga taaaacaaat catgtgttta gcttgactcc 120
agacaaggac aacctgttcc ttcataactc tctagagaaa aaaaggagtt gttagtagat 180
actaaaaaaa gtggatgaat aatctggata tttttcctaa aaagattcct tgaaacacat 240
taggaaaatg gagggcctta tgatcagaat gctagaatta gtccattgtg ctgaagcagg 300
gtttagggga gggagtggag gataaaagaa ggaaaaaag aagagtgaga aaacctattt 360
atcaaagcag gtgctatcac tcaatgtag gcctgctct ttt 403

```

<210> 397

<211> 100

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(100)

<223> n = A,T,C or G

<400> 397

```

actagtncag tgtggtgga ttcgcggccg cgtcgacctc naanccatct ctatagcaaa 60
tccatccccg ctctggttg gtnacagaat gactgacaaa 100

```

<210> 398

<211> 278

<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(278)
<223> n = A,T,C or G

<400> 398
gcggccgcgt cgacagcagt tccgccagcg ctccgccctg ggtggggatg tgctgcacgc 60
ccacctggac atctggaagt cagcggcctg gatgaaagag cggacttcac ctggggcgat 120
tcactactgt gcctcgacca gtgaggagag ctggaccgac agcgagggtg actcatcatg 180
ctccgggcag cccatccacc tgtggcagtt cctcaaggag ttgctactca agccccacag 240
ctatggccgc ttcattangt ggctcaacaa ggagaagg 278

<210> 399
<211> 298
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(298)
<223> n = A,T,C or G

<400> 399
acggagggtg aggaagcgnc cctgggatcg anaggatggg tcctgncatt gaccnccctn 60
gggggtgccng catggagcgc atgggcgcgg gcctgggcca cggcatggat cgcgtgggct 120
ccgagatcga gcgcattggc ctggtcatgg accgcatggg ctccgtggag cgcattgggt 180
ccggcattga gcgcattggc ccgctgggcc tcgaccacat ggcctccanc attganccga 240
tgggccagac catggagcgc attggctctg cgtgggagcn catgggtgcc ggcatggg 298

<210> 400
<211> 548
<212> DNA
<213> Homo sapiens

<400> 400
acatcaacta cttcctcatt ttaaggatg gcagttccct tcatcccctt ttctgcctt 60
gtacatgtac atgtatgaaa ttctcttctc ttaccgaact ctctccacac atcacaagg 120
caaagaacca cagccttaga agggtaagag ggcaccctat gaaatgaaat ggtgatttct 180
tgagtctctt ttttccacgt ttaaggggcc atggcaggac ttagagttgc gagttaagac 240
tgcagagggc tagagaatta ttcatatag gctttgaggc caccatgtc acttatccc 300
tataccctct caccatcccc ttgtctactc tgatgcccc aagatgcaac tgggcagcta 360
gttggcccca taattctggg cctttgttgt ttgttttaat tacttgggca tcccaggaag 420
ctttccagt atctcctacc atgggcccc ctccctggat caagccctc ccaggccctg 480
tccccagccc ctccctgccc agcccaaccg cttgccttgg tgctcagccc tccattggg 540
agcaggtt 548

<210> 401
<211> 355
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(355)
<223> n = A,T,C or G

<400> 401
 actgtttcca tggtatgttt ctacacattg ctacctcagt gtccttgaa acttagcttt 60
 tgatgtctcc aagtagtcca ccttcattta actctttgaa actgtatcat ctttgccaag 120
 taagagtggg ggctatttc agctgctttg acaaaatgac tggctcctga cttaacgttc 180
 tataaatgaa tgtgctgaag caaagtgtcc atgggtggcg cgaagaagan aaagatgtgt 240
 tttgttttgg actctctgtg gtcccttcca atgctgnggg tttccaacca ggggaagggt 300
 cccttttgca ttgccaagtg ccataaccat gagcactact ctaccatggn tctgc 355

<210> 402
 <211> 407
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(407)
 <223> n = A,T,C or G

<400> 402
 atggggcaag ctggataaag aaccaagacc cactggagta tgctgtcttc aagaaaccca 60
 tctcacatgc ggtggcatac ataggctcaa aataaaggaa tggagaaaaa tatttcaagc 120
 aaatggaaaa cagaaaaaag cagggtgttg actcctactt tctgacaaaa cagactatgc 180
 gaataaagat aaaaaagaga aggacattac aaagggtggtc ctgacctttg ataaatctca 240
 ttgcttgata ccaacctggg ctgttttaat tgcccaaacc aaaaggataa tttgctgagg 300
 ttgtggagct tctccctgc agagagtccc tgatctocca aaatttggtt gagatgtaag 360
 gntgattttg ctgacaactc cttttctgaa gttttactca tttccaa 407

<210> 403
 <211> 303
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(303)
 <223> n = A,T,C or G

<400> 403
 cagtatttat agccnaactg aaaagctagt agcaggcaag tctcaaattcc aggcacccaa 60
 tcctaagcaa gagccatggc atggtgaaaa tgcaaaagga gagtctggcc aatctacaaa 120
 tagagaacaa gacctactca gtcataaaca aaaaggcaga caccaacatg gatctcatgg 180
 gggattggat attgtaatta tagagcagga agatgacagt gatcgctatt tggcacaaca 240
 tcttaacaac gaccgaaacc cattatttac ataaacctcc attcggtaac catgttgaaa 300
 gga 303

<210> 404
 <211> 225
 <212> DNA
 <213> Homo sapiens

<400> 404
 aagtgtact tttaaaaatt tagtggattt tgaaaattct tagaggaaag taaaggaaaa 60
 attgttaatg cactcattta cctttacatg gtgaaagttc tctcttgatc ctacaaacag 120
 acattttcca ctggtgttcc catagttgtt aagtgtatca gatgtgttgg gcatgtgaat 180
 ctccaagtgc ctgtgtaata aataaagtat ctttatttca ttcatt 225

<210> 405

<211> 334
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(334)
<223> n = A,T,C or G

<400> 405
gagctgttat actgtgagtt ctactaggaa atcatcaaat ctgagggttg tctggaggac 60
ttcaatacac ctcccccat agtgaatcag cttccagggg gtccagtccc tctccttact 120
tcacccccat cccatgccaa aggaagaccc tccctccttg gctcacagcc ttctctaggc 180
ttcccagtg ctcaggaca gagggggta tgttttcagc tccatccttg ctgtgagtg 240
ctggtgcggt tgtgcctcca gcttctgctc agtgcttcat ggacagtgc cagcccatgt 300
cactctccac tctctcannng tggatccac ccct 334

<210> 406
<211> 216
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(216)
<223> n = A,T,C or G

<400> 406
tttcatacct aatgaggag ttganatnac atnnaaccag gaaatgcatg gatctcaang 60
gaaacaacaa cccaataaac tcggagtggc agactgacaa ctgtgagaca tgcacttgct 120
acnaaacaca aatttnatgt tgcacccttg tttctacacc tgtgggttat gacaaagaca 180
actgccaaag aatnttcaag aaggaggact gccant 216

<210> 407
<211> 413
<212> DNA
<213> Homo sapiens

<400> 407
gctgacttgc tagtatcatc tgcattcatt gaagcacaag aacttcacgc cttgactcat 60
gtaaatgcaa taggatta aaataaattt gatatcacat ggaaacagac aaaaaatatt 120
gtacaacatt gcacccagtg tcagattcta cacctggcca ctcaggaagc aagagttaat 180
cccagaggtc tatgtcctaa tgtgttatgg caaatggatg tcatgcacgt accttcattt 240
ggaaaattgt catttgtcca tgtgacagtt gatacttatt cacatttcat atgggcaacc 300
tgccagacag gagaaagtct tcccatgtta aaagacattt attatcttgt tttcctgtca 360
tgggagttcc agaaaaagtt aaaacagaca atgggccagg ttctgtagta aag 413

<210> 408
<211> 183
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(183)
<223> n = A,T,C or G

<400> 408

```
ggagctngcc ctcaattcct ccatntctat gttancatat ttaatgtctt ttgnnattaa 60
tnccttaacta gttaatcctt aaagggtan ntaatcccta actagtcctt ccattgtgag 120
cattatcctt ccagtattcn ccttctnttt tattttactcc ttcctggcta cccatgtact 180
ntt 183
```

<210> 409

<211> 250

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(250)

<223> n = A,T,C or G

<400> 409

```
cccacgcatg ataagctctt tattttctgta agtcctgcta ggaaatcatc aaatctgacg 60
gtggtttggg ggacctgaac aaacctcctg taattaatca gctttcagtt tctcccccta 120
gtccctcctt caacaacata ggaggatcct ccccttcttt ctgctcacgg ccttatctag 180
gcttcccagt gccccagga cagcgtgggc tatgtttaca gcgcntcctt gctggggggg 240
ggcctatgc 250
```

<210> 410

<211> 306

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(306)

<223> n = A,T,C or G

<400> 410

```
ggctggtttg caagaatgaa atgaatgatt ctacagctag gacttaacct tgaaatggaa 60
agtcttgcaa tcccatttgc aggatccgtc tgtgcacatg cctctgtaga gaggcagcatt 120
cccagggacc ttggaaacag ttggcactgt aaggtgcttg ctccccaaga cacatcctaa 180
aaggtgttgt aatggtgaaa accgcttcct tctttattgc cccttccttat ttatgtgaac 240
nactggttgg ctttttttgn atctttttta aactggaaag ttcaattgng aaaatgaata 300
tcntgc 306
```

<210> 411

<211> 261

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(261)

<223> n = A,T,C or G

<400> 411

```
agagatattn cttaggtnaa agttcataga gttcccatga actatatgac tggccacaca 60
ggatcttttg tatttaagga ttctgagatt ttgcttgagc aggattagat aaggctgttc 120
tttaaagtgc tgaaatggaa cagatttcaa aaaaaaaccc cacaatctag ggtgggaaca 180
aggaaggaaa gatgtgaata ggctgatggg caaaaaacca atttaccat cagttccagc 240
cttctctcaa ggngaggcaa a 261
```

<210> 412

<211> 241
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(241)
<223> n = A,T,C or G

<400> 412
gttcaatggt acctgacatt tctacaacac cccactcacc gatgtattcg ttgccagtg 60
ggaacatacc agcctgaatt tggaaaaaat aattgtgttt cttgccagc aaatactacg 120
actgactttg atggctccac aacataaacc cagtgtaaaa acagaagatg tggaggggag 180
ctgggagatt tctactggga cattgaattc ccaaactacc cangcaatta cccagccaac 240
a 241

<210> 413
<211> 231
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(231)
<223> n = A,T,C or G

<400> 413
aactcttaca atccaagtga ctcattctgtg tgettgaatc ctttccactg tctcatctcc 60
ctcatccaag tttctagtag cttctctttg ttgtgaagga taatcaaact gaacaacaaa 120
aagtttactc tctcattttg gaacctaaaa actctcttct tctgggtct gaggggtcca 180
agaatccttg aatcanttct cagatcattg gggacaccan atcaggaacc t 231

<210> 414
<211> 234
<212> DNA
<213> Homo sapiens

<400> 414
actgtccatg aagcactgag cagaagctgg aggcacaacg caccagacac tcacagcaag 60
gatggagctg aaacataaac ccactctgtc ctggaggcac tgggaagcct agagaaggct 120
gtgagccaag gagggagggt cttccttttg catgggatgg ggatgaagta aggagaggga 180
ctggaccccc tgggaagctga ttcactatgg ggggagggtg attgaagtcc tcca 234

<210> 415
<211> 217
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(217)
<223> n = A,T,C or G

<400> 415
gcataggatt aagactgagt atcttttcta cattctttta acttttctaag gggcacttct 60
caaaacacag accaggtagc aaatctccac tgctctaagg ntctcaccac cacttttctca 120
cacctagcaa tagtagaatt cagtctact tctgaggcca gaagaatggt tcagaaaaat 180
antggattat aaaaaataac aattaagaaa aataatc 217

<210> 416
 <211> 213
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(213)
 <223> n = A,T,C or G

<400> 416
 atgcataatnt aaagganact gcctcgcttt tagaagacat ctggncgtgct ctctgcatga 60
 ggcacagcag taaagctctt tgattcccag aatcaagaac tctccccttc agactattac 120
 cgaatgcaag gtggttaatt gaaggccact aattgatgct caaatagaag gatattgact 180
 atattggaac agatggagtc tctactacaa aag 213

<210> 417
 <211> 303
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(303)
 <223> n = A,T,C or G

<400> 417
 nagtcttcag gcccatcagg gaagttcaca ctggagagaa gtcatacata tgtactgtat 60
 gtgggaaagg ctttactctg agttcaaadc ttcaagccca tcagagagtc cacactggag 120
 agaagccata caaatgcaat gagtgtggga agagcttcag gagggattcc cattatcaag 180
 ttcatctagt ggtccacaca ggagagaaac cctataaatg tgagatatgt gggaagggct 240
 tcantcaaag ttcgatatctt caaatccatc ngaaggncct cagtatanan aaacctttta 300
 agt 303

<210> 418
 <211> 328
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(328)
 <223> n = A,T,C or G

<400> 418
 tttttggcgg tggtggggca gggacgggac angagtctca ctctgttgcc caggctggag 60
 tgcacaggca tgatctcggc tcaactacaac ccctgcctcc catgtccaag cgattcttgt 120
 gcctcagcct tccctgtagc tagaattaca ggcacatgcc accacacca gctagttttt 180
 gtatttttag tagagacagg gtttcacat gttggccagg ctggtctcaa actcctnacc 240
 tcagnggtca ggctgggtct aaactcctga cctcaagtga tctgcccacc tcagcctccc 300
 aaagtgtctan gattacaggc cgtgagcc 328

<210> 419
 <211> 389
 <212> DNA
 <213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(389)
<223> n = A,T,C or G

<400> 419
cctcctcaag acggcctgtg gtccgcctcc cggcaaccaa gaagcctgca gtgccatatg 60
acccctgagc catggactgg agcctgaaag gcagcgtaca ccctgtcct gatcttgctg 120
cttgtttctt ctctgtggct ccattcatag cacagttgtt gcaactgaggc ttgtgcaggc 180
cgagcaaggc caagctggct caaagagcaa ccagtcaact ctgccacggg gtgccaggca 240
ccggttctcc agccaccaac ctcaactcgt cccgcaaag gcacatcagt tcttctaccc 300
taaaggtagg accaaagggc atctgctttt ctgaagtct ctgctctatc agccatcacg 360
tggcagccac tcnggctgtg tcgacgcgg 389

<210> 420
<211> 408
<212> DNA
<213> Homo sapiens

<400> 420
gttctctcta actcctgcca gaaacagctc tcctcaacat gagagctgca cccctcctcc 60
tggccagggc agcaagcctt agccttggtt tcttgtttct gcttttttcc tggctagacc 120
gaagtgtact agccaaggag ttgaagtttg tgactttggt gtttcggcat ggagaccgaa 180
gtcccatgga cacttttccc actgacccca taaaggaatc ctcatggcca caaggatttg 240
gccaactcac ccagctgggc atggagcagc attatgaact tggagagtat ataagaaaga 300
gatatagaaa attcttgaat gagtccata aacatgaaca ggtttatatt cgaagcacag 360
acgttgaccg gactttgatg aagtgtatg acaaacctgg caagcccc 408

<210> 421
<211> 352
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(352)
<223> n = A,T,C or G

<400> 421
gtcaaaaat ctttttactg atnggcatgg ctacacaatc attgactatt acggaggcca 60
gaggagaatg aggcctggcc tgggagccct gtgcctacta naagcacatt agattatcca 120
ttcactgaca gaacagggtt tttttgggtc cttcttctcc accacnata acttgagtc 180
ctccttcttg aagattcttt ggagttgtc tttgtcataa cccacagggt tagaaacaag 240
ggtgcaacat gaaatttctg tttcgtagca agtgcagtgc tcacaagttg gcangtctgc 300
cactccgagt ttattgggtg tttgttctct ttgagatcca tgcatttctt gg 352

<210> 422
<211> 337
<212> DNA
<213> Homo sapiens

<400> 422
atgccacat gctggcaatg cagcgggcgg tcgaaggcct gcatatccag cccaagctgg 60
cgatgatcga cggcaaccgt tgcccgaagt tgccgatgcc agccgaagcg gtggtcaagg 120
gcgatagcaa ggtgccggcg atcgcggcgg cgtcaatcct ggccaaggtc agccgtgatc 180
gtgaaatggc agctgtcgaa ttgatctacc cgggttatgg catcggcggg cataagggtc 240
atccgacacc ggtgcacctg gaagccttgc agcggctggg gccgacgccg attcaccgac 300
gcttcttccg ccggtacggc tggcctatga aaattat 337

<210> 423
<211> 310
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(310)
<223> n = A,T,C or G

<400> 423
gctcaaaaat ctttttactg atatggcatg gctacacaat cattgactat tagaggccag 60
aggagaatga ggctggcctg gggagccctg tgcctactan aagcncatta gattatccat 120
tactgacag aacaggtctt ttttgggtcc ttcttctcca ccacgatata cttgcagtcc 180
tccttcttga agattctttg gcagttgtct ttgtcataac ccacaggtgt anaaacaagg 240
gtgcaacatg aaatttctgt ttcgtagcaa gtgcatgtct cacagttgtc aagtctgccc 300
tccgagttta 310

<210> 424
<211> 370
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(370)
<223> n = A,T,C or G

<400> 424
gctcaaaaat ctttttactg ataggcatgg ctacacaatc attgactatt agaggccaga 60
ggagaatgag gcctggcctg ggagccctgt gcctactaga agcacattag attatccatt 120
cactgacaga acaggtcttt tttgggtcct tcttctccac cagcatatac ttgcagtcc 180
ccttcttgaa gattcttttg cagttgtctt tgtcataacc cacaggtgta gaaacatcct 240
ggttgaatct cctggaactc cctcattag tatgaaatag catgatgcat tgcataaagt 300
cacgaaggtg gcaaagatca caacgctgcc cagganaaca ttcattgtga taagcaggac 360
tccgtcgacg 370

<210> 425
<211> 216
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(216)
<223> n = A,T,C or G

<400> 425
aattgctatn ttttattttg ccaactcaaaa taattaccaa aaaaaaaaaa tnttaaatga 60
taacaacnca acatcaaggn aaananaaca ggaatggntg actntgcata aatnggccga 120
anattatcca ttatnttaag ggttgacttc aggntacagc acacagacaa acatgcccag 180
gaggntntca ggaccgctcg atgtnttntg aggagg 216

<210> 426
<211> 596
<212> DNA
<213> Homo sapiens

<400> 426

```

cttccagtga ggataaccct gttgccccgg gccgagggtc tccattaggc tctgattgat 60
tggcagtcag tgatggaagg gtgttctgat cattccgact gccccaaggg tcgctggcca 120
gctctctgtt ttgctgagtt ggcagtagga cctaatttgt taattaagag tagatgggtga 180
gctgtccttg tattttgatt aacctaatgg ccttcccagc acgactcgga ttcagctgga 240
gacatcacgg caacttttaa tgaaatgatt tgaagggcca ttaagaggca cttcccgtaa 300
ttaggcagtt catctgcact gataacttct tggcagctga gctggtcgga gctgtggccc 360
aaacgcacac ttggcttttg gttttgagat acaactctta atcttttagt catgcttgag 420
ggtggatggc cttttcagct ttaacccaat ttgcactgcc ttggaagtgt agccaggaga 480
atacactcat atactcgtgg gcttagaggc cacagcagat gtcattggtc tactgcctga 540
gtcccgctgg tcccatccca ggaccttcca tcggcgagta cctgggagcc cgtgct 596

```

<210> 427

<211> 107

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(107)

<223> n = A,T,C or G

<400> 427

```

gaagaattca agttaggttt attcaaaggg cttacngaga atcctanacc caggncaccag 60
cccgggagca gccttanaga gtcctgttt gactgcccgg ctcagng 107

```

<210> 428

<211> 38

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(38)

<223> n = A,T,C or G

<400> 428

```

gaacttcna anaangactt tattcactat ttacatt 38

```

<210> 429

<211> 544

<212> DNA

<213> Homo sapiens

<400> 429

```

ctttgctgga cggaataaaa gtggacgcaa gcatgacctc ctgatgaggg cgctgcattt 60
attgaagagc ggctgcagcc ctgcggttca gattaaaatc cgagaattgt atagacgccg 120
atatccacga actcttgaag gactttctga tttatccaca atcaaatcat cggttttcag 180
tttggatggt ggctcatcac ctgtagaacc tgacttggcc gtggctggaa tccactcgtt 240
gccttccact tcagttacac ctcactcacc atcctctcct gttggttctg tgctgcttca 300
agatactaag ccacatttga agatgcagca gccatctccc ccaattcctc ctgtccatcc 360
tgatgtgcag ttaaaaaaatc tgccctttta tgatgtcctt gatgttctca tcaagcccac 420
gagtttagtt caaagcagta ttcagcgatt tcaagagaag ttttttattt ttgctttgac 480
acctcaacaa gttagagaga tatgcatatc cagggatttt ttgccaggtg gtaggagaga 540
ttat 544

```

<210> 430

<211> 507
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(507)
<223> n = A,T,C or G

<400> 430
cttatcncaa tggggctccc aaacttggct gtgcagtgga aactccgggg gaattttgaa 60
gaacaactgac acccatcttc caccocgaca ctctgattta attgggctgc agtgagaaca 120
gagcatcaat ttaaaaagct gcccagaatg ttntcctggg cagcgttggt atctttgccn 180
ccttcgtgac tttatgcaat gcatcatgct atttcatacc taatgaggga gttccaggag 240
attcaaccag gatgtttcta cncctgtggg ttatgacaaa gacaactgcc aaagaatntt 300
caagaaggag gactgcaagt atatcggtgt ggagaagaag gacccaaaaa agacctgttc 360
tgtcagttaa tggataatct aatgtgcttc tagtaggcac agggctccca ggccaggcct 420
cattctcttc tggcctctaa tagtcaatga ttgtgtagcc atgcctatca gtaaaaagat 480
ttttgagcaa aaaaaaaaaa aaaaaaa 507

<210> 431
<211> 392
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(392)
<223> n = A,T,C or G

<400> 431
gaaaattcag aatggataaa aacaaatgaa gtacaaaata tttcagattt acatagcgat 60
aaacaagaaa gcacttatca ggaggactta caaatggaag tacactctan aaccatcatc 120
tatcatggct aaatgtgaga ttagcacagc tgtattattt gtacattgca aacacctaga 180
aagagatggg aaacaaaatc ccaggagttt tgtgtgtgga gtccctgggt ttccaacaga 240
catcattcca gcattctgag attagggnga ttggggatca ttctggagtt ggaatgttca 300
acaaaagtga tgttggttagg taaaatgtac aacttctgga tctatgcaga cattgaaggt 360
gcaatgagtc tggcttttac tctgctgttt ct 392

<210> 432
<211> 387
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(387)
<223> n = A,T,C or G

<400> 432
ggtatccnta cataatcaaa tatagctgta gtacatgttt tcattggngt agattaccac 60
aatgcaagg caacatgtgt agatctcttg tcttattctt ttgtctataa tactgtattg 120
ngtagtccaa gctctcgga gtccagccac tngaaacat gctcccttta gattaacctc 180
gtggacnctn ttgttgnatt gtctgaactg tagngccctg tattttgctt ctgtctgnga 240
attctgttgc ttctggggca tttccttgng atgcagagga ccaccacaca gatgacagca 300
atctgaattg ntccaatcac agctgcgatt aagacatact gaaatcgtag aggaccggga 360
acaacgtata gaacactgga gtccttt 387

<210> 433
<211> 281
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(281)
<223> n = A,T,C or G

<400> 433
ttcaactagc anagaanact gcttcagggn gtgtaaaatg aaaggcttcc acgcagttat 60
ctgattaaag aacactaaga gagggacaag gctagaagcc gcaggatgtc tacactatag 120
caggcnctat ttgggttggc tggaggagct gtggaaaaca tggagagatt ggcgctggag 180
atcgccgtgg ctattcctcn ttgntattac accagnagg ntctctgtnt gccactggg 240
tnnaaaaccg ntatacaata atgatagaat aggacacaca t 281

<210> 434
<211> 484
<212> DNA
<213> Homo sapiens

<400> 434
ttttaaaata agcatttagt gctcagtcct tactgagtac tctttctctc cctcctctg 60
aatttaattc tttcaacttg caatttgcaa ggattacaca ttccactgtg atgtatatg 120
tgttgcaaaa aaaaaaagt gtctttgttt aaaattactt ggtttgtgaa tccatcttgc 180
tttttcccca ttggaactag tcattaaccc atctctgaac tggtagaaaa acatctgaag 240
agctagtcta tcagcatctg acaggtgaat tggatgggtc tcagaacccat ttcaccaga 300
cagcctgttt ctatcctgtt taataaatta gtttgggttc tctacatgca taacaaacc 360
tgctccaatc tgtcacataa aagtctgtga cttgaagttt agtcagcacc cccaccaaac 420
tttatTTTTc tatgtgtttt ttgcaacata tgagtgtttt gaaaataaag taccatgtc 480
ttta 484

<210> 435
<211> 424
<212> DNA
<213> Homo sapiens

<400> 435
gcgcccgtca gagcagggtca ctttctgcct tccacgtcct ccttcaagga agccccatgt 60
gggtagcttt caatatcgca gggtcttact cctctgcctc tataagctca aaccaccaa 120
cgatcgggca agtaaaccct ctccctcgcc gacttcggaa ctggcgagag ttcagcgag 180
atgggcctgt ggggaggggg caagatagat gagggggagc ggcatgggtc ggggtgacc 240
cttgagagaga ggaaaaaggc cacaagaggg gctgccaccg cactaacgg agatggccct 300
ggtagagacc tttgggggtc tggaaacctt ggactcccca tgctctaact cccacactct 360
gctatcagaa acttaaacctt gaggattttc tctgtttttc actcgcaata aattcagagc 420
aaac 424

<210> 436
<211> 667
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(667)
<223> n = A,T,C or G

<400> 436

```
accttgggaa nactctcaca atataaaggg tcgtagactt tactccaaat tccaaaaagg 60
tcctggccat gtaatcctga aagttttccc aaggttagcta taaaatcctt ataagggtgc 120
agcctcttct ggaattcctc tgattttcaa gtctcactct caagttcttg aaaacgaggg 180
cagttcctga aaggcaggta tagcaactga tcttcagaaa gaggaactgt gtgcaccggg 240
atgggctgcc agagtaggat aggattccag atgctgacac cttctggggg aaacaggggt 300
gccaggtttg tcatagcact catcaaagtc cgggtcaacgt ctgtgcttcg aatataaacc 360
tgttcatggt tataggactc attcaagaat tttctatatc tctttcttat atactctcca 420
agttcataat gctgctccat gccagctgg gtgagttggc caaatccttg tggccatgag 480
gattccttta tggggtcagt gggaaagggt tcaatgggac ttgggtctcc atgccgaaac 540
accaaagtcg caaacttcaa ctccttgggt agtacacttc ggtctagcca gaaaaaaagc 600
agaaacaaga agccaaggct aaggcttggt gcctcgccag gagggagggg gcagctctca 660
tgttgag 667
```

<210> 437

<211> 693

<212> DNA

<213> Homo sapiens

<400> 437

```
ctacgtctca accctcattt ttaggtaagg aatcttaagt ccaaagatat taagtgactc 60
acacagccag gtaaggaaag ctggattggc aactaggac tctaccatac cgggttttgt 120
taaagctcag gtaggagggc tgataagctt ggaaggaaact tcagacagct ttttcagatc 180
ataaaagata attcttagcc catgttcttc tccagagcag acctgaaatg acagcacagc 240
aggtaactct ctattttcac cctcttgcct tctactctct ggcagtcaga cctgtgggag 300
gccatgggag aaagcagctc tctggatggt tgtacagatc atggactatt ctctgtggac 360
catttctcca ggttacccta ggtgtcacta ttggggggag agccagcatc tttagcttcc 420
atgttagttt ctgtctgtct tcagtagagg aaacttttgc tcttcacact tcacatctga 480
acacctaact gctgttgctc ctgaggtggt gaaagacaga tatagagctt acagtattta 540
tcctatttct aggcactgag ggctgtgggg taccttgttg tgccaaaaca gatcctgttt 600
taaggacatg ttgcttcaga gatgtctgta actatctggg ggctctgttg gctctttacc 660
ctgcatcatg tgctctcttg gctgaaaatg acc 693
```

<210> 438

<211> 360

<212> DNA

<213> Homo sapiens

<400> 438

```
ctgcttatca caatgaatgt tctcctgggc agcgttgtga tctttgccac cttcgtgact 60
ttatgcaatg catcatgcta tttcatacct aatgagggag ttccaggaga ttcaaccagg 120
atgtttctac acctgtgggt tatgacaaag acaactgcc aagaatcttc aagaaggagg 180
actgcaagta tatctggtgg agaagaagga cccaaaaaag acctgttctg tcagtgaatg 240
gataatctaa tgtgcttcta gtaggcacag ggctcccagg ccaggcctca ttctcctctg 300
gcctctaata gtcaataatt gtgtagccat gcctatcagt aaaaagattt ttgagcaaac 360
```

<210> 439

<211> 431

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(431)

<223> n = A,T,C or G

<400> 439

```
gttcctnnta actcctgcc aaacacagctc tcctcaacat gagagctgca cccctcctcc 60
```

```

tggccagggc agcaagcctt agccttggct tcttgtttct gctttttttc tggctagacc 120
gaagtgtact agccaaggag ttgaagtttg tgacttttgg gtttcggcat ggagaccgaa 180
gtcccattga cacctttccc actgacccca taaaggaatc ctcatggcca caaggatttg 240
gccaactcac ccagctgggc atggagcagc attatgaact tggagagtat ataagaaaga 300
gatatagaaa attcttgaat gagtccata aacatgaaca ggtttatatt cgaagcacag 360
acgttgaccg gactttgatg agtgctatga caaacctggc agcccgtcga cgcggccgcg 420
aatttagtag t                                     431

```

<210> 440

<211> 523

<212> DNA

<213> Homo sapiens

<400> 440

```

agagataaag cttaggtcaa agttcataga gttcccatga actatatgac tggccacaca 60
ggatcttttg tatttaagga ttctgagatt ttgcttgagc aggattagat aaggctgttc 120
tttaaatgtc tgaaatggaa cagatttcaa aaaaaaaccc cacaatctag ggtgggaaca 180
aggaaggaaa gatgtgaata ggctgatggg caaaaaacca atttaccat cagttccagc 240
cttctctcaa ggagaggcaa agaaaggaga tacagtggag acatctggaa agttttctcc 300
actggaaaac tgctactatc tgtttttata tttctgttaa aatatatgag gctacagaac 360
taaaaattaa aacctctttg tgtcccttgg tcctggaaca tttatgttcc ttttaaagaa 420
acaaaaatca aactttacag aaagatttga tgtatgtaat acatatagca gctcttgaag 480
tatatatatc atagcaaata agtcatctga tgagaacaag cta                                     523

```

<210> 441

<211> 430

<212> DNA

<213> Homo sapiens

<400> 441

```

gttcctccta actcctgcca gaaacagctc tcctcaacat gagagctgca cccctcctcc 60
tggccagggc agcaagcctt agccttggct tcttgtttct gctttttttc tggctagacc 120
gaagtgtact agccaaggag ttgaagtttg tgacttttgg gtttcggcat ggagaccgaa 180
gtcccattga cacctttccc actgacccca taaaggaatc ctcatggcca caaggatttg 240
gccaactcac ccagctgggc atggagcagc attatgaact tggagagtat ataagaaaga 300
gatatagaaa attcttgaat gagtccata aacatgaaca ggtttatatt cgaagcacag 360
acgttgaccg gactttgatg agtgctatga caaacctggc agcccgtcga cgcggccgcg 420
aatttagtag                                     430

```

<210> 442

<211> 362

<212> DNA

<213> Homo sapiens

<400> 442

```

ctaaggaatt agtagtggtc ccatcacttg tttggagtgt gctattctaa aagattttga 60
tttcttgtaa tgacaattat attttaactt tgggtgggga aagagttata ggaccacagt 120
cttcacttct gatacttgta aattaatctt ttattgcact tgttttgacc attagctat 180
atgttttagaa atggtcattt tacggaaaaa ttagaaaaat tctgataata gtgcagaata 240
aatgaattaa tgttttactt aatttatatt gaactgtcaa tgacaaataa aaattctttt 300
tgattatttt ttgttttcat ttaccagaat aaaaactaag aattaaaagt ttgattacag 360
tc                                     362

```

<210> 443

<211> 624

<212> DNA

<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(624)
<223> n = A,T,C or G

<400> 443
tttttttttt gcaacacaaat atacatcaca gtgaaatgtg taatccttgc aaattgcaag 60
ttgaaagaat taaattcaga ggaggggaga gaaagagtag tcagtaggga ctgagcacta 120
aatgcttatt ttaaaagaaa tgtaaagagc agaaagcaat tcaggctacc ctgccttttg 180
tgctggctag tactccggtc ggtgtcagca gcacgtggca ttgaacattg caatgtggag 240
cccaaaccac agaaaatggg gtgaaattgg ccaactttct attaacttgg cttcctgttt 300
tataaaatat tgtgaataat atcacctact tcaaagggca gttatgaggc ttaaatgaac 360
taacgcctac aaaacactta aacatagata acatagggtgc aagtactatg tatctggtag 420
atggtaaaaca tccttattat taaagtcaac gctaaaatga atgtgtgtgc atagtctaata 480
agtacagaga gagggcactt aaaccaacta agggcctgga gggaagggtt cctgggaaaga 540
ngatgcttgt gctgggtcca aatcttgggtc tactatgacc ttggccaaat tatttaaact 600
ttgtccctat ctgctaaaca gatc 624

<210> 444
<211> 425
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(425)
<223> n = A,T,C or G

<400> 444
gcacatcatt nntcttgcatt tctttgagaa taagaagatc agtaaatagt tcagaagtgg 60
gaagctttgt ccaggcctgt gtgtgaaccc aatgttttgc ttagaaatag aacaagtaag 120
ttcattgcta tagcataaca caaaatttgc ataagtgggtg gtcagcaaat ccttgaatgc 180
tgcttaatgt gagaggttgg taaaatcctt tgtgcaacac tctaactccc tgaatgtttt 240
gctgtgctgg gacctgtgca tgccagacaa ggccaagctg gctgaaagag caaccagcca 300
cctctgcaat ctgccacctc ctgctggcag gatttgtttt tgcacacctg gaagagccaa 360
ggaggcaccg gggcataagt gagtagactt atggtcgacg cggccgcgaa tttagtagta 420
gtaga 425

<210> 445
<211> 414
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(414)
<223> n = A,T,C or G

<400> 445
catgtttatg nttttggatt actttgggca cctagtgttt ctaaatcgtc tatcattctt 60
ttctgttttt caaaagcaga gatggccaga gtctcaacaa actgtatctt caagtctttg 120
tgaaattctt tgcattgtggc agattattgg atgtagtctt ctttaactag catataaatc 180
tggtgtgttt cagataaatg aacagcaaaa tgggtgggaa ttaccatttg gaacattgtg 240
aatgaaaaat tgtgtctcta gattatgtaa caaataacta tttcctaacc attgatcttt 300
ggatttttat aatcctactc acaaatgact aggettctcc tcttgtattt tgaagcagtg 360
tgggtgctgg attgataaaa aaaaaaaaag tcgacgcggc cgcgaattta gtag 414

<210> 446

<211> 631
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(631)
<223> n = A,T,C or G

<400> 446
acaaattaga anaaagtgcc agagaacacc acataccttg tccggaacat tacaatggct 60
tctgcatgca tgggaagtgt gagcattcta tcaatatgca ggagccatct tgcaggtgtg 120
atgctggtta tactggacaa cactgtgaaa aaaaggacta cagtgttcta tacgttggtc 180
ccggtcctgt acgatttcag tatgtcttaa tcgcagctgt gattggaaca attcagattg 240
ctgtcatctg tgtggtggtc ctctgcatca caagggccaa actttaggta atagcattgg 300
actgagattt gtaaaactttc caaccctcca ggaaatgccc cagaagcaac agaattcaca 360
gacagaagca aaatacaggg cactacagtt cagacaatac aacaagagcg tccacgaggt 420
taatctaaag ggagcatggt tcacagtggc tggactaccg agagcttgga ctacacaata 480
cagtattata gacaaaagaa taagacaaga gatctacaca tgttgccctg catttggtgt 540
aatctacacc aatgaaaaca tgtactacag ctatatattga ttatgtatgg atatatttga 600
aatagtatac attgtcttga tgttttttct g 631

<210> 447
<211> 585
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(585)
<223> n = A,T,C or G

<400> 447
ccttgggaaa antntcacia tataaagggt cgtagacttt actccaaatt ccaaaaaggt 60
cctggccatg taatcctgaa agttttccca aggtagctat aaaatcctta taagggtgca 120
gcctcttctg gaattcctct gatttcaaag tctcactctc aagtctctga aaacgagggc 180
agttcctgaa aggcaggtat agcaactgat cttcagaaag aggaactgtg tgcaccggga 240
tgggctgcca gagtaggata ggattccaga tgctgacacc ttctggggga aacagggctg 300
ccaggtttgt catagcactc atcaaagtcc ggtcaacgtc tgtgcttcga atataaacct 360
gttcagtgtt ataggactca ttcaagaatt ttctatatct ctttcttata tactctccaa 420
gttcataatg ctgctccatg ccagctggg tgagttggcc aaatccttgt ggccatgagg 480
attcctttat ggggtcagtg ggaaagggtg caatgggact tcggtctcca tgccgaaaca 540
ccaaagtcac aaacttcaac tccttggtta gtacacttcg gtcta 585

<210> 448
<211> 93
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(93)
<223> n = A,T,C or G

<400> 448
tgctcgtggg tcattctgan ncccgaactg accntgccag ccctgccgan ggccnccat 60
ggctccctag tgccctggag agganggggc tag 93

<210> 449
 <211> 706
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(706)
 <223> n = A,T,C or G

<400> 449
 ccaagttcat gctntgtgct ggacgctgga cagggggcaa aagcnnttgc tcgtgggtca 60
 ttctganqac cgaactgacc atgccagccc tgccgatggc cctccatggc tccctagtgc 120
 cctggagagg aggtgtctag tcagagagta gtccctggaag gtggcctctg ngaggagcca 180
 cggggacagc atcctgcaga tggtcgggag cgtcccatc gccattcagg ctgcgcaact 240
 gttggaagg gcgatcggtg cgggcctctt cgctattacg ccagctggcg aaagggggat 300
 gtgctgcaag gcgattaagt tgggtaacgc caggggtttc ccagtcncga cgttgtaaaa 360
 cgacggccag tgaattgaat ttaggtgacn ctatagaaga gctatgacgt cgcatgcacg 420
 cgtacgtaag ctggatcct ctagagcggc cgcctactac tactaaatc gcggccgctg 480
 cgacgtggga tcncactga gagagtggag agtgacatgt gctggacnct gtccatgaag 540
 cactgagcag aagctggagg cacaacgcnc cagacactca cagctactca ggaggctgag 600
 aacaggttga acctgggagg tggaggttgc aatgagctga gatcaggccn ctgcncacca 660
 gcatggatga cagagtgaag ctatcatctta aaaaaaaaaa aaaaaa 706

<210> 450
 <211> 493
 <212> DNA
 <213> Homo sapiens

<400> 450
 gagacggagt gtcactctgt tgcccaggct ggagtgcagc aagacactgt ctaagaaaaa 60
 acagttttaa aaggtaaaac aacataaaaa gaaatatacct atagtggaaa taagagagtc 120
 aaatgaggct gagaacttta caaagggatc ttacagacat gtccccaata tcactgcatg 180
 agcctaagta taagaacaac ctttggggag aaaccatcat ttgacagtga ggtacaattc 240
 caagtcaagg agtgaaatgg gtggaattaa actcaaatta atcctgccag ctgaaacgca 300
 agagacactg tcagagagtt aaaaagttag ttctatccat gaggtgattc cacagtcttc 360
 tcaagtcaac acatctgtga actcacagac caagttctta aaccactgtt caaactctgc 420
 tacacatcag aatcacctgg agagctttac aaactcccat tgccgagggt cgacgcggcc 480
 gcgaatttag tag 493

<210> 451
 <211> 501
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(501)
 <223> n = A,T,C or G

<400> 451
 gggcgcgctc cattcgccat tcaggctgag caactgttgg gaaggcgcat cgggtcgggc 60
 ctcttcgcta ttacgccagc tggcgaaagg gggatgtgct gcaaggcgat taagttgggt 120
 aacgccaggg ttttcccagt cncgacgttg taaaacgacg gccagtgaat tgaatttagg 180
 tgacnctata gaagagctat gacgtcgcat gcacgcgtac gtaagcttgg atcctctaga 240
 gcggccgctt actactacta aattcgcgcc gcgctcgacg tgggatccnc actgagagag 300
 tggagagtga catgtgctgg acnctgtcca tgaagcactg agcagaagct ggaggcacia 360
 cgcncacagc actcacagct actcaggagg ctgagaacag gttgaacctg ggaggtggag 420

gttgcaatga gctgagatca ggccnctgcn ccccgatg gatgacagag tgaaactcca 480
tcttaaaaaa aaaaaaaaaa a 501

<210> 452
<211> 51
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(51)
<223> n = A,T,C or G

<400> 452
agacggtttc accnttacaa cnccttttag gatgggnntt ggggagcaag c 51

<210> 453
<211> 317
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(317)
<223> n = A,T,C or G

<400> 453
tacctcttgc tttttcccca ttggaactag tcattaaccc atctctgaac tggtagaaaa 60
acatctgaag agctagtcta tcagcatctg gcaagtgaat tggatgggtc tcagaaccat 120
ttcacccana cagcctgttt ctatcctgtt taataaatta gtttgggttc tctacatgca 180
taacaaaccc tgcctcaatc tgtcacataa aagtctgtga cttgaagttt antcagcacc 240
cccacaaac tttatttttc tatgtgtttt ttgcaacata tgagtgtttt gaaaataagg 300
taccatgtc tttatta 317

<210> 454
<211> 231
<212> DNA
<213> Homo sapiens

<400> 454
ttcgaggtag aatcaactct cagagtgtag tttccttcta tagatgagtc agcattaata 60
taagccacgc cagctcttgc aaggagtctt gaattctcct ctgctcactc agtagaacca 120
agaagaccaa attcttctgc atcccagctt gcaaacaaaa ttgttcttct aggtctccac 180
ccttcctttt tcagtgttcc aaagctcctc acaatttcat gaacaacagc t 231

<210> 455
<211> 231
<212> DNA
<213> Homo sapiens

<400> 455
taccaaagag ggcataataa tcagtctcac agtaggggtc accatcctcc aagtgaaaaa 60
cattgttccg aatgggcttt ccacaggcta cacacacaaa acaggaaaca tgccaagttt 120
gtttcaacgc attgatgact tctccaagga tcttcctttg gcatcgacca cattcagggg 180
caaagaattt ctcatagcac agctcacaat acagggtctc tttctcctct a 231

<210> 456
<211> 231

<212> DNA

<213> Homo sapiens

<400> 456

```
ttggcaggta cccttcaaaa gaagacacca taccttatgc gttattaggt ggaataatca 60
ttccattcag tattatcggtt attattcttg gagaaaccct gtctgtttac tgtaaccttt 120
tgcactcaaa ttcctttatc aggaataact acatagccac tatttcaaaa gccattggaa 180
cctttttatt tgggtgcagct gctagtcagt ccctgactga cattgccaag t 231
```

<210> 457

<211> 231

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(231)

<223> n = A,T,C or G

<400> 457

```
cgaggtagccc aggggtctga aaatctctnn ttantagtc gatagcaaaa ttgttcatca 60
gcattcctta atatgatctt gctataatta gatttttctc cattagagtt catacagttt 120
tatttgattt tattagcaat ctctttcaga agacccttga gatcattaag ctttgtatcc 180
agttgtctaa atcgatgcct catttcctct gaggtgtcgc tggcttttgt g 231
```

<210> 458

<211> 231

<212> DNA

<213> Homo sapiens

<400> 458

```
aggtctgggt cccccactt ccactccct ctactctctc taggactggg ctgggccaaag 60
agaagagggg tggttaggga agccgttgag acctgaagcc ccacctcta cttccttca 120
acaccctaac cttgggtaac agcatttgga attatcattt gggatgagta gaatttccaa 180
ggtcctgggt taggcatttt ggggggccag accccaggag aagaagattc t 231
```

<210> 459

<211> 231

<212> DNA

<213> Homo sapiens

<400> 459

```
ggtaccgagg ctgctgaca cagagaaacc ccaacgcgag gaaaggaatg gccagccaca 60
ccttcgcgaa acctgtggtg gccaccagt cctaaccggga caggacagag agacagagca 120
gccctgact gttttccctc caccacagcc atcctgtccc tcattggctc tgtgctttcc 180
actatacaca gtcaccgtcc caatgagaaa caagaaggag caccctccac a 231
```

<210> 460

<211> 231

<212> DNA

<213> Homo sapiens

<400> 460

```
gcaggtataa catgtgcaa caacagatgt gactaggaac ggccggtgac atggggaggg 60
cctatcaccc tattcttggg ggctgcttct tcacagtgat catgaagcct agcagcaaat 120
cccacctccc cacacgcaca cggccagcct ggagcccaca gaagggtcct cctgcagcca 180
gtggagcttg gtccagcctc cagtccaccc ctaccaggct taaggataga a 231
```


<210> 461
<211> 231
<212> DNA
<213> Homo sapiens

<400> 461
cgaggtttga gaagctctaa tgtgcagggg agccgagaag caggcggcct agggagggtc 60
gcgtgtgctc cagaagagtg tgtgcatgcc agaggggaaa caggcgcctg tgtgtcctgg 120
gtgggggttca gtgaggagtg ggaaattggt tcagcagaac caagccgttg ggtgaataag 180
agggggattc catggcactg atagagccct atagtttcag agctgggaat t 231

<210> 462
<211> 231
<212> DNA
<213> Homo sapiens

<400> 462
aggtaccctc attgtagcca tgggaaaatt gatgttcagt ggggatcagt gaattaaatg 60
gggtcatgca agtataaaaa ttaaaaaaaa aagacttcat gcccaatctc atatgatgtg 120
gaagaactgt tagagagacc aacagggtag tgggttagag atttcagag tcttacattt 180
tctagaggag gtatttaatt tcttctcact catccagtgt tgtatttagg a 231

<210> 463
<211> 231
<212> DNA
<213> Homo sapiens

<400> 463
tactccagcc tggtagacaga gcgagaccct atcaccgccc cccacccac caaaaaaaaa 60
actgagtaga cagggtgtct cttggcatgg taagtcttaa gtcccctccc agatctgtga 120
catttgacag gtgtcttttc ctctggacct cgggtgtccc atctgagtga gaaaaggcag 180
tggggagggtg gatcttccag tcgaagcggg atagaagccc gtgtgaaaag c 231

<210> 464
<211> 231
<212> DNA
<213> Homo sapiens

<400> 464
gtactctaag attttatcta agttgccttt tctgggtggg aaagtttaac cttagtgcct 60
aaggacatca catatgaaga atgtttaagt tggaggtggc aacgtgaatt gcaaacaggg 120
cctgcttcag tgactgtgtg cctgtagtcc cagctactcg ggagtctgtg tgaggccagg 180
ggtgccagcg caccagctag atgctctgta acttotaggg cccattttcc c 231

<210> 465
<211> 231
<212> DNA
<213> Homo sapiens

<400> 465
catgttggtg tagctgtggt aatgctggct gcactcaga cagggttaac ttcagctcct 60
gtggcaaat agcaacaaat tctgacatca tatttatggt ttctgtatct ttgttgatga 120
aggatggcac aatttttgct tgtgttcata atatactcag attagttcag ctccatcaga 180
taaactggag acatgcagga cattagggta gtgtgttagc tctggtaatg a 231

<210> 466
<211> 231
<212> DNA

<213> Homo sapiens

<400> 466

```

caggtagctc tttccattgg atactgtgct agcaagcatg ctctccgggg tttttttaat 60
ggccttcgaa cagaacttgc cacataccca ggtataatag tttctaacat ttgccagga 120
cctgtgcaat caaatattgt ggagaattcc ctactgtgag aagtcacaaa gactataggc 180
aataatggag accagtccca caagatgaca accagtcgtt gtgtgcggct g          231

```

<210> 467

<211> 311

<212> DNA

<213> Homo sapiens

<400> 467

```

gtacaccctg gcacagtcca atctgaactg gtccggcact catctttcat gagatggatg 60
tggtggcttt tctccttttt catcaagact cctcagcagg gagcccagac cagcctgcac 120
tgtgccttaa cagaaggtct tgagattcta agtgggaatc atttcagtga ctgtcatgtg 180
gcatgggtct tcgcccaagc tcgtaatgag actatagcaa ggcggctgtg ggacgtcagt 240
tgtgacctgc tgggcctccc aatagactaa caggcagtcg cagttggacc caagagaaga 300
ctgcagcaga c          311

```

<210> 468

<211> 3112

<212> DNA

<213> Homo sapiens

<400> 468

```

cattgtgttg ggagaaaaac agaggggaga tttgtgtggc tgcagccgag ggagaccagg 60
aagatctgca tgggtgggaag gacctgatga tacagagttt gataggagac aattaaaggc 120
tggaaggcac tggatgcctg atgatgaagt ggactttcaa actggggcac tactgaaacg 180
atgggatggc cagagacaca ggagatgagt tggagcaagc tcaataacaa agtggttcaa 240
cgaggacttg gaattgcatg gagctggagc tgaagttagt cccaattggt tactagttag 300
gtgaatgttg atgattggat gatcatttct catctctgag cctcaggttc cccatccata 360
aaatgggata cacagtatga tctataaagt gggatatagt atgatctact tcaactgggt 420
atgtgaagga tgaattgaga taatttattt caggtgccta gaacaatgcc cagatttagt 480
catttggttg aactgagaaa tggcataaca ccaaatttaa tatatgtcag atgttactat 540
gattatcatt caatctcata gttttgtcat ggcccaattt atcctcactt gtgcctcaac 600
aaattgaact gttaacaaag gaatctctgg tcctgggtaa tggtgagca ccaactgagca 660
tttccattcc agttggcttc ttgggtttgc tagctgcac actagtcac ttaaataaat 720
gaagttttaa catttccca gtgatttttt tatctcacct ttgaagatac tatgttatgt 780
gattaaataa agaacttgag aagaacaggt ttcattaaac ataaaatcaa tgtagacgca 840
aattttctgg atgggcaata cttatgttca caggaaatgc tttaaaatat gcagaagata 900
attaaatggc aatggacaaa gtgaaaaact tagacttttt tttttttttt ggaagtatct 960
ggatgttcct tagtcaacta aaggagaact gaaaaatagc agtgagttcc acataatcca 1020
acctgtgaga ttaaggtctt ttgtggggaa ggacaaagat ctgtaaattt acagtttctt 1080
tccaaagcca acgtcgaatt ttgaaacata tcaaagctct tcttcaagac aaataatcta 1140
tagtacatct ttcttatggg atgcacttat gaaaaatggg ggctgtcaac atctagtcac 1200
tttagctctc aaaatgggtc attttaagag aaagttttag aatctcatat ttattcctgt 1260
ggaaggacag cattgtggct tggactttat aaggtcttta ttcaactaaa taggtgagaa 1320
ataagaaagg ctgctgactt taccatctga ggccacacat ctgctgaaat ggagataatt 1380
aacatcacta gaaacagcaa gatgacaata taatgtctaa gtagtgcacat gtttttgcac 1440
atttccagcc cctttaaata tccacacaca caggaagcac aaaaggaagc acagagatcc 1500
ctgggagaaa tgcccgcccg ccattctggg tcatcgatga gcctcgccct gtgcctggtc 1560
ccgcttgtga ggggaaggaca ttagaaaatg aattgatgtg ttccttaaaag gatgggcagg 1620
aaaacagatc ctgttttgga tatttatgtg aacgggatta cagatttgaa atgaagtcac 1680
aaagtgagca ttaccaatga gagggaaaaca gacgagaaaa tcttgatggc ttcacaagac 1740
atgcaacaaa caaaatggaa tactgtgatg acatgaggca gccaaactgg ggaggagata 1800
accacggggc agagggtcag gattctggcc ctgctgccta aactgtgcgt tcataaccaa 1860

```

```

atcatttcat atttctaacc ctcaaaacaa agctgttgta atatctgac tctacgggtc 1920
cttctggggc caacattctc catatatcca gccacactca tttttaatat ttagttccca 1980
gatctgtact gtgaccttct tacactgtag aataacatta ctcatittgt tcaaagacc 2040
ttcgtgttgc tgcctaatat gtagctgact gtttttcta aggagtgttc tggcccagg 2100
gatctgtgaa caggctggga agcatctcaa gatctttcca gggttatact tactagcaca 2160
cagcatgac attacggagt gaattatcta atcaacatca tcctcagtgt ctttgcccat 2220
actgaaattc atttccact tttgtgcca ttctcaagac ctcaaatgt cattccatta 2280
atatcacag attaaccttt tttttaacc tggaagaatt caatgttaca tgcagctatg 2340
ggaatttaac tacatatatt gttttccagt gcaaagatga ctaagtcctt tatccctccc 2400
ctttgtttga tttttttccc agtataaagt taaaatgctt agccttgtag tgaggctgta 2460
tacagccaca gcctctcccc atccctccag ctttatctgt catcaccatc aaccctccc 2520
atgcacctaa acaaaatcta acttgtaatt ccttgaacat gtcaggcata cattattcct 2580
tctgcctgag aagctcttcc ttgtctctta aatctagaat gatgtaaagt tttgaataag 2640
ttgactatct tacttcatgc aaagaaggga cacatatgag attcatcatc acatgagaca 2700
gcaataacta aaagtgtaat ttgattataa gagtttagat aaatatatga aatgcaagag 2760
ccacagaggg aatgtttatg gggcacgttt gtaagcctgg gatgtgaagc aaaggcagg 2820
aacctcatag tatcttataa aatatacttc atttctctat ctctatcaca atatccaaca 2880
agcttttccac agaattcatg cagtgcacat ccccaaaggt aacctttatc catttcatg 2940
tgagtgcgct ttagaatttt ggcaaatcat actggtcact tatctcaact ttgagatgtg 3000
tttgtccttg tagttaattg aaagaaatag ggcactcttg tgagccactt tagggttcac 3060
tcctggcaat aaagaattta caaagagcaa aaaaaaaaaa aaaaaaaaaa aa 3112

```

<210> 469

<211> 2229

<212> DNA

<213> Homo sapiens

<400> 469

```

agctctttgt aaattcttta ttgccaggag tgaaccctaa agtggctcac aagagtgcc 60
tatttctttc aattaactac aaggacaaac acatctcaaa gttgagataa gtgaccagta 120
tgatttgcca aaattctaaa gcgcactcac catgaaatgg ataaaggta ctttgggga 180
ttgcaactgc atgaattctg tgaaaagctt gttggatatt gtgatagaga tagagaaatg 240
aagtatatta tataagatac tatgaggttc cctgcctttg cttcacatcc caggcttaca 300
aacgtgcccc ataaacattc cctctgtggc tcttgcatct catatattta tctaaactct 360
tataatcaaa tacactttta gtatttgctg tctcatgtga tgatgaatct catatgtgtc 420
ccttctttgc atgaagtaag atagtcaact tattcaaac tttacatcat tctagattta 480
agagacaagg aagagcttct caggcagaag gaataatgta tgcctgacat gttcaaggaa 540
ttacaagtta gattttgttt aggtgcatgg gaggggttga tgggtgatgac agataaggct 600
ggagggtggt ggagaggctg ttgctgtata cagcctcagt acaaggctaa gcattttaac 660
tttatactgg aaaaaaatc aaacaaaggg gagggataaa ggacttagtc atctttgac 720
tggaatacaa aatatgtaat taaattccca tagctgcatg taacattgaa ttcttccagg 780
ttaaaaaaaa agttaatcct gtgatattaa tggaaatgaca ttttgaggtc ttgagaatgg 840
gcacaaaagt gggaaatgaa ttccagtatg ggcaaagaca ctgaggatga tgttgattag 900
ataattcact ccgtaatgat catgctgtgt gctagtaagt ataaccctgg aaagatcttg 960
agatgcttcc cagcctgttc acagatcccc tgggccagaa cactccttag gaaaaacagt 1020
cagctacata ttaggcagca acacgaaggg tctttgaaca aaatgagtaa tgttattcta 1080
cagtgtagaa aggtcacagt acagatctgg gaactaaata ttaaaaatga gtgtggctgg 1140
atatatggag aatgttgggc ccagaaggaa ccgtagagat cagatattac aacagcttgg 1200
ttttgagggt tagaaatatg aaatgatttg gttatgaacg cacagtttag gcagcagggc 1260
cagaatcctg accctctgcc ccgtggttat ctctcccca gcttggctgc ctcatgtcat 1320
cacagtattc cattttgttt gtgcatgtc ttgtgaagcc atcaagattt tctcgtctgt 1380
tttctctca ttggtaatgc tcactttgtg acttcatttc aaatctgtaa tcccgttcaa 1440
ataaatatcc acaacaggat ctgttttctt gccatcctt taaggacac atcaattcat 1500
tttctaattg ccttccctca caagcgggac caggcacagg gcgaggctca tcatgaccc 1560
aagatggcgg ccgggcattt ctcccaggga tctctgtgct tctttttgtg cttcctgtgt 1620
gtgtggatat ttaagggggc tggaaatgtg caaaaacatg tcaactacta gacattatat 1680
tgtcatcttg ctgtttctag tgatgttaat tatctccatt tcagcagatg tgtggcctca 1740
gatggtaaag tcagcagcct ttcttatttc tcacctgaa atacatacga ccatttgagg 1800

```

```

agacaaatgg caaggtgtca gcataacctg aacttgagtt gagagctaca cacaatatta 1860
ttggtttccg agcatcacaa acacctctc tgtttcttca ctgggcacag aattttaata 1920
cttatttcag tgggctgttg gcaggaacaa atgaagcaat ctacataaag tcactagtgc 1980
agtgcctgac acacaccatt ctcttgaggt cccctctaga gatccacag gtcatatgac 2040
ttcttgggga gcagtggctc acacctgtaa tcccagcact ttgggaggct gaggcagggt 2100
ggtcacctga ggtcaggagt tcaagaccag cctggccaat atggtgaaac cccatctcta 2160
ctaaaaatac aaaaattagc tgggcgtgct ggtgcatgcc tgtaatcca gcccacac 2220
aatggaatt                                     2229

```

<210> 470

<211> 2426

<212> DNA

<213> Homo sapiens

<400> 470

```

gtaaattctt tattgccagg agtgaaccct aaagtggctc acaagagtgc cctatttctt 60
tcaatttaact acaaggacaa acacatctca aagttgagat aagtgaccag tatgatttgc 120
caaaatttcta aagcgactc accatgaaat ggataaagg tacccttggg gatttgcact 180
gcatgaattc tgtgaaaagc ttgttgata ttgtgataga gatagagaaa tgaagtatat 240
tatataagat actatgaggt tccctgcctt tgcttcacat cccaggctta caaacgtgcc 300
ccataaacat tccctctgtg gctcttgcac ttcatatatt tatctaaact cttataatca 360
aattacactt ttagtatttg ctgtctcatg tgatgatgaa tctcatatgt gtcccttctt 420
tgcatgaagt aagatagtca acttattcaa aactttacat cattctagat ttaagagaca 480
aggaagagct tctcaggcag aaggaataat gtatgcctga catgttcaag gaattacaag 540
ttagattttg tttagtgca tgggaggggt tgatgggtgat gacagataag gctggaggga 600
tggggagagg ctgtggctgt atacagcctc agtacaaggc taagcatttt aactttatac 660
tggaaaaaaa atcaaacaaa ggggagggat aaaggactta gtcacttttg cactggaaaa 720
caaaatatgt aattaaattc ccatagctgc atgtaacatt gaattcttcc aggttaaaaa 780
aaaaagttaa tcctgtgata ttaatggaat gacattttga ggtcttgaga atgggcacaa 840
aagtgggaaa tgaatttcag tatgggcaaa gacactgagg atgatgttga ttagataatt 900
cactccgtaa tgatcatgct gtgtgctagt aagtataacc ctggaaagat cttgagatgc 960
ttccagcctt gttcacagat cccctgggac agaacactcc ttaggaaaaa cagtcagcta 1020
catattaggc agcaacacga aggtcttttg aacaaaatga gtaatgttat tctacagtg 1080
agaaaggcca cagtacagat ctgggaacta aatattaaaa atgagtgttg ctggatatat 1140
ggagaatgtt gggcccagaa ggaaccgtag agatcagata ttacaacagc tttgttttga 1200
gggttagaaa tatgaaatga tttggttatg aacgcacagt ttaggcagca gggccagaat 1260
cctgaccctc tgcccctgtg ttatctcctc cccagcttgg ctgcctcatg tcatcacagt 1320
attccatttt gtttgttgca tgtcttgtga agccatcaag attttctcgt ctgttttctt 1380
ctcatttgta atgctcactt tgtgacttca tttcaaactc gtaatcccgt tcaaataaat 1440
atccacaaca ggatctgttt tctgtcccat cctttaagga acacatcaat tcattttcta 1500
atgtccttcc ctcacaagcg ggaccaggca caggggcagg ctcatcgatg acccaagatg 1560
gcgccggggc atttctccca gggatctctg tgcttccctt tgtgcttccg gtgtgtgtgg 1620
atattttaaag gggctggaaa tgtgcaaaaa catgtcacta cttagacatt atattgtcat 1680
cttgctgttt ctagtgtatg taattatctc catttcagca gatgtgtggc ctcagatggt 1740
aaagtcagca gcctttctta tttctcacct ggaatacat acgaccattt gaggagacaa 1800
atggcaagggt gtcagacata cctgaacttg agttgagagc tacacacaat attattggtt 1860
tccgagcatc acaaacaccc tctctgtttc ttcaactggc acagaatttt aatacttatt 1920
tcagtgggct gttggcagga acaaatgaag caatctacat aaagtcacta gtgcagtgcc 1980
tgacacacac cattctcttg aggtcccctc tagagatccc acaggtcata tgacttcttg 2040
gggagcagtg gctcacacct gtaatcccag cactttggga ggctgaggca ggtgggtcac 2100
ctgaggtcag gagttcaaga ccagcctggc caatatgggt aaaccccatc tctactaaaa 2160
atacaaaaat tagctgggag tgctgggtgca tgccgtgtaa cccagctact tgggagggtg 2220
aggcaggaga attgtcgaa catgggaggc ggaggttgca gtgagctgta attgtgccat 2280
tgactcgaa cctgggcgac agagtggaa tctgtttcca aaaaacaaac aaacaaaaaa 2340
ggcatagtca gatacaacgt ggggtgggat tgtaaataga agcaggatat aaagggtcat 2400
gggtgacggt tttgcccaac acaatg                                     2426

```

<210> 471

<211> 812
<212> DNA
<213> Homo sapiens

<400> 471
gaacaaaatg agtaatgtta ttctacagtg tagaaaggtc acagtacaga tctgggaact 60
aaatattaaa aatgagtgtg gctggatata tggagaatgt tgggccaga aggaaccgta 120
gagatcagat attacaacag ctttggtttg agggtttagaa atatgaaatg atttggttat 180
gaacgcacag tttaggcagc agggccagaa tcttgaccct ctgccccgtg gttatctcct 240
ccccagcttg gctgcctcat gtcacacag tattccattt tgtttgttgc atgtcttgtg 300
aagccatcaa gatcttctcg tctgttttcc tctcatttgt aatgctcact ttgtgacttc 360
atttcaaatc tgtaatcccg ttcaaataaa tatccacaac aggatctgtt ttctgcccc 420
tcctttaagg aacacatcaa ttcattttct aatgtccttc cctcacaagc gggaccaggc 480
acagggcgag gctcatcgat gacccaagat ggccggcggg catttctccc agggatctct 540
gtgcttcctt ttgtgcttcc tgtgtgtgtg gatattttaa ggggctggaa atgtgcaaaa 600
acatgtcact acttagacat tatattgtca tcttgctgtt tctagtgtg ttaattatct 660
ccatttcagc agatgtgtgg cctcagatgg taaagtcagc agcctttctt atttctcacc 720
tctgtatcat caggctcctc ccaccatgca gatcttctcg gtctccctcg gctgcagcca 780
cacaaatctc ccctctgttt ttctgatgcc ag 812

<210> 472
<211> 515
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(515)
<223> n = A,T,C or G

<400> 472
acggagactt attttctgat attgtctgca tatgtatggt ttaagagtc tggaaatagt 60
cttatgactt tcctatcatg cttattaata aataatacag cccagagaag atgaaaatgg 120
gttcagaat tattggtcct tgcagcccgg tgaatctcag caagaggaa caccaactga 180
caatcaggat attgaacctg gacaagagag agaaggaaca cctccgatcg aagaacgtaa 240
agtagaagg gattgccagg aatggatctt ggaaaagact cggagtgtgc gtggagatgg 300
ctctgatgta aaagagaaga ctccacctaa tcctaagcat gctaagacta aagaagcagg 360
agatgggcag ccataagtta aaaagaagac aagctgaagc tacacacatg gctgatgtca 420
cattgaaaat gtgactgaaa atttgaaaat tctctcaata aagtttgagt tttctctgaa 480
gaaaaaaaaa naaaaaaaaaa aaaaaaaaaa aaaaaa 515

<210> 473
<211> 5829
<212> DNA
<213> Homo sapiens

<400> 473
cgcatgccgg ggaagcccaa gctggctcga agagccacca gccacctgtg caagggtggg 60
cctggaccag ttggaccagc caccaagctc acctactcaa ggaagcagg atggccagg 120
tgcaacagcc tgagtggctg ccacctgata gctgatggag cagaggcctg aggaaaatca 180
gatggcacat ttagctcttt aatggatctt aagttaattt ttctataaag cacatggcac 240
cagtccatgc ctcagagctc gtatggcact gcggaccaca gcaggccgag ttcccaggat 300
tgccatccag gggggccttc tgtagccctg gccagacctt gcagagggtg ctgggtgctc 360
tttgagcgag ctgcgcctcc ctggcatgca caggccccag gtactgacac gctgctctga 420
gtgagcttgt cctgccttgg ctgccaccta actgctgatg gacagcggc cttaggaaaa 480
gcaaatggcg ctgtagccca actttagggt agaagaagat gtacctgtc cggccgctag 540
ttggtgactg gtgcacctgc tcttgccgta cccttgacga ggtgggtggg tgctctttgg 600
ccagcttggc cttgcctggc atgcacaagc ctcagtgcga caactgtcct acaaatggag 660

acacagagag	gaaacaagca	gcgggctcag	gagcagggtg	tgtgctgcct	ttggggctcc	720
agtcacatgcc	tcgggtcgta	tgggtactgca	ggcttcttgg	ttgccaaagag	gcggaccaca	780
ggccttcttg	aggaggactt	tacgttcaag	tgcagaaagc	agccaaaatt	accatccatg	840
agactaagcc	ttctgtggcc	ctggcgagac	ttaaaatttg	tgccaaggca	ggacaagctc	900
actcggagca	gcgtgtcagt	agctggggcc	tatgcatgcc	gggcagggcc	gggctggctg	960
aaggagcaac	cagccacctc	tgaagggtg	cgctagtgc	aggcggagca	tccaccacct	1020
cacccgctcg	aggaagtggg	gatggccagg	ttcccacagc	ctgagtgtct	gccaccttat	1080
tgctgatgga	gcagaggcct	taagaaaagc	agatggcact	gtggccctac	ctttagggtg	1140
gaagaagtga	tgtacatgtc	cggacgctaa	ttgggtactg	gtacaccggc	tcctgtctaca	1200
cctttgcaga	ggtggctggt	tgtcttttga	gccagcttgt	ccttgcccgg	catgcacaag	1260
tttcagtga	acaaactttg	cacaaatgga	gccatataga	ggaaacaaga	agcaggttca	1320
ggagaagggt	gtacctggcc	tttgggctc	cagtccatgc	ctcaggtgtc	acatggccta	1380
gcgggtctct	tgggtgccag	gaggcggacc	acaggccatc	ttggggagga	ctttgtgttc	1440
aagtgcagaa	agcagccagg	attgccatcc	agggggacct	tctatagccc	tggccaaacc	1500
ttgcagggtg	gtctggttgc	tctttgagcc	ggcttggcct	ccctggcatg	cacgggcccc	1560
aggtgctggc	acgctgctcc	gagtgtgctt	gtcctgcctt	ggctgccacc	tctgcggggg	1620
tgcgtctgga	gggggtggac	cggccaccaa	ccttaccagg	tcaagggaagt	ggatggccat	1680
gttccacag	cctgagtggc	tgccacctga	tggtgatgg	agcaaaggcc	ttaggaaaag	1740
cagatggccc	ttggccctac	ctttttgtta	gaagaactga	tgttccatgt	cctgcagcga	1800
gtgagcttgg	tggctgtgcc	cccagctcct	ggcgccctct	cgagaggtg	actggtgtgt	1860
cctttggccc	tcttggcctt	gcccagcatg	cacaagcctc	agtgtacta	ctgtgtctaca	1920
aatggagcca	tataggggaa	acgagcagcc	atctcaggag	caaggtgtat	gctgcctttg	1980
ggggctccag	tccttgccctc	aagggcttta	tgctactgtg	ggcttcttgg	ttgtcaagag	2040
gcagaccata	ggcgtcttgg	agagggactt	tatgttcaag	tgcagaaagc	agccaggatt	2100
gccaccctcg	ggactctgcc	ttctgtggcc	ctggccaaac	ttagaatttg	gccgtagaca	2160
ggacaggtc	acttggagta	gcgtgtccgt	agctgggggtc	tgtgcatgcc	gggcaaggcc	2220
gggctggctc	ggggagcaac	cagccacctc	tgccgggggtg	cgccctggagc	aggtggagca	2280
gccaccagct	cacccactcc	aggaagccgg	ggtagccagg	ttcccaaggc	ctgagtgggt	2340
gccaccta	ggctgaagaa	acagaggcct	tgggaaaacc	agatggcact	gtggccctac	2400
ctttatggta	gaagagctga	tttagcctga	ctggcagcgt	gtgggggttg	tggctgtgtc	2460
gcctgctgct	ggcgcatccg	tgaaggatg	gctgggttgc	ctttgagcca	gcttgccctt	2520
gcccggcatg	cgcaagcctc	agtgaacaa	ctgtgctgca	aatggggcca	tatagaggaa	2580
aggagcagct	ggctctggag	catgggtgtg	actcccttgg	ggccttcagt	ccatgtctca	2640
tgggtcggtat	gcactgcgg	gcttgttgg	tgccaagagg	cagaccacag	gtcatcttga	2700
ggaggacttt	atgttccagt	ccagaaagca	gccagtggta	ccaccaggg	gacttgtgct	2760
tctgtgcca	ggccagacgt	agaatttgac	aaagtcagga	cggtctcagt	cagagcggcg	2820
tgtcggtccc	cggggcctgt	gcatgccggg	cagggccggg	ctggcttggg	gagcaagcag	2880
ccacctctgt	taagggtgtg	cctggagcag	gtggagcagc	caccaacctc	acgcactgaa	2940
agaagcaggg	atggccagg	tccaacatcc	tgagtggctg	ccacctgatg	gctgatggag	3000
cagaggcctg	agtaaaagca	gatggcactg	ctttgtagt	ctgttcttgg	tctctcttga	3060
tcttttccag	ttaatgtctg	ttttatcaga	gactaggatt	gcaaaccctg	ctcttttttg	3120
ctttccattt	gcttggtaaa	tattcctcca	tccctttatt	ttaagcctat	gtgtgtcttt	3180
gcacatgaga	tgggtctcct	gaatacagga	caacaatggg	tctttactct	ttatccaact	3240
tgccagtctg	tgtcttttaa	ctggggcatt	tagccattt	acatttaagt	ttagtattgt	3300
tacatgtgaa	atttatcctg	tcagtatgtt	gctagctttt	tatttttccc	attagtttgc	3360
agtttcttta	tagtgtcaat	ggtctttaca	attcgatatg	ttttttagt	ggctggta	3420
ggtttttcc	ttctacgttt	agtgtctcct	tcaggagctc	ttgtaacaca	agaatgtgga	3480
tttatttctt	gtaaggtaaa	tatgtggatt	tatttcttgg	gactgtattc	tatggccttt	3540
accccaagaa	tcattacttt	ttaaaatgca	attcaaatta	gcataaaaca	tttacagcct	3600
atggaaaggc	ttgtggcatt	agaatcctta	tttataggat	tatttttgtg	ttttttgaga	3660
tatggtcttt	gtcatcgagg	cagaagtgcc	gtggtttgat	cataattcac	cacagccctg	3720
aactcttgag	tccaagccat	ccttttgcct	taatctccca	accagttgga	tctgcaggca	3780
taaggcatca	tgcgtggcta	attttttcac	gttttttttt	tttttttgtc	gagattatgg	3840
tgtcactgtg	tgtctctggc	tgatctcaaa	tgtttgacct	caagggatct	ttctgccacg	3900
gcctcctaaa	gtgctaggat	tatatgcatg	atacaccatg	cctattgtag	agtattacat	3960
tattttcaaa	gtcttattgt	aagagccatt	tattgccttt	ggcctaaata	actcaatata	4020
atatctctga	aacttttttt	tgacaaattt	tggggcgtga	tgatgagaga	aggggggttg	4080
aaactttcta	ataagagtta	acttagagcc	atttaagaaa	ggaaaaaaca	caaattatca	4140

```

gaaaaacaac agtaagatca agtgcaaaag ttctgtggca aagatgatga gagtaaagaa 4200
tatatgtttg tgactcatgg tggtttttac tttgttcttg aatttctgag tacgggttaa 4260
catttaaaga atctacatta tagataacat tttattgcaa gtaaagtgtat ttcaaaattt 4320
gttattgggt ttgtatgaga ttattctcag cctacttcat tatcaagcta tattatttta 4380
ttaatgtagt tcatgatctt tacagcaaaag ctgaaagctg tatcttcaaa atatgtctat 4440
ttgactaaaa agttattcaa caggagttat tatctataaa aaaaatacaa caggaatata 4500
aaaaacttga ggataaaaag atgttggaaa aagtaattatt aaatcttaaa aaacatatgg 4560
aaactacaca atggtgaaga cacattgggtg aagtacaaaa atataaattg gatctagaag 4620
aaaggccaat gcaggcaata gaaaaattag tagaaatccc tttaaagggt agtttgtaaa 4680
atcaggtaag tttatttata atttgctttc atttatttca ctgcaaatta tattttggat 4740
atgtatata atgtgtcttc ctctgcctgt cttacagcaa tttgccttgc agagttctag 4800
gaaaaagggt gcatgtgttt ttactttcaa aatattttaa tttccatcat tataacaaaa 4860
tcaatttttc agagtaatga ttctcactgt ggagtcattt gattattaag acccgttggc 4920
ataagattac atcctctgac tataaaaatc ctggaagaaa acctaggaaa tattcgtctg 4980
gacattgcac ttggcaatga atttatgggt aaccactgat ccacttccag tcaactatcca 5040
tgagttttta tttccagata catgaaatca tatgagttga aactttcttt tgattgagca 5100
gtttgaaaac cgtctttttg tagaatctgc aagtggatat ttggaaccct ttgaggccta 5160
tgctgaaaaa agaaatatct tcactacatg atgaccacca gcagcagctg gggaaccag 5220
caccctgtgg aattccatac ggtgcataga atacatcttc ccttcagtcg gcttgggtca 5280
acttaggtca tgggccacct ggctgatagc agtttccaca gaaatgcttc aagatgaaag 5340
tggatgaccg ggccaccctc caccactgcc ctgtaagacc atgggacaca caggccacca 5400
gttcttttca tgtggtcatc ccctgttaga tgggagaaaa tacacctgcc tcatttttgt 5460
accttctgtg tgaacattcc acggcagact gtcgctaaat gtggatgaag aattgaatga 5520
atgaatgaat atgagagaaa atgaataaat ggttcagatc ctgggctgga aggtgtgta 5580
tgaggatggt gggtagagga gggctctgtt ttcttgcttc taagtcacta attgtcactt 5640
tggggcagga gcacaggctt tgaatgcaga ccgactggac ttaattctg gctttactag 5700
ttgtgattgt gtgaccttgt gaaagttact taaacctct gtgcctgttt ctttatctgt 5760
aaaatggaga taataagatg tcaaggact gtggaagaa ttaaatgctt taaaaaaaaa 5820
aaaaaaaaa

```

<210> 474

<211> 1594

<212> DNA

<213> Homo sapiens

<400> 474

```

atztatggat cattaatgcc tctttagtag tttagagaaa acgtcaaaag aaatggcccc 60
agaataagct tcttgatttg taaaattcta tgtcattggc tcaaatgtgt atagtatctc 120
aaaatataaa tatatagaca tctcagataa tatatttgaa atagcaaatt cctgttagaa 180
aataatagta cttaactaga tgagaataac aggtcgccat tatttgaatt gtctcctatt 240
cgtttttcat ttgttgtgtt actcatgttt tacttatgag ggatatatat aacttccact 300
gttttcagaa ttattgtatg cagtcagtat gagaatgcaa tttaaagttc cttgatgctt 360
tttcacactt ctattactag aaataagaat acagtaatat tggcaaagaa aattgaccag 420
ttcaataaaa ttttttagta aatctgattg aaaataaaca ttgcttatgg ctttcttaca 480
tcaatattgt tatgtcctag acaccttato tgaaattacg gtttcaaaat tctaattatg 540
tgcaaatgtg taaaatatca atactttatg ttcaagctgg ggcctcttca ggcgtcctgg 600
gctgagagag aaagatgcta gctccgcaag ccggagaggg aacaccgcca cattgttaca 660
cggacacacc gccacgtgga cacatgacca gactcacatg tacagacaca cggagacatt 720
accacatgga gacaccgtca cacagtcaca cggacacact ggcatagtca catggacgga 780
cacacagaca tatggagaaa tcacatggac acaccaccac actatcacag ggacacagac 840
acacggagac atcaccacat ggacacactg tcacactacc acagggacac gagacatcac 900
actgtcacat ggacacacca tcacacacat gaacacaccg acacactgcc atatggacac 960
tggcacacac actgccacac tgtcacatgg acacacctcc acaccatcac accaccacac 1020
acactgcctg tggacacaag gacacacaga cactgtcaca cagatacaca aaacactgtc 1080
acacggagac atcaccatgc agatacacca ccactctggg gccgtctgaa ttaccctgct 1140
ggggggacag cagtggcata ctcatgccta agtgactggc tttcacccca gtagtgattg 1200
ccctccatca acactgcca ccccaggttg gggctacccc agcccatctt taaaaacag 1260
ggcaaggtga actaatggag tgggtggagg agttggaaga aatcccagcg tcagtcaccg 1320

```

```

ggatagaatt cccaaggaac cctctttttg gaggatgggt tccatttctg gaggcgatct 1380
gccgacaggg tgaatgcctt cttgcttgct ttctggggaa tcagagagag tccgttttgt 1440
ggtgggaaga gtgtggctgt gtactttgaa ctctgtataa ttctctgact catgtccaca 1500
aaaccaacag ttttgtgaat gtgtctggag gcaagggaag ggccactcag gatctatgtt 1560
gaagggaaga ggcttggggc tggagtattc gctt 1594

```

<210> 475

<211> 2414

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (33)

<223> n=A,T,C or G

<400> 475

```

cccaacacaa tggctttata agaatgcttc acntgtgaaa aacaaatatt aaagtcttct 60
tgtagattat ttttaaggac aaatctttat tccatgttta atttatttag ctttccctgt 120
agctaattat tcatgctgaa cacattttta atgctgtaaa ttagataat gtaatttatg 180
tatcattaat gcctctttag tagtttagag aaaacgtcaa aagaaatggc cccagaataa 240
gcttcttgat ttgtaaaatt ctatgtcatt ggctcaaatt tgtatagtat ctcaaaatat 300
aaatatatag acatctcaga taatatattt gaaatagcaa attcctgtta gaaaataata 360
gtacttaact agatgagaat aacaggctgc cattatttga attgtctcct attcgttttt 420
catttgttgt gttactcatg ttttacttat ggggggatat atataacttc cgctgttttc 480
agaagtattg tatgcagtca gtatgagaat gcaatttaag ttcccttgat gctttttcac 540
acttctatta ctagaaataa gaatacagta atattggcaa agaaaattga ccagttcaat 600
aaaatttttt agtaaatctg attgaaaata aacattgctt atggctttct tacatcaata 660
ttgttatgtc ctagacacct tatctgaaat tacggcttca aaattctaata tatgtgcaaa 720
tgtgtaaaat atcaatactt tatgttcaag ctggggcctc ttcaggcgctc ctgggctgag 780
agagaaagat gctagctccg caagccgggg agggaacacc gccacattgt tacatggaca 840
caccgccacg tggacacatg accagactca catgtacaga cacacggaga cattaccaca 900
tggagacacc gtcacacagt cacacgagca cactggcata gtcacatgga cggacacaca 960
gacatatgga gaaatcacac tgacacacca ccacactatc acagggacac agacacacgg 1020
agacatcacc acatggacac actgtcacac taccacaggg acacgagaca tcacactgtc 1080
acatggacac accatcacac acatgaacac accgacacac tgccatatgg aactgccac 1140
acacactgcc aactgtcac atggacacac ctccatacca tcacaccacc acacacactg 1200
ccatgtggac acaaggacac acagacactg tcacacagat acacaaaaca ctgtcacacg 1260
gagacatcac catgcagata caccaccaca tggacatagc accagacact ctgccacaca 1320
gatacaccac cagacagaaa tgcggacaca ctgccacaca gacaccacca catcggtgcc 1380
acactttcat gtgtcagctg gcggtgtggg cccacgactc ctgggctcta atcgagaaat 1440
tacttggaca tatagtgaag gcaaaatttt tttttatttt ctgggtaacc aagcgcgact 1500
ctgtctcaaa aaaagaaaaa aaaagcaata tactgtgtaa tcgttgacag cataattcac 1560
tattatgtag atcggagagc agaggattct gaatgcatga acatatcatt aacatttcaa 1620
tacattactc ataattactg atgaactaaa gagaaccaa gaaattatgg tgatagttat 1680
attgacctgg agaaatgtag acacaaaaga accgtaagat gagaaatgtg ttaacacagt 1740
ctataagggc atgcaagaat aaaaataggg gagaaaacag gagagttttt caagagcttt 1800
ctggctcatgt aagtcaactt gtatcggtta atttttaaaa ggtttattta catgcaataa 1860
actgcacata cttcaattgt acatttttgt aattcttggc attttagctt ctataaaacc 1920
agcaacatat taaaatagca aacatatcca ttacctttac caccaaagtt ttcttgtgtt 1980
ttttctactc actttttcct gcctatcccc ccatctcttc cacaggtaac cactgatcca 2040
cttcagtcac ctatccatga gtttttattt ccaaatatcat gaaatcatat gaatttctgg 2100
tttttctgtt tggagcccaa ggagcaaggg cagaatgagg aacatgatgt ttcttwccga 2160
cagttactca tgactctcc atccaggact gaggggggca tccttctcca tctaggactg 2220
ggggcatcct tctccatcca gtattggggg tcatccttct ccatccagta ttgggggtca 2280
tctctctcca tccaggacct gaggggtgtc cttttctgog cttccttggg tggcagtcct 2340
tcccttcatg tttatagtra cttaccatta aatcactgtg ccgttttttc ctaaaataaa 2400
aaaaaaaaaa aaaa 2414

```


<210> 476
<211> 3434
<212> DNA
<213> Homo sapiens

<400> 476

```
ctgtgctgca aatggggcca tatagaggaa aggagcagct ggctctggag catggtgtgc 60
actccctttg ggccttcagt ccatgtctca tgggtcgtat gacactgcgg gcttgttgggt 120
tgccaagagg cagaccacag gtcatcttga ggaggacttt atgttccagt ccagaaagca 180
gccagtggta ccaccaggg gacttgtgct tctgtggccc aggccagacg tagaatttga 240
caaagtacag acggtctcag tcagagcagc atgtcgggtcc ccggggcctg tgcattgccgg 300
gcagggccag gctggcttaa ggagcaagca gccacctctg ttaggggtgt gcctggagca 360
ggtggagcag ccaccaacct cacgcactga aagaagcagg gatggccagg ttccaacatc 420
ctgagtggct gccacctgat ggctgatgga gcagaggcct gaggaaaagc agatggcact 480
gctttttagt gctgttcttt gtctctcttg atctttttca gttaatgtct gttttatcag 540
agactaggat tgcaaacctt gctctttttt gctttccatt tgccttggta atattcctcc 600
atccctttat ttttaagccta tgtgtgtctt tgcacatgag atgggtctcc tgaatacagg 660
acaacaatgg tcttttactc tttatccaac ttgccagtct gtgtctttta actggggcct 720
ttagccattt tacatttaag tttagtattt gttacatgtg aaatttatcc tgtcatgatg 780
ttgctagctt tttatttttc ccattagttt gcagtttctt tatagtgtca atgggtctta 840
caattcgata tgtttttgta gtggctggta ctgggttttc ctttctacgt ttagtgtctc 900
cttcaggagc tcttgaataa caagaatgtg gatttatttc ttgtaaggta aatatgtgga 960
tttattctgg gactgtattc tatggccttt accccaagaa tcattacttt ttaaaatgca 1020
attcaaatta gcataaaaca tttacagcct atggaaaggc ttgtggcatt agaatcctta 1080
tttataggat tattttgtgt ttttttgaga taatgtcttt gtcatcgagg cagaagtgcc 1140
gtggtttgat cataattcac cacagccctg aactcttgag tccaagccat ccttttgctc 1200
taatctccca accagttgga tctacaagca taaggcatca tgcgtggcta attttttcac 1260
gttttttttt tttttgtcga gattatggta tcaactgtgtt gctctggctg atctcaaag 1320
tttgacctca aggatctttt ctgccacagc ctctaaagt gctaggatta tatgcatgat 1380
acaccatgcc tattgtagag tattacatta ttttcaaagt cttattgtaa gagccattta 1440
ttgccttttg cctaaataac tcaatataat atctctgaaa cttttttttg acaaattttg 1500
gggcgtgatg atgagagaag ggggtttgaa acttttcta atagagttac ttagagccat 1560
ttaagaaaag aaaaaaacaca aattatcaga aaaacaacag taagatcaag tgcaaaaagt 1620
ctgtggcaaa gatgatgaga gtaaagaata tatgtttgtg actcatgggt gcttttactt 1680
tgttcttgaa tttctgagta cgggttaaca tttaaagaat ctacattata gataacattt 1740
tattgcaagt aaatgtattt caaaatttgt tattggtttt gtatgagatt attctcagcc 1800
tacttcatta tcaagctata ttattttatt aatgtagttc gatgatctta cagcaaagct 1860
gaaagctgta tcttcaaaat atgtctattt gactaaaaag ttattcaaca ggagttatta 1920
tctataaaaa aatataacag gaatataaaa aacttgagga taaaagatg ttggaaaaag 1980
taatattaaa tcttaaaaaa catatggaaa ctacacaatg gtgaagacac attgggtgaag 2040
tacaaaaata taaattggat ctagaagaaa gggcaatgca ggcaatagaa aaattagtag 2100
aaatcccttt aaaggttagt ttgtaaaatc aggttaagtt atttataatt tgctttcatt 2160
tatttctactg caaattatat tttggatatg tatatatatt gtgcttcctc tgcctgtctt 2220
acagcaatth gccttgacga gttctaggaa aaagggtggca tgtgttttta ctttcaaaat 2280
atttaaatth ccattcattat aacaaaatca atttttcaga gtaatgattc tcaactgtgga 2340
gtcatttgat tattaagacc cgttggcata agattacatc ctctgactat aaaaatcctg 2400
gaagaaaacc taggaaatat tctgtctggac attgcaactg gcaatgaatt tatgggcgct 2460
ttggaatcct gcagatataa taatgataat taaacaaaac actcagagaa actgccaacc 2520
ctaggatgaa gtatattgtt actgtgcttt gggattaaaa taagtaacta cagttttatag 2580
aacttttata ctgatacaca gactataaaa agggaaaggg ttttagatgag aagctctgct 2640
atgcaatcaa gaatctcagc cactcatttc tgtaggggct gcaggagctc cctgtaaaaga 2700
gaggttatgg agtctgtagc ttcaggtaag atacttaaaa cccttcagag tttctccatt 2760
ttttcccata gtttcccaa aaaggttatg acactttata agaatgcttc acttgtgaaa 2820
aacaatatc aaagtcttct tgtagattat ttttaaggac aaatctttat tccattgtta 2880
atatttttag ctttccctgt agctaataat tcatgctgaa cacattttta atgctgtaaa 2940
tgtagataat gtaatttatg tatcattaat gcctctttag tagtttagag aaaacgtcaa 3000
aagaaatggc cccagaataa gcttcttgat ttgtaaaatt ctatgtcatt ggctcaaatt 3060
```

tgtatagtat ctcaaaatat aaatatatag acatctcaga taatatattt gaaatagcaa 3120
 attcctgtta gaaaataata gtacttaact agatgagaat aacaggtcgc cattatttga 3180
 attgtctcct attcggtttt catttggtgt gttactcatg ttttacttat ggggggatat 3240
 atataacttc cgtgttttc agaagtattg tatgcagtca gtatgagaat gcaatttaag 3300
 tttccttgat gctttttcac acttctatta ctagaataa gaatacagta atattggcaa 3360
 agaaaattga ccagttcaat aaaatttttt agtaaacttg attgaaaata aaaaaaaaaa 3420
 aaaaaaaaaa aaaa 3434

<210> 477

<211> 140

<212> PRT

<213> Homo sapiens

<400> 477

Met Asp Gly His Thr Asp Ile Trp Arg Asn His Met Asp Thr Pro Pro
 5 10 15

His Tyr His Arg Asp Thr Asp Thr Arg Arg His His His Met Asp Thr
 20 25 30

Leu Ser His Tyr His Arg Asp Thr Arg His His Thr Val Thr Trp Thr
 35 40 45

His His His Thr His Glu His Thr Asp Thr Leu Pro Tyr Gly His Trp
 50 55 60

His Thr His Cys His Thr Val Thr Trp Thr His Leu His Thr Ile Thr
 65 70 75 80

Pro Pro His Thr Leu Pro Val Asp Thr Arg Thr His Arg His Cys His
 85 90 95

Thr Asp Thr Gln Asn Thr Val Thr Arg Arg His His His Ala Asp Thr
 100 105 110

Pro Pro Leu Trp Cys Arg Leu Asn Tyr Pro Ala Gly Gly Thr Ala Val
 115 120 125

Ala Tyr Ser Cys Leu Ser Asp Trp Leu Ser Pro Gln
 130 135 140

<210> 478

<211> 143

<212> PRT

<213> Homo sapiens

<400> 478

Met Tyr Arg His Thr Glu Thr Leu Pro His Gly Asp Thr Val Thr Gln
 5 10 15

Ser His Gly His Thr Gly Ile Val Thr Trp Thr Asp Thr Gln Thr Tyr
 20 25 30

Gly Glu Ile Thr Trp Thr His His His Thr Ile Thr Gly Thr Gln Thr
 35 40 45

His Gly Asp Ile Thr Thr Trp Thr His Cys His Thr Thr Thr Gly Thr

166.

50 55 60
 Arg Asp Ile Thr Leu Ser His Gly His Thr Ile Thr His Met Asn Thr
 65 70 75 80
 Pro Thr His Cys His Met Asp Thr Gly Thr His Thr Ala Thr Leu Ser
 85 90 95
 His Gly His Thr Ser Thr Pro Ser His His His Thr His Cys Leu Trp
 100 105 110
 Thr Gln Gly His Thr Asp Thr Val Thr Gln Ile His Lys Thr Leu Ser
 115 120 125
 His Gly Asp Ile Thr Met Gln Ile His His His Ser Gly Ala Val
 130 135 140

<210> 479

<211> 222

<212> PRT

<213> Homo sapiens

<400> 479

Met Tyr Arg His Thr Glu Thr Leu Pro His Gly Asp Thr Val Thr Gln
 5 10 15
 Ser His Glu His Thr Gly Ile Val Thr Trp Thr Asp Thr Gln Thr Tyr
 20 25 30
 Gly Glu Ile Thr Leu Thr His His His Thr Ile Thr Gly Thr Gln Thr
 35 40 45
 His Gly Asp Ile Thr Thr Trp Thr His Cys His Thr Thr Thr Gly Thr
 50 55 60
 Arg Asp Ile Thr Leu Ser His Gly His Thr Ile Thr His Met Asn Thr
 65 70 75 80
 Pro Thr His Cys His Met Asp Thr Ala Thr His Thr Ala Thr Leu Ser
 85 90 95
 His Gly His Thr Ser Ile Pro Ser His His His Thr His Cys His Val
 100 105 110
 Asp Thr Arg Thr His Arg His Cys His Thr Asp Thr Gln Asn Thr Val
 115 120 125
 Thr Arg Arg His His His Ala Asp Thr Pro Pro His Gly His Ser Thr
 130 135 140
 Arg His Ser Ala Thr Gln Ile His His His Thr Glu Met Arg Thr His
 145 150 155 160
 Cys His Thr Asp Thr Thr Thr Ser Leu Pro His Phe His Val Ser Ala
 165 170 175
 Gly Gly Val Gly Pro Thr Thr Leu Gly Ser Asn Arg Glu Ile Thr Trp

167

180 185 190

Thr Tyr Ser Glu Gly Lys Ile Phe Phe Tyr Phe Leu Gly Asn Gln Ala
195 200 205

Arg Leu Cys Leu Lys Lys Arg Lys Lys Lys Gln Tyr Thr Val
210 215 220

<210> 480
<211> 144
<212> PRT
<213> Homo sapiens

<400> 480

Met Glu Pro Tyr Arg Gly Asn Glu Gln Pro Ser Gln Glu Gln Gly Val
5 10 15

Cys Cys Leu Trp Gly Leu Gln Ser Leu Pro Gln Gly Ser Tyr Val Thr
20 25 30

Val Gly Phe Leu Val Val Lys Arg Gln Thr Ile Gly Arg Leu Glu Arg
35 40 45

Asp Phe Met Phe Lys Cys Arg Lys Gln Pro Gly Leu Pro Pro Ser Gly
50 55 60

Leu Cys Leu Leu Trp Pro Trp Pro Asn Leu Glu Phe Gly Arg Arg Gln
65 70 75 80

Asp Arg Leu Thr Trp Ser Ser Val Ser Val Ala Gly Val Cys Ala Cys
85 90 95

Arg Ala Arg Pro Gly Trp Leu Gly Glu Gln Pro Ala Thr Ser Ala Gly
100 105 110

Val Arg Leu Glu Gln Val Glu Gln Pro Pro Ala His Pro Leu Gln Glu
115 120 125

Ala Gly Val Ala Arg Phe Pro Arg Pro Glu Trp Val Pro Pro Asn Gly
130 135 140

<210> 481
<211> 167
<212> PRT
<213> Homo sapiens

<400> 481

Met His Gly Pro Gln Val Leu Ala Arg Cys Ser Glu Cys Ala Cys Pro
5 10 15

Ala Leu Ala Ala Thr Ser Ala Gly Val Arg Leu Glu Gly Val Asp Arg
20 25 30

Pro Pro Thr Leu Pro Ser Gln Gly Ser Gly Trp Pro Cys Ser His Ser
 35 40 45
 Leu Ser Gly Cys His Leu Met Ala Asp Gly Ala Lys Ala Leu Gly Lys
 50 55 60
 Ala Asp Gly Pro Trp Pro Tyr Leu Phe Val Arg Arg Thr Asp Val Pro
 65 70 75 80
 Cys Pro Ala Ala Ser Glu Val Gly Gly Cys Ala Pro Ser Ser Trp Arg
 85 90 95
 Ala Leu Ala Glu Val Thr Gly Cys Ser Leu Gly Pro Leu Gly Leu Ala
 100 105 110
 Gln His Ala Gln Ala Ser Val Leu Leu Leu Cys Tyr Lys Trp Ser His
 115 120 125
 Ile Gly Glu Thr Ser Ser His Leu Arg Ser Lys Val Tyr Ala Ala Phe
 130 135 140
 Gly Gly Ser Ser Pro Cys Leu Lys Gly Leu Met Ser Leu Trp Ala Ser
 145 150 155 160
 Trp Leu Ser Arg Gly Arg Pro
 165

<210> 482

<211> 143

<212> PRT

<213> Homo sapiens

<400> 482

Met Glu Pro Tyr Arg Gly Asn Lys Lys Gln Val Gln Glu Lys Gly Val
 5 10 15
 Pro Cys Leu Trp Gly Ser Ser Pro Cys Leu Arg Cys His Met Ala Leu
 20 25 30
 Arg Ala Ser Trp Leu Pro Gly Gly Gly Pro Gln Ala Ile Leu Gly Arg
 35 40 45
 Thr Leu Cys Ser Ser Ala Glu Ser Ser Gln Asp Cys His Pro Gly Gly
 50 55 60
 Pro Ser Ile Ala Leu Ala Lys Pro Cys Arg Gly Val Trp Leu Leu Phe
 65 70 75 80
 Glu Pro Ala Trp Pro Pro Trp His Ala Arg Ala Pro Gly Ala Gly Thr
 85 90 95
 Leu Leu Arg Val Cys Leu Ser Cys Leu Gly Cys His Leu Cys Gly Gly
 100 105 110
 Ala Ser Gly Gly Gly Gly Pro Ala Thr Asn Leu Thr Gln Ser Arg Lys
 115 120 125

169

Trp Met Ala Met Phe Pro Gln Pro Glu Trp Leu Pro Pro Asp Gly
 130 135 140

<210> 483
 <211> 143
 <212> PRT
 <213> Homo sapiens

<400> 483
 Met Glu Thr Gln Arg Gly Asn Lys Gln Arg Ala Gln Glu Gln Gly Val
 5 10 15
 Cys Cys Leu Trp Gly Ser Ser Pro Cys Leu Gly Ser Tyr Gly Thr Ala
 20 25 30
 Gly Phe Leu Val Ala Lys Arg Arg Thr Thr Gly Leu Leu Glu Glu Asp
 35 40 45
 Phe Thr Phe Lys Cys Arg Lys Gln Pro Lys Leu Pro Ser Met Arg Leu
 50 55 60
 Ser Leu Leu Trp Pro Trp Arg Asp Leu Lys Phe Val Pro Arg Gln Asp
 65 70 75 80
 Lys Leu Thr Arg Ser Ser Val Ser Val Ala Gly Ala Tyr Ala Cys Arg
 85 90 95
 Ala Gly Pro Gly Trp Leu Lys Glu Gln Pro Ala Thr Ser Ala Arg Val
 100 105 110
 Arg Leu Val Gln Ala Glu His Pro Pro Pro His Pro Leu Glu Glu Val
 115 120 125
 Gly Met Ala Arg Phe Pro Gln Pro Glu Cys Leu Pro Pro Tyr Cys
 130 135 140

<210> 484
 <211> 30
 <212> PRT
 <213> Homo Sapien

<400> 484
 Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe
 1 5 10 15
 Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile
 20 25 30

<210> 485
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Made in a lab

<400> 485
 gggaagctta tcacctatgt gccgcctctg c

<210> 486
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Made in a lab

<400> 486
 gcgaattctc acgctgagta ttggcc 27

<210> 487
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Made in a lab

<400> 487
 cccgaattct tagctgccca tccgaacgcc ttcac 36

<210> 488
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Made in a lab

<400> 488
 gggaagcttc ttccccggct gcaccagctg tgc 33

<210> 489
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in a lab

<400> 489
 Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg Ala Val Tyr Leu Ala
 1 5 10 15
 Ser Val Ala

<210> 490
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in a lab

<400> 490
 Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala Thr Cys

```

1          5          10          15
Leu Ser His Ser
20

<210> 491
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 491
Thr Cys Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu
1          5          10          15
Thr Gly Phe Thr
20

<210> 492
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 492
Ala Leu Thr Gly Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr
1          5          10          15
Leu Ala Ser Leu
20

<210> 493
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 493
Tyr Thr Leu Ala Ser Leu Tyr His Arg Glu Lys Gln Val Phe Leu Pro
1          5          10          15
Lys Tyr Arg Gly
20

<210> 494
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 494
Leu Pro Lys Tyr Arg Gly Asp Thr Gly Gly Ala Ser Ser Glu Asp Ser
1          5          10          15
Leu Met Ile Ser

```


20

<210> 495
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in a lab

<400> 495
 Asp Ser Leu Met Thr Ser Phe Leu Pro Gly Pro Lys Pro Gly Ala Pro
 1 5 10 15
 Phe Pro Asn Gly
 20

<210> 496
 <211> 21
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in a lab

<400> 496
 Ala Pro Phe Pro Asn Gly His Val Gly Ala Gly Gly Ser Gly Leu Leu
 1 5 10 15
 Pro Pro Pro Pro Ala
 20

<210> 497
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in a lab

<400> 497
 Leu Leu Pro Pro Pro Ala Leu Cys Gly Ala Ser Ala Cys Asp Val
 1 5 10 15
 Ser Val Arg Val
 20

<210> 498
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in a lab

<400> 498
 Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala Arg Val
 1 5 10 15
 Val Pro Gly Arg
 20

<210> 499
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in a lab

<400> 499
 Arg Val Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp
 1 5 10 15
 Ser Ala Phe Leu
 20

<210> 500
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in a lab

<400> 500
 Leu Asp Ser Ala Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met
 1 5 10 15
 Gly Ser Ile Val
 20

<210> 501
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in a lab

<400> 501
 Phe Met Gly Ser Ile Val Gln Leu Ser Gln Ser Val Thr Ala Tyr Met
 1 5 10 15
 Val Ser Ala Ala
 20

<210> 502
 <211> 414
 <212> DNA
 <213> Homo Sapien

<220>
 <221> misc_feature
 <222> (1)...(414)
 <223> n=A,T,C or G

<400> 502
 caccatggag acaggcctgc gctggctttt cctggctcgt gtgctcaaag gtgtccaatg 60
 tcagtgcgtg gaggagtccg ggggtcgcct ggtcacgcct gggacacctt tgacantcac 120
 ctgtagagtt tttggaatng acctcagtag caatgcaatg agctgggtcc gccaggctcc 180
 agggaagggg ctggaatgga tcggagccat tgataattgt ccacantacg cgacctgggc 240

```

gaaaggccga ttnatnattt ccaaaacctn gaccacgggtg gatttgaaaa tgaccagtcc 300
gacaaccgag gacacggcca cctatntttg tggcagaatg aatactggtg atagtgggtg 360
gaagaatatt tggggcccag gcaccctggg caccgtntcc tcagggaac ctaa 414

```

```

<210> 503
<211> 379
<212> DNA
<213> Homo Sapien

```

```

<220>
<221> misc_feature
<222> (1)...(379)
<223> n=A,T,C or G

```

```

<400> 503
atncgatggt gcttgggtcaa aggtgtccag tgtcagtcgg tggaggagtc cgggggtcgc 60
ctggtcacgc ctgggacacc cctgacactc acctgcaccg tntctggatt ngacatcagt 120
agctatggag tgagctgggt ccgccaggct ccagggaagg ggctggnata catcggtatca 180
ttagtagtag tgggtacattt tacgcgagct gggcgaaagg ccgattcacc atttccaaaa 240
cctngaccac ggtggatttg aaaatcacca gtttgacaac cgaggacacg gccacctatt 300
tntgtgccag aggggggttt aattataaag acatttgggg cccaggcacc ctggtcaccg 360
tntccttagg gcaacctaa 379

```

```

<210> 504
<211> 19
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Made in a lab

```

```

<400> 504
Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp Ser Pro Tyr Phe Lys Glu
1 5 10 15
Asn Ser Ala

```

```

<210> 505
<211> 20
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Made in a lab

```

```

<400> 505
Lys Glu Asn Ser Ala Phe Pro Pro Phe Cys Cys Asn Asp Asn Val Thr
1 5 10 15
Asn Thr Ala Asn
20

```

```

<210> 506
<211> 407
<212> DNA
<213> Homo Sapien

```

```

<400> 506

```

```

atggagacag gcctgcgctg gcttctcctg gtcgctgctg tcaaaggtgt ccagtgtcag    60
tcgctggagg agtccggggg tcgcctgggc acgcctggga caccctgac actcacctgc    120
accgtctctg gattctccct cagtagcaat gcaatgatct gggtcgcgca ggctccaggg    180
aaggggctgg aatacatcgg atacattagt tatgggtgta gcgcatacta cgcgagctgg    240
gtgaaaggcc gattcaccat ctccaaaacc tcgaccacgg tggatctgag aatgaccagt    300
ctgacaaccg aggacacggc cacctatttc tgtgccagaa atagtgattt tagtggtatg    360
ttgtggggcc caggcacccct ggtcacccgc tcctcagggc aacctaa                407

```

<210> 507
 <211> 422
 <212> DNA
 <213> Homo Sapien

```

<400> 507
atggagacag gcctgcgctg gcttctcctg gtcgctgtgc tcaaaggtgt ccagtgtcag    60
tcgctggagg agtccggggg tcgcctgggc acgcctggga caccctgac actcacctgt    120
acagtctctg gattctccct cagcaactac gacctgaact gggtcgcgca ggctccaggg    180
aaggggctgg aatggatcgg gatcattaat tatgttggtg ggacggacta cgcgaactgg    240
gcaaaaggcc gggtcaccat ctccaaaacc tcgaccacgg tggatctcaa gatcgccagt    300
ccgacaaccg aggacacggc cacctatttc tgtgccagag ggtggaagtg cgatgagtct    360
ggctcgtgct tgcgcatctg gggcccaggc accctgggtca ccgtctcctt agggcaacct    420
aa                                                                422

```

<210> 508
 <211> 411
 <212> DNA
 <213> Homo Sapien

<220>
 <221> misc_feature
 <222> (1)...(411)
 <223> n=A,T,C or G

```

<400> 508
atggagacag gcctgcgctg cttctcctgg tcgctgtgct caaaggtgtc cagtgtcagt    60
cgggtggagg gtccgggggt cgcttggtca cgctgggac acccctgaca ctcacctgca    120
cagtctctgg aatcgacctc agtagctact gcatgagctg ggtccgcccag gctccaggga    180
aggggctgga atggatcgga atcattggta ctcttggtga cacatactac gcgaggtggg    240
cgaaaggccg attcaccatc tccaaaacct cgaccacggt gcatntgaaa atcnccagtc    300
cgacaaccga ggacacggcc acctatttct gtgccagaga tcttcgggat ggtagtagta    360
ctggttatta taaaatctgg ggcccaggca ccctgggtcac cgtctccttg g                411

```

<210> 509
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in a lab

```

<400> 509
Leu Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser
 1              5              10             15

```

<210> 510
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Made in a lab

<400> 510

Pro	Glu	Tyr	Asn	Arg	Pro	Leu	Leu	Ala	Asn	Asp	Leu	Met	Leu	Ile
1				5					10					15

<210> 511

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 511

Tyr	His	Pro	Ser	Met	Phe	Cys	Ala	Gly	Gly	Gly	Gln	Asp	Gln	Lys
1				5					10					15

<210> 512

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 512

Asp	Ser	Gly	Gly	Pro	Leu	Ile	Cys	Asn	Gly	Tyr	Leu	Gln	Gly	Leu
1				5					10					15

<210> 513

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 513

Ala	Pro	Cys	Gly	Gln	Val	Gly	Val	Pro	Asx	Val	Tyr	Thr	Asn	Leu
1				5					10					15

<210> 514

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 514

Leu	Cys	Lys	Phe	Thr	Glu	Trp	Ile	Glu	Lys	Thr	Val	Gln	Ala	Ser
1				5					10					15

<210> 515

<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 515
Met Val Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg
1 5 10 15

<210> 516
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 516
Val Ser Glu Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln
1 5 10 15

<210> 517
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 517
Glu Val Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met
1 5 10 15

<210> 518
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 518
Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly
1 5 10 15

<210> 519
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 519
Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg Asn Tyr Asp Glu Gly Cys
1 5 10 15

Gly

<210> 520
 <211> 25
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in a lab

<400> 520
 Val Gly Glu Gly Leu Tyr Gln Gly Val Pro Arg Ala Glu Pro Gly Thr
 1 5 10 15
 Glu Ala Arg Arg His Tyr Asp Glu Gly
 20 25

<210> 521
 <211> 21
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in a lab

<400> 521
 Ala Pro Phe Pro Asn Gly His Val Gly Ala Gly Gly Ser Gly Leu Leu
 1 5 10 15
 Pro Pro Pro Pro Ala
 20

<210> 522
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in a lab

<400> 522
 Leu Leu Val Val Pro Ala Ile Lys Lys Asp Tyr Gly Ser Gln Glu Asp
 1 5 10 15
 Phe Thr Gln Val
 20

<210> 523
 <211> 254
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in a lab

<220>
 <221> VARIANT
 <222> (1)...(254)
 <223> Xaa = any amino acid

<400> 523

Met Ala Thr Ala Gly Asn Pro Trp Gly Trp Phe Leu Gly Tyr Leu Ile
 1 5 10 15
 Leu Gly Val Ala Gly Ser Leu Val Ser Gly Ser Cys Ser Gln Ile Ile
 20 25 30
 Asn Gly Glu Asp Cys Ser Pro His Ser Gln Pro Trp Gln Ala Ala Leu
 35 40 45
 Val Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln
 50 55 60
 Trp Val Leu Ser Ala Thr His Cys Phe Gln Asn Ser Tyr Thr Ile Gly
 65 70 75 80
 Leu Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met
 85 90 95
 Val Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu
 100 105 110
 Leu Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu
 115 120 125
 Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala
 130 135 140
 Gly Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg
 145 150 155 160
 Met Pro Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu Glu
 165 170 175
 Val Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys
 180 185 190
 Ala Gly Gly Gly Gln Xaa Gln Xaa Asp Ser Cys Asn Gly Asp Ser Gly
 195 200 205
 Gly Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly
 210 215 220
 Lys Ala Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn Leu
 225 230 235 240
 Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser
 245 250

<210> 524

<211> 765

<212> DNA

<213> Homo sapien

<400> 524

atggccacag caggaaatcc ctggggctgg ttcttggggg acctcatcct tgggtgtcgca 60
 ggatcgctcg tctctggtag ctgcagccaa atcataaacg gcgaggactg cagcccgcac 120
 tcgcagccct ggcaggcggc actggtcatg gaaaacgaat tggtctgctc gggcgctctg 180
 gtgcacccgc agtgggtgct gtcagccgca cactgtttcc agaactccta caccatcggtg 240
 ctgggcctgc acagtcttga ggccgaccaa gagccaggga gccagatggt ggaggccagc 300
 ctctccgtac ggcacccaga gtacaacaga cccttgtctg ctaacgacct catgctcatc 360
 aagttggacg aatccgtgtc cgagtctgac accatccgga gcatcagcat tgcttcgcag 420
 tgccctaccg cggggaactc ttgcctcgtt tctggctggg gtctgctggc gaacggcaga 480
 atgcctaccg tgctgcagtg cgtgaacgtg tcggtggtgt ctgaggaggt ctgcagtaag 540
 ctctatgacc cgctgtacca cccagcatg ttctgcgccg gcggagggca agaccagaag 600
 gactcctgca acggtgactc tggggggccc ctgatctgca acgggtactt gcagggcctt 660
 gtgtctttcg gaaaagcccc gtgtggccaa gttggcgtgc caggtgtcta caccaacctc 720
 tgcaaattca ctgagtggat agagaaaacc gtccaggcca gtttaa 765

<210> 525

<211> 254

<212> PRT

<213> Homo sapien

<400> 525

Met Ala Thr Ala Gly Asn Pro Trp Gly Trp Phe Leu Gly Tyr Leu Ile
 1 5 10 15
 Leu Gly Val Ala Gly Ser Leu Val Ser Gly Ser Cys Ser Gln Ile Ile
 20 25 30
 Asn Gly Glu Asp Cys Ser Pro His Ser Gln Pro Trp Gln Ala Ala Leu
 35 40 45
 Val Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln
 50 55 60
 Trp Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly
 65 70 75 80
 Leu Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met
 85 90 95
 Val Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu
 100 105 110
 Leu Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu
 115 120 125
 Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala
 130 135 140
 Gly Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg
 145 150 155 160
 Met Pro Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu Glu
 165 170 175
 Val Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys
 180 185 190
 Ala Gly Gly Gly Gln Asp Gln Lys Asp Ser Cys Asn Gly Asp Ser Gly
 195 200 205
 Gly Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly
 210 215 220
 Lys Ala Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn Leu
 225 230 235 240
 Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser
 245 250

<210> 526

<211> 963

<212> DNA

<213> Homo sapiens

<400> 526

atgagttcct gcaacttcac acatgccacc tttgtgctta ttggtatccc aggattagag 60
 aaagcccatt tctgggttgg cttcccctc ctttccatgt atgtagtggc aatgttttga 120
 aactgcatcg tggcttctcat cgtaaggacg gaacgcagcc tgcacgctcc gatgtacctc 180
 tttctctgca tgcttgacgc cattgacctg gccttatcca catccaccat gcctaagatc 240
 cttgcccttt tctggtttga ttcccagagag attagctttg aggcctgtct taccagatg 300
 ttctttattc atgccctctc agccattgaa tccaccatcc tgctggccat ggcctttgac 360
 cgttatgtgg ccattcgcca cccactgcgc catgctgcag tgctcaacaa tacagtaaca 420
 gccagattg gcacgtggc tgtggtccgc ggatccctct ttttttccc actgcctctg 480
 ctgatcaagc ggctggcctt ctgccactcc aatgtcctct cgcactccta ttgtgtccac 540
 caggatgtaa tgaagtggc ctatgcagac actttgccca atgtggtata tggctttact 600
 gccattctgc tggctcatggg cgtggacgta atgttcactc ccttgtccta ttttctgata 660
 atacgaacgg ttctgcaact gccttccaag tcagagcggg ccaaggcctt tggaacctgt 720
 gtgtcaacaa ttggtgtggg actgccttc tatgtgccac ttattggcct ctcagttgta 780
 caccgctttg gaaacagcct tcattcccatt gtgcgtgttg tcatgggtga catctacctg 840
 ctgctgcctc ctgtcatcaa tcccatcatc tatggtgccaa aaaccaaaca gatcagaaca 900
 cgggtgctgg ctatgttcaa gatcagctgt gacaaggact tgcaggctgt gggaggcaag 960
 tga 963

Met Ser Ser Cys Asn Phe Thr His Ala Thr Phe Val Leu Ile Gly Ile
5 10 15

Pro Gly Leu Glu Lys Ala His Phe Trp Val Gly Phe Pro Leu Leu Ser
20 25 30

Met Tyr Val Val Ala Met Phe Gly Asn Cys Ile Val Val Phe Ile Val
35 40 45

Arg Thr Glu Arg Ser Leu His Ala Pro Met Tyr Leu Phe Leu Cys Met
50 55 60

Leu Ala Ala Ile Asp Leu Ala Leu Ser Thr Ser Thr Met Pro Lys Ile
65 70 75 80

Leu Ala Leu Phe Trp Phe Asp Ser Arg Glu Ile Ser Phe Glu Ala Cys
85 90 95

Leu Thr Gln Met Phe Phe Ile His Ala Leu Ser Ala Ile Glu Ser Thr
100 105 110

Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys His Pro
115 120 125

Leu Arg His Ala Ala Val Leu Asn Asn Thr Val Thr Ala Gln Ile Gly
130 135 140

Ile Val Ala Val Val Arg Gly Ser Leu Phe Phe Phe Pro Leu Pro Leu
145 150 155 160

Leu Ile Lys Arg Leu Ala Phe Cys His Ser Asn Val Leu Ser His Ser
165 170 175

Tyr Cys Val His Gln Asp Val Met Lys Leu Ala Tyr Ala Asp Thr Leu
180 185 190

Pro Asn Val Val Tyr Gly Leu Thr Ala Ile Leu Leu Val Met Gly Val
195 200 205

Asp Val Met Phe Ile Ser Leu Ser Tyr Phe Leu Ile Ile Arg Thr Val
210 215 220

Leu Gln Leu Pro Ser Lys Ser Glu Arg Ala Lys Ala Phe Gly Thr Cys
225 230 235 240

Val Ser His Ile Gly Val Val Leu Ala Phe Tyr Val Pro Leu Ile Gly
245 250 255

Leu Ser Val Val His Arg Phe Gly Asn Ser Leu His Pro Ile Val Arg
260 265 270

Val Val Met Gly Asp Ile Tyr Leu Leu Leu Pro Pro Val Ile Asn Pro
275 280 285

Ile Ile Tyr Gly Ala Lys Thr Lys Gln Ile Arg Thr Arg Val Leu Ala
290 295 300

Met Phe Lys Ile Ser Cys Asp Lys Asp Leu Gln Ala Val Gly Gly Lys
305 310 315 320

<210> 528
<211> 20
<212> DNA
<213> Homo Sapien

<400> 528
actatggtcc agaggctgtg 20

<210> 529
<211> 20
<212> DNA
<213> Homo Sapien

<400> 529
atcacctatg tgccgcctct 20

<210> 530
<211> 1852
<212> DNA
<213> Homo sapiens

<400> 530
ggcacgagaa ttaaaaccct cagcaaaaca ggcatagaag ggacatacct taaagtaata 60
aaaaccacct atgacaagcc cacagccaac ataatactaa atggggaaaa gttagaagca 120
tttcctctga gaactgcaac aataaataca aggatgctgg attttgtcaa atgccttttc 180
tgtgtctgtt gagatgctta tgtgactttg cttttaattc tgtttatgtg attatcacat 240
ttattgactt gcctgtgtta gaccggaaga gctgggggtg ttctcaggag ccaccgtgtg 300
ctgcgcgagc ttcgggataa cttgaggctg catcactggg gaagaaacac aytccgtgcc 360
gtggcgctga tggctgagga cagagcttca gtgtggcttc tctgcgactg gcttcttcgg 420
ggagtcttcc cttcatagtt catccatatt gctccagagg aaaattatat tattttgtta 480
tggatgaaga gtattacgtt gtgcagatat actgcagtgt cttcatctct tgatgtgtga 540
ttgggtaggt tccaccatgt tgccgcagat gacatgattt cagtacctgt gtctggctga 600
aaagtgtttg tttgtgaatg gatattgtgg tttctggatc tcatcctctg tgggtggaca 660
gctttctcca ccttgctgga agtgacctgc tgtccagaag tttgatggct gaggagtata 720
ccatcgtgca tgcattcttc atttcctgca tttcttcctc cctggatgga cagggggagc 780
ggcaagagca acgtgggcac ttctggagac cacaacgact cctctgtgaa gacgcttggg 840
agcaagaggt gcaagtgggt ctgccactgc tccccctgct gcagggggag cggcaagagc 900
aacgtggtcg cttggggaga ctacgatgac agcgcttca tggatcccag gtaccacgtc 960
catggagaag atctggacaa gctccacaga gctgcctggt ggggtaaaagt ccccgaaaag 1020
gatctcatcg tcatgctcag ggacacggat gtgaacaaga gggacaagca aaagaggact 1080
gctctacatc tggcctctgc caatgggaat tcagaagtag taaaactcgt gctggacaga 1140
cgatgtcaac ttaattgtct tgacaacaaa aagaggacag ctctgacaaa ggccgtacaa 1200
tgccaggaag atgaatgtgc gttaatgttg ctggaacatg gcactgatcc aaatattcca 1260
gatgagtatg gaaataccac tctacactat gctgtctaca atgaagataa attaatggcc 1320
aaagcactgc tcttatacgg tgetgatatc gaatcaaaaa acaagcatgg cctcacacca 1380
ctgctacttg gtatacatga gcaaaaacag caagtgtgtg aatttttaat caagaaaaaa 1440
gcgaatttaa atcgctgtga tagatatgga agaactgtct tcatacttgc tgtatgttgt 1500
ggatcagcaa gtatagtcag cctctactt gagcaaaatg ttgatgtatc ttctcaagat 1560
ctggaagagc ggccagagag tatgctgttt ctatgcatca tcatgtaatt tgccagttac 1620

tttctgacta caaagaaaaa cagatgttaa aaatctcttc tgaaaacagc aatccagaac 1680
 aagacttaaa gctgacatca gaggaagagt cacaaaggct taaaggaagt gaaaacagcc 1740
 agccagagct agaagattta tggctattga agaagaatga agaacacgga agtactcatg 1800
 tgggattccc agaaaacctg actaacggtg ccgctgctgg caatggtgat ga 1852

<210> 531
 <211> 879
 <212> DNA
 <213> Homo sapiens

<400> 531
 atgcatcttt catttcctgc atttcttctt ccctggatgg acagggggag cggcaagagc 60
 aacgtgggca cttctggaga ccacaacgac tcctctgtga agacgcttgg gagcaagagg 120
 tgcaagtggg gctgccactg cttcccttgc tgcaggggga gcggcaagag caacgtgggc 180
 gcttggggag actacgatga cagcgcttgc atggatccca ggtaccacgt ccatggagaa 240
 gatctggaca agctccacag agctgcctgg tggggtaaaag tccccagaaa ggatctcatc 300
 gtcattgctca gggacacgga tgtgaacaag agggacaagc aaaagaggac tgctctacat 360
 ctggcctctg ccaatgggaa ttcagaagta gtaaaactcg tgctggacag acgatgtcaa 420
 cttaatgtcc ttgacaacaa aaagaggaca gctctgacaa aggccgtaca atgccaggaa 480
 gatgaatgtg cgtaaatgtt gctggaacat ggcactgatc caaatattcc agatgagtat 540
 ggaaatacca ctctacacta tgctgtctac aatgaagata aattaatggc caaagcactg 600
 ctcttatacg gtgctgatat cgaatcaaaa aacaagcatg gcctcacacc actgctactt 660
 ggtatacatg agcaaaaaca gcaagtgggtg aaatttttaa tcaagaaaaa agcgaattta 720
 aatgcgctgg atagatatgg aagaactgct ctcatacttg ctgtatgttg tggatcagca 780
 agtatagtca gccctctact tgagcaaaat gttgatgtat cttctcaaga tctggaaaga 840
 cggccagaga gtatgctgtt tctagtcac atcatgtaa 879

<210> 532
 <211> 292
 <212> PRT
 <213> Homo sapiens

<400> 532
 Met His Leu Ser Phe Pro Ala Phe Leu Pro Pro Trp Met Asp Arg Gly
 5 10 15
 Ser Gly Lys Ser Asn Val Gly Thr Ser Gly Asp His Asn Asp Ser Ser
 20 25 30
 Val Lys Thr Leu Gly Ser Lys Arg Cys Lys Trp Cys Cys His Cys Phe
 35 40 45
 Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Val Val Ala Trp Gly Asp
 50 55 60
 Tyr Asp Asp Ser Ala Phe Met Asp Pro Arg Tyr His Val His Gly Glu
 65 70 75 80
 Asp Leu Asp Lys Leu His Arg Ala Ala Trp Trp Gly Lys Val Pro Arg
 85 90 95
 Lys Asp Leu Ile Val Met Leu Arg Asp Thr Asp Val Asn Lys Arg Asp
 100 105 110
 Lys Gln Lys Arg Thr Ala Leu His Leu Ala Ser Ala Asn Gly Asn Ser
 115 120 125
 Glu Val Val Lys Leu Val Leu Asp Arg Arg Cys Gln Leu Asn Val Leu

130 135 140
 Asp Asn Lys Lys Arg Thr Ala Leu Thr Lys Ala Val Gln Cys Gln Glu
 145 150 155 160
 Asp Glu Cys Ala Leu Met Leu Leu Glu His Gly Thr Asp Pro Asn Ile
 165 170 175
 Pro Asp Glu Tyr Gly Asn Thr Thr Leu His Tyr Ala Val Tyr Asn Glu
 180 185 190
 Asp Lys Leu Met Ala Lys Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu
 195 200 205
 Ser Lys Asn Lys His Gly Leu Thr Pro Leu Leu Leu Gly Ile His Glu
 210 215 220
 Gln Lys Gln Gln Val Val Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu
 225 230 235 240
 Asn Ala Leu Asp Arg Tyr Gly Arg Thr Ala Leu Ile Leu Ala Val Cys
 245 250 255
 Cys Gly Ser Ala Ser Ile Val Ser Pro Leu Leu Glu Gln Asn Val Asp
 260 265 270
 Val Ser Ser Gln Asp Leu Glu Arg Arg Pro Glu Ser Met Leu Phe Leu
 275 280 285
 Val Ile Ile Met
 290

<210> 533
 <211> 801
 <212> DNA
 <213> Homo sapiens

<400> 533
 atgtacaagc ttcaagtcaa caactgtgct acaaattggag ccacagagag gaaacaagca 60
 gcaggctcag gaggagggtg tgcgtgcct tcggctctcc aatccatgcc tcagggtccc 120
 tatgccactg cagcattctt ggttgccaag aggccaaacca caggccatct tgagaaggag 180
 tttatgttcc actgcagaaa gcagccagga tcaccatcca ggggacttgg tcttctgttg 240
 ccctggccag acatagaatt tgtgccaagg caggacaagc tcaactcagag cagcgtgtta 300
 gtacctcaaa tctgtgcgtg ccagacaagg ccaaactggc tcaatgagca accagccacc 360
 tctgcagggg tgcgtctgga ggaggtggac cagccaccaa ccttaccag tcaagggaagt 420
 ggatggccat gttccacag cctgagtgcc tgccacctga tggctgatat agcaaaggcc 480
 ttaggaaaag cagatggccc ttggccctac ctttttggtt gaagaactga tgttccatgt 540
 cctgcagcga gtgaggttgg tggctgtgcc cccagctcct ggcacaccct cgcagagggtg 600
 actggttgc tttgagccc tcttagcctt gccagcatg cacaagcctc agtgctacta 660
 ctgtgctaca aatggagcca tataggggaa acgagcagcc atctcaggag caaggtgtat 720
 gctgcctttg ggggtccag tccttgccctc aagggtctta tgtcactgtg ggcttcttgg 780
 ttgccaagag gcagaccata g 801

<210> 534
 <211> 266
 <212> PRT
 <213> Homo sapiens

<210> 535

<211> 6082

<212> DNA

<213> Homo sapiens

<400> 535

```

cctccactat tacagcttat aggaaattac aatccacttt acaggcctca aaggttcatt 60
ctggccgagc ggacaggcgt ggcggccgga gccccagcat ccctgcttga ggtccaggag 120
cggagcccgc ggcactgcc gcctgatcag cgcgaccccg gcccgcgccc gccccgcccg 180
gcaaatgctt gccgtgttac caggaggtga agcccaaccc gctgcaggac gcgaacctct 240
gtcacgcgtg ttcttctctg tggtcgaatc ccttggttaa aattggccat aaacggagat 300
tagaggaaga tgatatgtat tcagtgtctc cagaagaccg ctcacagcac cttggagagg 360
agttgcaagg gttctgggat aaagaagttt taagagctga gaatgacgca cagaagcctt 420
ctttaacaag agcaatcata aagtgttact ggaaatctta tttagttttg ggaattttta 480
cgtaatttga ggaaagtgcc aaagtaatcc agcccatatt tttgggaaaa attattaatt 540
attttgaaaa ttatgatccc atggattctg tggctttgaa cacagcgtac gcctatgcca 600
cggtgctgac tttttgcacg ctcatcttgg ctatactgca tcacttatat ttttatcacg 660
ttcagtgtgc tgggagtagg ttacgagtag ccagtgtgcca tatgatttat cggaggagac 720
ttcgtcttag taacatggcc atggggaaga caaccacagg ccagatagtc aatctgctgt 780
ccaatgatgt gaacaagttt gatcaggtga cagtgttctt acacttcctg tgggcaggac 840
cactgcaggc gatcgagtg actgccctac tctggatgga gataggaata tcgtgccttg 900
ctgggatggc agttctaata attctcctgc ccttgcaaaag ctgttttggg aagttgttct 960
catcactgag gagtaaaact gcaactttca cggatgccag gatcaggacc atgaatgaag 1020
ttataactgg tataaggata ataaaaatgt acgcctggga aaagtcattt tcaaatctta 1080
ttaccaattt gagaaagaag gagatttcca agattctgag aagttcctgc ctcaggggga 1140
tgaatttggc ttctgttttc agtgcaagca aaatcatcgt gtttgtgacc ttcaccacct 1200
acgtgtcctt cggcagtggt atcacagcca gccgcgtgtt cgtggcagtg acgctgtatg 1260
gggctgtgog gctgacggtt accctcttct tcccctcagc cattgagagg gtgtcagagg 1320
caatcgtcag catccgaaga atccagacct ttttgctact tgatgagata tcacagcgca 1380
accgtcagct gccgtcagat ggtaaaaaga tgggtcatgt gcaggatttt actgcttttt 1440
gggataaggc atcagagacc ccaactctac aaggcctttc ctttactgtc agacctggcg 1500
aattgttagc tgtgttcggc cccgtgggag cagggaagtc atcactgtta agtgcctgac 1560
tcggggaatt ggccccaagt cacgggctgg tcagcgtgca tggagaattt gcctatgtgt 1620
ctcagcagcc ctgggtgttc tcgggaactc tgaggagtaa tattttattt gggaagaaat 1680
acgaaaagga acgatatgaa aaagtcataa aggcttgtgc tctgaaaaag gatttacagc 1740
tggttgaggga tgggtgatctg actgtgatag gagatcgggg aaccacgctg agtggagggc 1800
agaaagcacg ggtaaacctt gcaagagcag tgtatcaaga tgctgacatc tatctcctgg 1860
acgatcctct cagtgcagta gatgcggaag ttacgagaca cttgttcgaa ctgtgtattt 1920
gtcaaatttt gcatgagaag atcacaattt tagtgactca tcagtgtcag tacttcaaa 1980
ctgcaagtca gattctgata ttgaaagatg gtaaaatggt gcagaagggg acttacactg 2040
agttcctaaa atctgttata gattttggct cccttttaaa gaaggataat gaggaaagt 2100
aacaacctcc agttccagga actcccacac taaggaatcg taccttctca gagtcttcgg 2160
tttggtctca acaatcttct agaccctcct tgaagatgg tgctctggag agccaagata 2220
cagagaatgt cccagttaca ctatcagagg agaaccgttc tgaaggaaaa gttggttttc 2280
aggcctataa gaattacttc agagctgggt ctcactggat tgtcttcatt ttccttatte 2340
tcctaaacac tgcagtcag gttgcctatg tgcttcaaga ttggtggctt tcatactggg 2400
caaacaacaa aagtatgcta aatgtcactg taaatggagg aggaaatgta accgagaagc 2460
tagatcttaa ctggtactta ggaatttatt cagggttaac tgtagctacc gttctttttg 2520
gcatagcaag atctctattg gtattctacg tccttggtta ctcttcacaa actttgcaca 2580
acaaaatggt tgagtcaatt ctgaaagctc cgttattatt ctttgataga aatccaatag 2640
gaagaatttt aaatcgtttc tccaaagaca ttggacactt ggatgatttg ctgccgctga 2700
cgtttttaga tttcatccag acattgctac aagtgggttg tgtggtctct gtggtctgtg 2760
ccgtgattcc ttggtcgcga atacccttgg tccccttgg aatcattttc atttttcttc 2820
ggcgatattt tttggaacg tcaagagatg tgaagcgcct ggaatctaca actcggagtc 2880
cagtgttttc ccacttgtea tcttctctcc aggggtctct gaccatccgg gcatacaaa 2940
cagaagagag gtgtcaggaa ctggttgatg cacaccagga tttacattca gaggcttggt 3000
tcttggtttt gacaacgtcc cgctggttcg ccgtccgtct ggatgccatc tgtgccatgt 3060
ttgtcatcat cgttgccctt gggtcctcga tcttgcaaaa aactctggat gccgggcagg 3120
ttggtttggc actgtcctat gccctcacgc tcattgggat gtttcagtgg tgtgttcgac 3180
aaagtgtcga agtgagaat atgatgatc cagtagaag ggtcattgaa tacacagacc 3240
ttgaaaaaga agcaccttgg gaatatcaga aacgccacc accagcctgg ccccatgaag 3300
gagtataat ctttgacaat gtgaacttca tgtacagtc aggtgggcct ctggtactga 3360

```

```

agcatctgac agcactcatt aaatcacaaag aaaaggttgg cattgtggga agaaccggag 3420
ctggaaaaag ttccctcatc tcagcccttt ttagattgtc agaaccggaa ggtaaaaattt 3480
ggattgataa gatcttgaca actgaaattg gacttcacga ttttaaggaag aaaatgtcaa 3540
tcatacctca ggaacctgtt ttgttctactg gaacaatgag gaaaaacctg gatcccttta 3600
atgagcacac ggatgaggaa ctgtggaatg ccttacaaga ggtacaactt aaagaaacca 3660
ttgaagatct tcctggtaaa atggatactg aattagcaga atcaggatcc aatttttagtg 3720
ttggacaaag acaactggtg tgccttgcca gggcaattct caggaaaaat cagatattga 3780
ttattgatga agcgacggca aatgtggatc caagaactga tgagttaata caaaaaaat 3840
ccgggagaaa ttgtcccact gcaccgtgct aaccattgca cacagattga acaccattat 3900
tgacacggac aagataatgg ttttagattc aggaagactg aaagaatatg atgagccgta 3960
tgttttgctg caaaaataag agagcctatt ttacaagatg gtgcaacaac tgggcaaggc 4020
agaagccgct gccctcactg aaacagcaaa acagggtatac ttcaaaagaa attatccaca 4080
tattgtgcac actgaccaca tggttacaaa cacttccaat ggacagccct cgaccttaac 4140
tattttcgag acagcactgt gaatccaacc aaaatgtcaa gtccgttccg aaggcatttg 4200
ccactagttt ttggactatg taaaccacat tgtacttttt tttacttttg caacaaatat 4260
ttatacatac aagatgctag ttcatctgaa tatttctccc aacttatcca aggatctcca 4320
gctctaacaa aatggtttat ttttatttaa atgtcaatag ttgtttttta aaatccaaat 4380
cagaggtgca ggccaccagt taaatgccgt ctatcagggt ttgtgcctta agagactaca 4440
gagtcaaagc tcatttttaa aggagtagga cagagttgtc acaggttttt gttgtgtgtt 4500
ttattgcccc caaaattaca tgttaatttc catttataac agggattcta tttacttgaa 4560
gactgtgaag ttgccatttt gtctcattgt tttctttgac ataactagga tccattatit 4620
cccctgaagg ctctctgtta gaaaatagta cagttacaac caataggaac aacaaaaaga 4680
aaaagtttgt gacattgtag tagggagtgt gtacccctta ctcccatca aaaaaaaa 4740
tggatagatg gttaaaggat agaagggcaa tattttatca tatgttctaa aagagaagga 4800
agagaaaata ctactttctc aaaatggaag cccttaaagg tgctttgata ctgaaggaca 4860
caaatgtgac cgtccatcct ccttttagat tgcatgactt ggacacggta actgttgagc 4920
tttttagactc agcattgtga cacttcccaa gaaggccaaa cctctaaccg acattcctga 4980
aatacgtggc attattcttt tttggatttc tcatttatgg aaggctaacc ctctgttgac 5040
tgtaagcctt ttggtttggg ctgtattgaa atcctttcta aattgcatga ataggctctg 5100
ctaactgtat gagacaaact gaaaattatt gcaagcattg actataatta tgcagtacgt 5160
tctcagatg catcaggagg ttcatatttc tgagcctgtc caggttagtt tactcctgac 5220
cactaatagc attgtcattt gggtttctg ttgaatgaat caacaaacca caatacttcc 5280
tgggaccttt tgtactttat ttgaactatg agtctttaat ttttctgat gatggtggct 5340
gtaatatgtt gagttcagtt tactaaagggt tttactatta tgggttgaa tggagtctca 5400
tgacctctca gaataagggtg tcacctccct gaaattgcat atatgtatat agacatgcac 5460
acgtgtgcat ttgtttgtat acatatatit gtccctcgta tagcaagttt tttgctcatc 5520
agcagagagc aacagatgtt ttattgagtg aagccttaaa aagcacacac cacacacagc 5580
taactgccaa aatacattga ccgtagtagc tgttcaactc ctagtactta gaaatacacg 5640
tatggttaat gttcagttca acaaaaccaca cacagtaaat gtttattaat agtcatgggt 5700
cgtatttttag gtgactgaaa ttgcaacagt gatcataatg aggtttgtta aaatgatagc 5760
tatattcaaa atgtctatat gtttattttg acttttgagg ttaaagacag tcatataaac 5820
gtcctgtttc tgttttaatg ttatcataga attttttaat gaaactaaat tcaattgaaa 5880
taaattgatag ttttcatctc caaaaaaaa aaaaaaaagg gcggccgctc gagtctagag 5940
ggcccgttta aaccgctga tcagcctcga ctgtgccttc tagttgccag ccatctgtt 6000
tttgccctc ccccgctgct tccttgacct tgggaaggtgc cactccact gtcctttcct 6060
aataaaatga ggaaattgca tc 6082

```

<210> 536

<211> 6140

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(6140)

<223> n=A,T,C or G

<400> 536

cagtggcgca	gtctcagctc	actgcagcct	ccacctcctg	tgttcaagca	gtcctcctgc	60
ctcagccacc	agactagcag	gtctcccccg	cctctttcct	ggaaggacac	ttgccattgg	120
atthagcacc	cacttgagata	atccaggatg	atgtcttcac	tccaacatcc	tcagtttaat	180
tccatgtgca	aatacccttt	tcccaaataa	cattcaattc	tttaccagga	aaggtggctc	240
aatcccttgt	ttaaaattgg	ccataaacgg	agattagagg	aagatgatat	gtattcagtg	300
ctgccagaag	accgctcaca	gcaccttgga	gaggagttgc	aagggttctg	ggataaagaa	360
gttttaagag	ctgagaatga	cgcacagaag	ccttctttta	caagagcaat	cataaagtgt	420
tactggaaat	cttatttagt	tttgggaatt	tttacgttaa	ttgaggaaag	tgccaaagta	480
atccagccca	tatttttggg	aaaaattatt	aattattttg	aaaattatga	tccatggat	540
tctgtggctt	tgaacacagc	gtacgcctat	gccacggtgc	tgaacttttg	cacgctcatt	600
ttggctatac	tgcatcactt	atatttttat	cacgttcagt	gtgctgggat	gaggttacga	660
gtagccatgt	gccatatgat	ttatcggaag	gcacttcgtc	ttagtaacat	ggccatgggg	720
aagacaacca	caggccagat	agtcaatctg	ctgtccaatg	atgtgaacaa	gtttgatcag	780
gtgacagtgt	tcttacactt	cctgtgggca	ggaccactgc	aggcgatcgc	agtgactgcc	840
ctactctgga	tggagatagg	aatatcgtgc	cttgcctgga	tggcagttct	aatcattctc	900
ctgcccttgc	aaagctgttt	tgggaagtgt	tctcatcac	tgaggagtaa	aactgcaact	960
ttcacggatg	ccaggatcag	gacctgaat	gaagttataa	ctggtataag	gataataaaa	1020
atgtacgcct	gggaaaagtc	attttcaaat	cttattacca	atttgagaaa	gaaggagatt	1080
tccaagattc	tgagaagtgc	ctgcctcagg	gggatgaatt	tggcttcggt	tttcagtgc	1140
agcaaaatca	tcgtgtttgt	gaccttcacc	acctacgtgc	tcctcggcag	tgtgatcaca	1200
gccagccgog	tgctcgtggc	agtgcgctg	tatggggctg	tgccgctgac	ggttaccctc	1260
ttcttccctt	cagccattga	gaggtgtgca	gaggcaatcg	tcagcatccg	agaatccag	1320
acctttttgc	tacttgatga	gatatcacag	cgcacacgtc	agctgccgtc	agatggtaaa	1380
aagatggtgc	atgtgcagga	ttttactgct	ttttgggata	aggcatcaga	gaccccaact	1440
ctacaaggcc	tttcttttac	gtcagacct	ggcgaattgt	tagctgtggt	cggccccgtg	1500
ggagcaggga	agtcacact	gttaagtgcc	gtgctcgggg	aattggcccc	aagtcacggg	1560
ctggtcagcg	tgcatggaag	aattgcctat	gtgtctcagc	agccctgggt	gttctcggga	1620
actctgagga	gtaataat	atttgggaag	aaatacgaaa	aggaacgata	tgaaaaagtc	1680
ataaaggctt	gtgctctgaa	aaaggattta	cagctgttgg	aggatggtga	tctgactgtg	1740
atagtagatc	ggggaaccac	gctgagtga	gggcagaaa	cacgggtaaa	ccttgcaaga	1800
gcagtgtatc	aagatgctga	catctatctc	ctggacgac	ctctcagtc	agtagatcgc	1860
gaagttagca	gacacttggt	cgaactgtgt	atttgtcaaa	ttttgcatga	gaagatcaca	1920
attttagtga	ctcatcagtt	gcagtacctc	aaagctgcaa	gtcagattct	gatattgaaa	1980
gatgttaaaa	tggtcagaaa	ggggacttac	actgagttcc	taaaatctgg	tatagatttt	2040
ggctcccttt	taaagaagga	taattgaggaa	agtgaacaac	ctccagttcc	aggaactccc	2100
acactaagga	atcgtaacct	ctcagagctc	tcggtttggt	ctcaacaatc	ttctagaccc	2160
tccttgaaag	atggtgctct	ggagagccaa	gatacagaga	atgtccagat	tacactatca	2220
gaggagaacc	gttctgaagg	aaaagttggt	tttcaggcct	ataagaatta	cttcagagct	2280
ggtgctcact	ggattgtcct	cattttcctt	attctcctaa	acactgcagc	tcaggttgcc	2340
tatgtgcttc	aagattggtg	gctttcatac	tgggcaaa	aacaaagtat	gctaaatgct	2400
actgtaaatg	gaggaggaaa	tgtaacggag	aagctagatc	tttaactggt	cttaggaatt	2460
tattcaggtt	taactgtagc	taccgttctt	tttggcatag	caagatctct	attggtattc	2520
tacgtccttg	tttaactctt	acaaactttg	cacaacaaaa	tgtttgagtc	aattctgaaa	2580
gctccggtat	tattctttga	tagaaatcca	ataggaagaa	ttttaaatcg	tttctccaaa	2640
gacattggac	acttggatga	tttgctgccg	ctgacgtttt	tagatttcat	ccagacattg	2700
ctacaagtgg	ttggtgtggt	ctctgtggct	gtggccgtga	ttccttggtg	cgcaataccc	2760
ttggttcccc	ttggaatcat	tttcattttt	cttcggcgat	attttttgga	aacgtcaaga	2820
gatgtgaage	gcctggaatc	tacaactcgg	agtcacagtg	tttcccactt	gtcatcttct	2880
ctccaggggc	tctggacat	cgggcatcac	aaagcagaag	agaggtgtca	ggaactgttt	2940
gatgcacacc	aggattttaca	ttcagaggct	tggttcttgt	ttttgacaac	gtcccgtctg	3000
ttcgccgtcc	cttgggatgc	catctgtgcc	atgtttgtca	tcacgtgtgc	ctttgggtcc	3060
ctgattctgg	caaaaactct	ggatgcgggg	caagtttggt	tggcactgtc	ctatgccctc	3120
acgctcatgg	ggatgtttca	gtggtgtggt	cgacaaagtg	ctgaagttga	gaatatgatg	3180
atctcagtag	aaagggtcat	tgaatacaca	gaccttgaaa	aagaagcacc	ttgggaatat	3240
cagaaacgcc	caccaccagc	ctggccccat	gaaggagtga	taatctttga	caatgtgaac	3300
ttcatgtaca	gtccagggtg	gcctctggta	ctgaagcatc	tgacagcact	cattaaatca	3360
caagaaaagg	ttggcattgt	gggaagaacc	ggagctggaa	aaagttccct	catctcagcc	3420
cttttagat	tgtcagaacc	cgaaggtaaa	atttggattg	ataagatctt	gacaactgaa	3480

```

attggacttc acgattttaag gaagaaaatg tcaatcatac ctcaggaacc tgttttggtc 3540
actggaacaa tgaggaaaaa cctggatccc tttaatgagc acacggatga ggaactgtgg 3600
aatgccttac aagaggtaca acttaaagaa accattgaag atcttcctgg taaaatggat 3660
actgaattag cagaatcagg atccaatttt agtggtggac aaagacaact ggtgtgcctt 3720
gccaggggcaa ttctcaggaa aaatcagata ttgattattg atgaagcgac ggcaaatgtg 3780
gatccaagaa ctgatgagtt aatacaaaaa aaaatccggg agaaatttgc ccactgcacc 3840
gtgctaacca ttgcacacag attgaacacc attattgaca gcgacaagat aatgggttta 3900
gattcaggaa gactgaaaga atatgatgag ccgtatgttt tgctgcaaaa taaagagagc 3960
ctattttaca agatggtgca acaactgggc aaggcagaag ccgctgccct cactgaaaca 4020
gcaaaacaga gatgggggtt caccatgttg gccaggctgg tctcaaacct ctgacctcaa 4080
gtgatccacc tgccttggcc tcccaaacct ctgagattac aggtgtgagc caccacgccc 4140
agcctgagta tacttcaaaa gaaattatcc acatattggt cactactgacc acatggttac 4200
aaacacttcc aatggacagc cctcgacctt aactattttc gagacagcac tgtgaatcca 4260
accaaagtgt caagtccggt ccgaaggcat ttgcccactag tttttggact atgtaaacca 4320
cattgtactt ttttttactt tggcaacaaa tatttataca tacaagatgc tagttcattt 4380
gaatatttct cccaacttat ccaaggatct ccagctctaa caaaatggtt tatttttatt 4440
taaattgtcaa tagtkgkttt ttaaaatcca aatcagaggt gcaggccacc agttaaatgc 4500
cgtctatcag gttttgtgcc ttaagagact acagnagtca gaagctcatt tttaaaggag 4560
taggacagag ttgtcacagg tttttgttgg tgtttktatt gcccccaaaa ttacatgtta 4620
atttccattt atatcagggg attctattta cttgaagact gtgaagttgc cattttgtct 4680
cattgttttc ttgacatam ctaggatcca ttatttccc tgaaggcttc ttgkagaaaa 4740
tagtacagtt acaaccaata ggaactamca aaaagaaaaa gtttgtgaca ttgtagtagg 4800
gagtgtgtac ccttacttcc ccatcaaaaa aaaaaatgga tacatggtta aaggatagaa 4860
gggcaatatt ttatcatatg ttctaaaaga gaaggaagag aaaatactac tttctcaaaa 4920
tggaagccct taaaggtgct ttgatactga aggacacaaa tgtgaccgtc catcctcctt 4980
tagagttgca tgacttggac acggttaactg ttgcagtttt agactcagca ttgtgacact 5040
tcccaagaag gccaaacctc taaccgacat tcctgaaata cgtggcatta ttcttttttg 5100
gattttctcat ttaggaaggc taaccctctg ttgamtgatm kccttttggt ttgggctgta 5160
ttgaaatcct ttctaattg catgaatagg ctctgctaac cgtgatgaga caaactgaaa 5220
attattgcaa gcattgacta taattatgca gtacgttctc aggatgcata caggggttca 5280
ttttcatgag cctgtccagg ttagtttact cctgaccact aatagcattg tcatttgggc 5340
tttctgttga atgaatcaac aaaccacaat acttcctggg accttttgta ctttatttga 5400
actatgagtc tttaattttt cctgatgatg gtggctgtaa tatgttgagt tcagtttact 5460
aaaggtttta ctattatggt ttgaagggag tctcatgacc tctcagaaaa ggtgcacctc 5520
cctgaaattg catatatgta tatagacatg cacacgtgtg catttgtttg tatacatata 5580
tttgtccttc gtatagcaag ttttttgctc atcagcagag agcaacagat gttttattga 5640
gtgaagcctt aaaaagcaca caccacacac agctaactgc caaaatacat tgaccgtagt 5700
agctgttcaa ctccatgtac ttagaaatac acgtatggtt aatgttcagt ccaacaaacc 5760
acacacagta aatgtttatt aatagtcagt gttcgtattt taggtgactg aaattgcaac 5820
agtgatcata atgaggtttg ttaaaatgat agctatattc aaaatgtcta tatgtttatt 5880
tggaactttt aggttaaaga cagtcataata aacgtcctgt ttctgtttta atgttatcat 5940
agaatttttt aatgaaacta aattcaattg aaataaatga tagttttcat ctccaaaaaa 6000
aaaaaaaagg ggcggcccgc tcgagtcctag agggcccgtt ttaaaccgcg tgatcagcct 6060
cgactgtgcc ttctagtgtc cagccatctg ttgtttggcc ctccccctg ccttccttga 6120
ccctggaagg ggccactccc                                     6140

```

<210> 537

<211> 1228

<212> PRT

<213> Homo sapiens

<400> 537

```

Met Leu Pro Val Tyr Gln Glu Val Lys Pro Asn Pro Leu Gln Asp Ala
                    5                                10                    15

```

```

Asn Leu Cys Ser Arg Val Phe Phe Trp Trp Leu Asn Pro Leu Phe Lys
                20                    25                    30

```

Ile Gly His Lys Arg Arg Leu Glu Glu Asp Asp Met Tyr Ser Val Leu
 35 40 45
 Pro Glu Asp Arg Ser Gln His Leu Gly Glu Glu Leu Gln Gly Phe Trp
 50 55 60
 Asp Lys Glu Val Leu Arg Ala Glu Asn Asp Ala Gln Lys Pro Ser Leu
 65 70 75 80
 Thr Arg Ala Ile Ile Lys Cys Tyr Trp Lys Ser Tyr Leu Val Leu Gly
 85 90 95
 Ile Phe Thr Leu Ile Glu Glu Ser Ala Lys Val Ile Gln Pro Ile Phe
 100 105 110
 Leu Gly Lys Ile Ile Asn Tyr Phe Glu Asn Tyr Asp Pro Met Asp Ser
 115 120 125
 Val Ala Leu Asn Thr Ala Tyr Ala Tyr Ala Thr Val Leu Thr Phe Cys
 130 135 140
 Thr Leu Ile Leu Ala Ile Leu His His Leu Tyr Phe Tyr His Val Gln
 145 150 155 160
 Cys Ala Gly Met Arg Leu Arg Val Ala Met Cys His Met Ile Tyr Arg
 165 170 175
 Lys Ala Leu Arg Leu Ser Asn Met Ala Met Gly Lys Thr Thr Thr Gly
 180 185 190
 Gln Ile Val Asn Leu Leu Ser Asn Asp Val Asn Lys Phe Asp Gln Val
 195 200 205
 Thr Val Phe Leu His Phe Leu Trp Ala Gly Pro Leu Gln Ala Ile Ala
 210 215 220
 Val Thr Ala Leu Leu Trp Met Glu Ile Gly Ile Ser Cys Leu Ala Gly
 225 230 235 240
 Met Ala Val Leu Ile Ile Leu Leu Pro Leu Gln Ser Cys Phe Gly Lys
 245 250 255
 Leu Phe Ser Ser Leu Arg Ser Lys Thr Ala Thr Phe Thr Asp Ala Arg
 260 265 270
 Ile Arg Thr Met Asn Glu Val Ile Thr Gly Ile Arg Ile Ile Lys Met
 275 280 285
 Tyr Ala Trp Glu Lys Ser Phe Ser Asn Leu Ile Thr Asn Leu Arg Lys
 290 295 300
 Lys Glu Ile Ser Lys Ile Leu Arg Ser Ser Cys Leu Arg Gly Met Asn
 305 310 315 320
 Leu Ala Ser Phe Phe Ser Ala Ser Lys Ile Ile Val Phe Val Thr Phe
 325 330 335
 Thr Thr Tyr Val Leu Leu Gly Ser Val Ile Thr Ala Ser Arg Val Phe

340	345	350
Val Ala Val Thr Leu Tyr Gly Ala Val Arg Leu Thr Val Thr Leu Phe		
355	360	365
Phe Pro Ser Ala Ile Glu Arg Val Ser Glu Ala Ile Val Ser Ile Arg		
370	375	380
Arg Ile Gln Thr Phe Leu Leu Leu Asp Glu Ile Ser Gln Arg Asn Arg		
385	390	395
Gln Leu Pro Ser Asp Gly Lys Lys Met Val His Val Gln Asp Phe Thr		
405	410	415
Ala Phe Trp Asp Lys Ala Ser Glu Thr Pro Thr Leu Gln Gly Leu Ser		
420	425	430
Phe Thr Val Arg Pro Gly Glu Leu Leu Ala Val Val Gly Pro Val Gly		
435	440	445
Ala Gly Lys Ser Ser Leu Leu Ser Ala Val Leu Gly Glu Leu Ala Pro		
450	455	460
Ser His Gly Leu Val Ser Val His Gly Arg Ile Ala Tyr Val Ser Gln		
465	470	475
Gln Pro Trp Val Phe Ser Gly Thr Leu Arg Ser Asn Ile Leu Phe Gly		
485	490	495
Lys Lys Tyr Glu Lys Glu Arg Tyr Glu Lys Val Ile Lys Ala Cys Ala		
500	505	510
Leu Lys Lys Asp Leu Gln Leu Leu Glu Asp Gly Asp Leu Thr Val Ile		
515	520	525
Gly Asp Arg Gly Thr Thr Leu Ser Gly Gly Gln Lys Ala Arg Val Asn		
530	535	540
Leu Ala Arg Ala Val Tyr Gln Asp Ala Asp Ile Tyr Leu Leu Asp Asp		
545	550	555
Pro Leu Ser Ala Val Asp Ala Glu Val Ser Arg His Leu Phe Glu Leu		
565	570	575
Cys Ile Cys Gln Ile Leu His Glu Lys Ile Thr Ile Leu Val Thr His		
580	585	590
Gln Leu Gln Tyr Leu Lys Ala Ala Ser Gln Ile Leu Ile Leu Lys Asp		
595	600	605
Gly Lys Met Val Gln Lys Gly Thr Tyr Thr Glu Phe Leu Lys Ser Gly		
610	615	620
Ile Asp Phe Gly Ser Leu Leu Lys Lys Asp Asn Glu Glu Ser Glu Gln		
625	630	635
Pro Pro Val Pro Gly Thr Pro Thr Leu Arg Asn Arg Thr Phe Ser Glu		
645	650	655

Ser. Ser Val Trp Ser Gln Gln Ser Ser Arg Pro Ser Leu Lys Asp Gly
 660 665 670
 Ala Leu Glu Ser Gln Asp Thr Glu Asn Val Pro Val Thr Leu Ser Glu
 675 680 685
 Glu Asn Arg Ser Glu Gly Lys Val Gly Phe Gln Ala Tyr Lys Asn Tyr
 690 695 700
 Phe Arg Ala Gly Ala His Trp Ile Val Phe Ile Phe Leu Ile Leu Leu
 705 710 715 720
 Asn Thr Ala Ala Gln Val Ala Tyr Val Leu Gln Asp Trp Trp Leu Ser
 725 730 735
 Tyr Trp Ala Asn Lys Gln Ser Met Leu Asn Val Thr Val Asn Gly Gly
 740 745 750
 Gly Asn Val Thr Glu Lys Leu Asp Leu Asn Trp Tyr Leu Gly Ile Tyr
 755 760 765
 Ser Gly Leu Thr Val Ala Thr Val Leu Phe Gly Ile Ala Arg Ser Leu
 770 775 780
 Leu Val Phe Tyr Val Leu Val Asn Ser Ser Gln Thr Leu His Asn Lys
 785 790 795 800
 Met Phe Glu Ser Ile Leu Lys Ala Pro Val Leu Phe Phe Asp Arg Asn
 805 810 815
 Pro Ile Gly Arg Ile Leu Asn Arg Phe Ser Lys Asp Ile Gly His Leu
 820 825 830
 Asp Asp Leu Leu Pro Leu Thr Phe Leu Asp Phe Ile Gln Thr Leu Leu
 835 840 845
 Gln Val Val Gly Val Val Ser Val Ala Val Ala Val Ile Pro Trp Ile
 850 855 860
 Ala Ile Pro Leu Val Pro Leu Gly Ile Ile Phe Ile Phe Leu Arg Arg
 865 870 875 880
 Tyr Phe Leu Glu Thr Ser Arg Asp Val Lys Arg Leu Glu Ser Thr Thr
 885 890 895
 Arg Ser Pro Val Phe Ser His Leu Ser Ser Ser Leu Gln Gly Leu Trp
 900 905 910
 Thr Ile Arg Ala Tyr Lys Ala Glu Glu Arg Cys Gln Glu Leu Phe Asp
 915 920 925
 Ala His Gln Asp Leu His Ser Glu Ala Trp Phe Leu Phe Leu Thr Thr
 930 935 940
 Ser Arg Trp Phe Ala Val Arg Leu Asp Ala Ile Cys Ala Met Phe Val
 945 950 955 960

Ile Ile Val Ala Phe Gly Ser Leu Ile Leu Ala Lys Thr Leu Asp Ala
 965 970 975
 Gly Gln Val Gly Leu Ala Leu Ser Tyr Ala Leu Thr Leu Met Gly Met
 980 985 990
 Phe Gln Trp Cys Val Arg Gln Ser Ala Glu Val Glu Asn Met Met Ile
 995 1000 1005
 Ser Val Glu Arg Val Ile Glu Tyr Thr Asp Leu Glu Lys Glu Ala Pro
 1010 1015 1020
 Trp Glu Tyr Gln Lys Arg Pro Pro Pro Ala Trp Pro His Glu Gly Val
 1025 1030 1035 1040
 Ile Ile Phe Asp Asn Val Asn Phe Met Tyr Ser Pro Gly Gly Pro Leu
 1045 1050 1055
 Val Leu Lys His Leu Thr Ala Leu Ile Lys Ser Gln Glu Lys Val Gly
 1060 1065 1070
 Ile Val Gly Arg Thr Gly Ala Gly Lys Ser Ser Leu Ile Ser Ala Leu
 1075 1080 1085
 Phe Arg Leu Ser Glu Pro Glu Gly Lys Ile Trp Ile Asp Lys Ile Leu
 1090 1095 1100
 Thr Thr Glu Ile Gly Leu His Asp Leu Arg Lys Lys Met Ser Ile Ile
 1105 1110 1115 1120
 Pro Gln Glu Pro Val Leu Phe Thr Gly Thr Met Arg Lys Asn Leu Asp
 1125 1130 1135
 Pro Phe Asn Glu His Thr Asp Glu Glu Leu Trp Asn Ala Leu Gln Glu
 1140 1145 1150
 Val Gln Leu Lys Glu Thr Ile Glu Asp Leu Pro Gly Lys Met Asp Thr
 1155 1160 1165
 Glu Leu Ala Glu Ser Gly Ser Asn Phe Ser Val Gly Gln Arg Gln Leu
 1170 1175 1180
 Val Cys Leu Ala Arg Ala Ile Leu Arg Lys Asn Gln Ile Leu Ile Ile
 1185 1190 1195 1200
 Asp Glu Ala Thr Ala Asn Val Asp Pro Arg Thr Asp Glu Leu Ile Gln
 1205 1210 1215
 Lys Lys Ser Gly Arg Asn Leu Pro Thr Ala Pro Cys
 1220 1225
 <210> 538
 <211> 1261
 <212> PRT
 <213> Homo sapiens
 <400> 538
 Met Tyr Ser Val Leu Pro Glu Asp Arg Ser Gln His Leu Gly Glu Glu

194

5					10					15					
Leu	Gln	Gly	Phe	Trp	Asp	Lys	Glu	Val	Leu	Arg	Ala	Glu	Asn	Asp	Ala
			20					25					30		
Gln	Lys	Pro	Ser	Leu	Thr	Arg	Ala	Ile	Ile	Lys	Cys	Tyr	Trp	Lys	Ser
		35					40					45			
Tyr	Leu	Val	Leu	Gly	Ile	Phe	Thr	Leu	Ile	Glu	Glu	Ser	Ala	Lys	Val
	50					55					60				
Ile	Gln	Pro	Ile	Phe	Leu	Gly	Lys	Ile	Ile	Asn	Tyr	Phe	Glu	Asn	Tyr
	65					70					75				80
Asp	Pro	Met	Asp	Ser	Val	Ala	Leu	Asn	Thr	Ala	Tyr	Ala	Tyr	Ala	Thr
				85					90					95	
Val	Leu	Thr	Phe	Cys	Thr	Leu	Ile	Leu	Ala	Ile	Leu	His	His	Leu	Tyr
			100					105					110		
Phe	Tyr	His	Val	Gln	Cys	Ala	Gly	Met	Arg	Leu	Arg	Val	Ala	Met	Cys
		115					120					125			
His	Met	Ile	Tyr	Arg	Lys	Ala	Leu	Arg	Leu	Ser	Asn	Met	Ala	Met	Gly
	130					135					140				
Lys	Thr	Thr	Thr	Gly	Gln	Ile	Val	Asn	Leu	Leu	Ser	Asn	Asp	Val	Asn
	145					150					155				160
Lys	Phe	Asp	Gln	Val	Thr	Val	Phe	Leu	His	Phe	Leu	Trp	Ala	Gly	Pro
			165					170						175	
Leu	Gln	Ala	Ile	Ala	Val	Thr	Ala	Leu	Leu	Trp	Met	Glu	Ile	Gly	Ile
			180					185					190		
Ser	Cys	Leu	Ala	Gly	Met	Ala	Val	Leu	Ile	Ile	Leu	Leu	Pro	Leu	Gln
		195					200					205			
Ser	Cys	Phe	Gly	Lys	Leu	Phe	Ser	Ser	Leu	Arg	Ser	Lys	Thr	Ala	Thr
	210					215					220				
Phe	Thr	Asp	Ala	Arg	Ile	Arg	Thr	Met	Asn	Glu	Val	Ile	Thr	Gly	Ile
	225					230					235				240
Arg	Ile	Ile	Lys	Met	Tyr	Ala	Trp	Glu	Lys	Ser	Phe	Ser	Asn	Leu	Ile
			245						250					255	
Thr	Asn	Leu	Arg	Lys	Lys	Glu	Ile	Ser	Lys	Ile	Leu	Arg	Ser	Ser	Cys
			260					265					270		
Leu	Arg	Gly	Met	Asn	Leu	Ala	Ser	Phe	Phe	Ser	Ala	Ser	Lys	Ile	Ile
		275					280					285			
Val	Phe	Val	Thr	Phe	Thr	Thr	Tyr	Val	Leu	Leu	Gly	Ser	Val	Ile	Thr
	290					295					300				
Ala	Ser	Arg	Val	Phe	Val	Ala	Val	Thr	Leu	Tyr	Gly	Ala	Val	Arg	Leu
	305					310					315				320

Thr Val Thr Leu Phe Phe Pro Ser Ala Ile Glu Arg Val Ser Glu Ala
 325 330 335
 Ile Val Ser Ile Arg Arg Ile Gln Thr Phe Leu Leu Leu Asp Glu Ile
 340 345 350
 Ser Gln Arg Asn Arg Gln Leu Pro Ser Asp Gly Lys Lys Met Val His
 355 360 365
 Val Gln Asp Phe Thr Ala Phe Trp Asp Lys Ala Ser Glu Thr Pro Thr
 370 375 380
 Leu Gln Gly Leu Ser Phe Thr Val Arg Pro Gly Glu Leu Leu Ala Val
 385 390 395 400
 Val Gly Pro Val Gly Ala Gly Lys Ser Ser Leu Leu Ser Ala Val Leu
 405 410 415
 Gly Glu Leu Ala Pro Ser His Gly Leu Val Ser Val His Gly Arg Ile
 420 425 430
 Ala Tyr Val Ser Gln Gln Pro Trp Val Phe Ser Gly Thr Leu Arg Ser
 435 440 445
 Asn Ile Leu Phe Gly Lys Lys Tyr Glu Lys Glu Arg Tyr Glu Lys Val
 450 455 460
 Ile Lys Ala Cys Ala Leu Lys Lys Asp Leu Gln Leu Leu Glu Asp Gly
 465 470 475 480
 Asp Leu Thr Val Ile Gly Asp Arg Gly Thr Thr Leu Ser Gly Gly Gln
 485 490 495
 Lys Ala Arg Val Asn Leu Ala Arg Ala Val Tyr Gln Asp Ala Asp Ile
 500 505 510
 Tyr Leu Leu Asp Asp Pro Leu Ser Ala Val Asp Ala Glu Val Ser Arg
 515 520 525
 His Leu Phe Glu Leu Cys Ile Cys Gln Ile Leu His Glu Lys Ile Thr
 530 535 540
 Ile Leu Val Thr His Gln Leu Gln Tyr Leu Lys Ala Ala Ser Gln Ile
 545 550 555 560
 Leu Ile Leu Lys Asp Gly Lys Met Val Gln Lys Gly Thr Tyr Thr Glu
 565 570 575
 Phe Leu Lys Ser Gly Ile Asp Phe Gly Ser Leu Leu Lys Lys Asp Asn
 580 585 590
 Glu Glu Ser Glu Gln Pro Pro Val Pro Gly Thr Pro Thr Leu Arg Asn
 595 600 605
 Arg Thr Phe Ser Glu Ser Ser Val Trp Ser Gln Gln Ser Ser Arg Pro
 610 615 620

Ser Leu Lys Asp Gly Ala Leu Glu Ser Gln Asp Thr Glu Asn Val Pro
 625 630 635 640
 Val Thr Leu Ser Glu Glu Asn Arg Ser Glu Gly Lys Val Gly Phe Gln
 645 650 655
 Ala Tyr Lys Asn Tyr Phe Arg Ala Gly Ala His Trp Ile Val Phe Ile
 660 665 670
 Phe Leu Ile Leu Leu Asn Thr Ala Ala Gln Val Ala Tyr Val Leu Gln
 675 680 685
 Asp Trp Trp Leu Ser Tyr Trp Ala Asn Lys Gln Ser Met Leu Asn Val
 690 695 700
 Thr Val Asn Gly Gly Gly Asn Val Thr Glu Lys Leu Asp Leu Asn Trp
 705 710 715 720
 Tyr Leu Gly Ile Tyr Ser Gly Leu Thr Val Ala Thr Val Leu Phe Gly
 725 730 735
 Ile Ala Arg Ser Leu Leu Val Phe Tyr Val Leu Val Asn Ser Ser Gln
 740 745 750
 Thr Leu His Asn Lys Met Phe Glu Ser Ile Leu Lys Ala Pro Val Leu
 755 760 765
 Phe Phe Asp Arg Asn Pro Ile Gly Arg Ile Leu Asn Arg Phe Ser Lys
 770 775 780
 Asp Ile Gly His Leu Asp Asp Leu Leu Pro Leu Thr Phe Leu Asp Phe
 785 790 795 800
 Ile Gln Thr Leu Leu Gln Val Val Gly Val Val Ser Val Ala Val Ala
 805 810 815
 Val Ile Pro Trp Ile Ala Ile Pro Leu Val Pro Leu Gly Ile Ile Phe
 820 825 830
 Ile Phe Leu Arg Arg Tyr Phe Leu Glu Thr Ser Arg Asp Val Lys Arg
 835 840 845
 Leu Glu Ser Thr Thr Arg Ser Pro Val Phe Ser His Leu Ser Ser Ser
 850 855 860
 Leu Gln Gly Leu Trp Thr Ile Arg Ala Tyr Lys Ala Glu Glu Arg Cys
 865 870 875 880
 Gln Glu Leu Phe Asp Ala His Gln Asp Leu His Ser Glu Ala Trp Phe
 885 890 895
 Leu Phe Leu Thr Thr Ser Arg Trp Phe Ala Val Arg Leu Asp Ala Ile
 900 905 910
 Cys Ala Met Phe Val Ile Ile Val Ala Phe Gly Ser Leu Ile Leu Ala
 915 920 925
 Lys Thr Leu Asp Ala Gly Gln Val Gly Leu Ala Leu Ser Tyr Ala Leu

930	935	940
Thr Leu Met Gly Met Phe Gln Trp Cys Val Arg Gln Ser Ala Glu Val 945 950 955 960		
Glu Asn Met Met Ile Ser Val Glu Arg Val Ile Glu Tyr Thr Asp Leu 965 970 975		
Glu Lys Glu Ala Pro Trp Glu Tyr Gln Lys Arg Pro Pro Pro Ala Trp 980 985 990		
Pro His Glu Gly Val Ile Ile Phe Asp Asn Val Asn Phe Met Tyr Ser 995 1000 1005		
Pro Gly Gly Pro Leu Val Leu Lys His Leu Thr Ala Leu Ile Lys Ser 1010 1015 1020		
Gln Glu Lys Val Gly Ile Val Gly Arg Thr Gly Ala Gly Lys Ser Ser 1025 1030 1035 1040		
Leu Ile Ser Ala Leu Phe Arg Leu Ser Glu Pro Glu Gly Lys Ile Trp 1045 1050 1055		
Ile Asp Lys Ile Leu Thr Thr Glu Ile Gly Leu His Asp Leu Arg Lys 1060 1065 1070		
Lys Met Ser Ile Ile Pro Gln Glu Pro Val Leu Phe Thr Gly Thr Met 1075 1080 1085		
Arg Lys Asn Leu Asp Pro Phe Asn Glu His Thr Asp Glu Glu Leu Trp 1090 1095 1100		
Asn Ala Leu Gln Glu Val Gln Leu Lys Glu Thr Ile Glu Asp Leu Pro 1105 1110 1115 1120		
Gly Lys Met Asp Thr Glu Leu Ala Glu Ser Gly Ser Asn Phe Ser Val 1125 1130 1135		
Gly Gln Arg Gln Leu Val Cys Leu Ala Arg Ala Ile Leu Arg Lys Asn 1140 1145 1150		
Gln Ile Leu Ile Ile Asp Glu Ala Thr Ala Asn Val Asp Pro Arg Thr 1155 1160 1165		
Asp Glu Leu Ile Gln Lys Lys Ile Arg Glu Lys Phe Ala His Cys Thr 1170 1175 1180		
Val Leu Thr Ile Ala His Arg Leu Asn Thr Ile Ile Asp Ser Asp Lys 1185 1190 1195 1200		
Ile Met Val Leu Asp Ser Gly Arg Leu Lys Glu Tyr Asp Glu Pro Tyr 1205 1210 1215		
Val Leu Leu Gln Asn Lys Glu Ser Leu Phe Tyr Lys Met Val Gln Gln 1220 1225 1230		
Leu Gly Lys Ala Glu Ala Ala Ala Leu Thr Glu Thr Ala Lys Gln Arg 1235 1240 1245		

Trp Gly Phe Thr Met Leu Ala Arg Leu Val Ser Asn Ser
1250 1255 1260

<210> 539
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 539
Cys Leu Ser His Ser Val Ala Val Val Thr
1 5 10

<210> 540
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 540
Ala Val Val Thr Ala Ser Ala Ala Leu
1 5

<210> 541
<211> 14
<212> PRT
<213> Homo sapiens

<400> 541
Leu Ala Gly Leu Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu
5 10

<210> 542
<211> 15
<212> PRT
<213> Homo sapiens

<400> 542
Thr Gln Val Val Phe Asp Lys Ser Asp Leu Ala Lys Tyr Ser Ala
5 10 15

<210> 543
<211> 12
<212> PRT
<213> Homo sapiens

<400> 543
Phe Met Gly Ser Ile Val Gln Leu Ser Gln Ser Val
5 10

Met Thr

```
<210> 545
<211> 18
<212> PRT
<213> Homo sapiens
```

Ser Val

```
<210> 546
<211> 29
<212> PRT
<213> Homo sapiens
```

Thr Glu Ala Arg Arg His Tyr Asp Glu Gly Val Arg Met
20 25

```
<210> 547
<211> 58
<212> PRT
<213> Homo sapiens
```

Ser Ala Pro Ser Leu Ser Pro His Cys Cys Pro Cys Arg Ala Arg Leu
20 25 30

Cys Arg Met Pro Arg Thr Leu Arg Arg Leu
50 55

200

<210> 548
<211> 18
<212> PRT
<213> Homo sapiens

<400> 548
Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu Gly Thr Gln Glu
5 10 15

Glu Cys

<210> 549
<211> 18
<212> PRT
<213> Homo sapiens

<400> 549
Leu Glu Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg
5 10 15

Gln Ala

<210> 550
<211> 14
<212> PRT
<213> Homo sapiens

<400> 550
Ser Asp His Trp Arg Gly Arg Tyr Gly Arg Arg Arg Pro Phe
5 10

<210> 551
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 551
Phe Asp Lys Ser Asp Leu Ala Lys Tyr Ser Ala
5 10

<210> 552
<211> 2577
<212> DNA
<213> Homo sapiens

<400> 552
agcatatgta acatgacctg tgcttcagtg ttcttttggtg atcaaaaatt ccttactttt 60
agttttttat ctatggtaga accaccaga gcaggggtcc tcaactccca ggccacagac 120
tcataccagt ccacggacta ttatgaacca caccacacag gaggaggtga gcactaggca 180
agccaaggaa gcttcacctg tacttacagc cacacgcat ggctcatatt acagcctgaa 240

```

ctctgcctcc actcagatca gtgataacat tagaaactca ttggagcacg aaccctgttg 300
tgaactgcct atccgaagga tctaggttgt gtgcttcgta tgagaatcta atgccagatg 360
atctatcatt gtctcacttt gcccccagat aagaccatct agttgcagaa aaataagctc 420
agagcttcca ctgattctac attatggata tgtgccgccc aagcaagcac aaagccctac 480
ttttacacat gcctagtgat gcttcatgga caaggcttgg ctctgttgag tccaactaac 540
ctacctgaga ttctgagatt tctcttcaat ggcttcctgt gagctagagt ttgaaaatat 600
cttaaaatct tgagctagag atggaagtag cttggacgat tttcattatc atgtaaatcg 660
gggtactcaa ggggccaacc acagctggga gccactgctc aggggaaggt tcatatggga 720
ctttctactg cccaagggttc tatacaggat ataaagggtgc ctcacagtat agatctggta 780
gcaaagaaga agaacaaac actgatctct ttctgccacc cctctgaccc tttggaactc 840
ctctgacctt ttaagaacaag cctacctaata atctgctaga gaaaagacca acaacggcct 900
caaaggatct cttaccatga aggtctcagc taattcttgg ctaagatgtg gggtccacat 960
taggttctga atatgggggg aagggtcaat ttgtctcattt tgtgtgtgga taaagtcagg 1020
atgcccaggg gccagagcag ggggctgctg ctttgggaac aatggctgag catataacca 1080
taggtatggg aacaaaaaac atcaaagtca ctgtatcaat tgccatgaag actcgaggga 1140
cctgaatcta ccgattcatc ttaaggcagc aggaccagtt tgagtggcaa caatgcagca 1200
gcagaatcaa tggaacaac agaattgatt caatgtcctt ttttttctcc tcttctgac 1260
ttgataaaag ggaccgtctt ccttggattt agtgaacccc tttggttcct gaaaaattca 1320
aggagtatct aggacatagt cccagaaga cagtacaaga ctttctgata aactggacat 1380
ttcaagrccc aaataactaa tcagaaaaat caaagatgtg atactatttt ttatcccatg 1440
catagtgctt acacttggat caaatgaaca atgttgggat ctytatggat aaaggtctta 1500
aaagtcttga gataaagaat cctgcaccca ctgttacttc taacttgtct tgttttttgt 1560
ctgwtttctg gctgatgcag gggactaact cactgccacg cgaaaactac ctgaactgaa 1620
ctatgacatc tcacctgata tgtaagatgt aactgttata attattttta acctcaattt 1680
agcattaact agccttttaa tgtaaacact tacacattat gaygactaga aacagcatat 1740
tctctggccg tctgtccaga tagatottga gaagatacat caatgttttg ctcaagtaga 1800
aggctgacta tacttgccga tccacaacat acagcaagta tgagagcagt tctaaaatga 1860
cagagatagg aacagtaata aagttattkt aaaagctaata ttgatatact ttaccaattt 1920
aacatcttgc ctgtccgtgc agaatacaac atttacctgc actaaaagac ataagcatct 1980
tcagtgtcca agtgttcac tttgtaaaa accaccaagg ttaaaaggaa gggacaaaaa 2040
aaaaaaaacc tcttatctca gtggggtatt gcatagcaga agctactaat ttgaagtcct 2100
ttgatggaca agaacaata ttagggccac ttatctgaaa tgaacaaaga tttaagtga 2160
gatttcatca cagcttccct agactgatat gctgtaatag aaaatcagct aggggggtaaa 2220
ataaataaga gctctctgca tgctgaaagc aagtaagatt aataataatg gtaagaatag 2280
tagtcacagg agtttcagtt aatgatgcca ataagcatgt gctaggcact gaattaaatg 2340
ccacatatat ctttcttatg cgcagcaaac tttgaaggat atattctcct acttttcata 2400
tatgacaaca tatttgggtg taaataacgt tcccaaggct acacacctag caagtaagaa 2460
agttaggaat taaacccagt attgtgtgaa tctaaagcct aacttttttc tctttatcac 2520
ccacctacgg cttgtcttca ttaaaggaaa agtgtatcca cttaaaaaaa aaaaaaa 2577

```

<210> 553

<211> 58

<212> PRT

<213> Homo sapiens

<400> 553

```

Ser Ile Cys Asn Met Thr Cys Ala Ser Val Phe Phe Cys Asp Gln Lys
          5                      10                      15

```

```

Phe Leu Thr Phe Ser Phe Leu Ser Met Val Glu Pro Pro Arg Ala Gly
          20                      25                      30

```

```

Val Leu Asn Ser Gln Ala Thr Asp Ser Tyr Gln Ser Thr Asp Tyr Tyr
          35                      40                      45

```

```

Glu Pro His His Thr Gly Gly Gly Glu His
          50                      55

```

<210> 554
 <211> 59
 <212> PRT
 <213> Homo sapiens

<400> 554
 Leu Gln Lys Asn Lys Leu Arg Ala Ser Thr Asp Ser Thr Leu Trp Ile
 5 10 15
 Cys Ala Ala Glu Ala Ser Thr Lys Pro Tyr Phe Tyr Thr Cys Leu Val
 20 25 30
 Met Leu His Gly Gln Gly Leu Ala Leu Leu Ser Pro Thr Asn Leu Pro
 35 40 45
 Glu Ile Leu Arg Phe Leu Phe Asn Gly Phe Leu
 50 55

<210> 555
 <211> 71
 <212> PRT
 <213> Homo sapiens

<400> 555
 Leu Gly Arg Phe Ser Leu Ser Cys Lys Ser Gly His Ser Arg Gly Gln
 5 10 15
 Pro Gln Leu Gly Ala Thr Ala Gln Gly Lys Val His Met Gly Leu Ser
 20 25 30
 Thr Ala Gln Gly Ser Ile Gln Asp Ile Lys Val Pro His Ser Ile Asp
 35 40 45
 Leu Val Ala Lys Lys Lys Lys Gln Thr Leu Ile Ser Phe Cys His Pro
 50 55 60
 Ser Asp Pro Leu Glu Leu Leu
 65 70

<210> 556
 <211> 81
 <212> PRT
 <213> Homo sapiens

<400> 556
 Asn His Pro Glu Gln Gly Ser Ser Thr Pro Arg Pro Gln Thr His Thr
 5 10 15
 Ser Pro Arg Thr Ile Met Asn His Thr Thr Gln Glu Glu Val Ser Thr
 20 25 30
 Arg Gln Ala Lys Glu Ala Ser Pro Val Leu Thr Ala Thr Arg His Gly
 35 40 45
 Ser Tyr Tyr Ser Leu Asn Ser Ala Ser Thr Gln Ile Ser Asp Asn Ile

203

50 55 60
 Arg Asn Ser Leu Glu His Glu Pro Cys Cys Glu Leu Pro Ile Arg Arg
 65 70 75 80

Ile

<210> 557
 <211> 54
 <212> PRT
 <213> Homo sapiens

<400> 557
 Ser Leu Ser Ala Thr Pro Leu Thr Leu Trp Asn Ser Ser Asp Pro Leu
 5 10 15

Glu Gln Ala Tyr Leu Ile Ser Ala Arg Glu Lys Thr Asn Asn Gly Leu
 20 25 30

Lys Gly Ser Leu Thr Met Lys Val Ser Ala Asn Ser Trp Leu Arg Cys
 35 40 45

Gly Phe His Ile Arg Phe
 50

<210> 558
 <211> 77
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (1)...(77)
 <223> Xaa = Any amino acid

<400> 558
 Asn Asp Arg Asp Arg Asn Ser Asn Lys Val Ile Xaa Lys Ala Asn Leu
 5 10 15

Ile Tyr Phe Thr Asn Leu Thr Ser Cys Leu Ser Val Gln Asn Gln Thr
 20 25 30

Phe Thr Cys Thr Lys Arg His Lys His Leu Gln Cys Ser Ser Val His
 35 40 45

Leu Cys Lys Ile Pro Pro Arg Leu Lys Gly Arg Asp Lys Lys Lys Lys
 50 55 60

Pro Ser Tyr Leu Ser Gly Val Leu His Ser Arg Ser Tyr
 65 70 75

<210> 559
 <211> 50
 <212> PRT

<213> Homo sapiens

<400> 559

Thr Leu Pro Pro Leu Arg Ser Val Ile Thr Leu Glu Thr His Trp Ser
 5 10 15
 Thr Asn Pro Val Val Asn Cys Leu Ser Glu Gly Ser Arg Leu Cys Ala
 20 25 30
 Ser Tyr Glu Asn Leu Met Pro Asp Asp Leu Ser Leu Ser His Phe Ala
 35 40 45
 Pro Arg
 50

<210> 560

<211> 56

<212> PRT

<213> Homo sapiens

<400> 560

Ile Gly Ser Leu Lys Gly Pro Thr Thr Ala Gly Ser His Cys Ser Gly
 5 10 15
 Glu Gly Ser Tyr Gly Thr Phe Tyr Cys Pro Arg Phe Tyr Thr Gly Tyr
 20 25 30
 Lys Gly Ala Ser Gln Tyr Arg Ser Gly Ser Lys Glu Glu Glu Thr Asn
 35 40 45
 Thr Asp Leu Phe Leu Pro Pro Leu
 50 55

<210> 561

<211> 57

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)...(57)

<223> Xaa = Any amino acid

<400> 561

Val Leu His Leu Asp Gln Met Asn Asn Val Gly Ile Xaa Met Asp Lys
 5 10 15
 Gly Leu Lys Ser Pro Glu Ile Lys Asn Pro Ala Pro Thr Gly Thr Ser
 20 25 30
 Asn Leu Ser Cys Phe Leu Ser Xaa Phe Trp Leu Met Gln Gly Thr Asn
 35 40 45
 Ser Leu Pro Arg Glu Asn Tyr Leu Asn
 50 55

```
<220>  
<221> VARIANT  
<222> (1)...(59)  
<223> Xaa = Any amino acid.
```

```

<400> 562
Asp Leu Tyr Pro Xaa Arg Ser Gln His Cys Ser Phe Asp Pro Ser Val
      5                      10                      15
Ala Pro Met His Gly Ile Lys Asn Ser Ile Thr Ser Leu Ile Phe Leu
      20                      25                      30
Ile Ser Tyr Leu Xaa Leu Glu Met Ser Ser Leu Ser Glu Ser Leu Val
      35                      40                      45
Leu Ser Ser Gly Asp Tyr Val Leu Asp Thr Pro
      50                      55

```

```
<210> 563
<211> 79
<212> PRT
<213> Homo sapiens
```

```
<400> 563  
Cys Phe Leu Phe Pro Tyr Leu Trp Leu Tyr Ala Gln Pro Leu Phe Pro  
          5                      10                      15  
  
Lys Gln Gln Pro Pro Ala Leu Ala Pro Gly His Pro Asp Phe Ile His  
      20                      25                      30  
  
Thr Gln Asn Glu Gln Ile Asp Pro Ser Pro His Ile Gln Asn Leu Met  
     35                      40                      45  
  
Trp Asn Pro His Leu Ser Gln Glu Leu Ala Glu Thr Phe Met Val Arg  
    50                      55                      60  
  
Asp Pro Leu Arg Pro Leu Leu Val Phe Ser Leu Ala Asp Ile Arg  
   65                      70                      75
```

```
<210> 564
<211> 64
<212> PRT
<213> Homo sapiens
```

<400> 564
Ala Cys Ser Lys Gly Ser Glu Glu Phe Gln Arg Val Arg Gly Val Ala
5 10 15
Glu Arg Asp Gln Cys Leu Phe Leu Leu Leu Cys Tyr Gln Ile Tyr Thr
20 25 30

Val Arg His Leu Tyr Ile Leu Tyr Arg Thr Leu Gly Ser Arg Lys Ser
 35 40 45

His Met Asn Leu Pro Leu Ser Ser Gly Ser Gln Leu Trp Leu Ala Pro
 50 55 60

<210> 565

<211> 57

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)...(57)

<223> Xaa = Any amino acid

<400> 565

Leu Tyr Tyr Cys Ser Tyr Leu Cys His Phe Arg Thr Ala Leu Ile Leu
 5 10 15

Ala Val Cys Cys Gly Ser Ala Ser Ile Val Ser Leu Leu Leu Glu Gln
 20 25 30

Asn Ile Asp Val Ser Ser Gln Asp Leu Ser Gly Gln Thr Ala Arg Glu
 35 40 45

Tyr Ala Val Ser Ser Xaa His Asn Val
 50 55

<210> 566

<211> 55

<212> PRT

<213> Homo sapiens

<400> 566

Ile Leu Leu Glu Phe Phe Arg Asn Gln Arg Gly Ser Leu Asn Pro Arg
 5 10 15

Lys Thr Val Pro Phe Ile Lys Ser Glu Gly Gly Glu Lys Lys Gly His
 20 25 30

Cys Asn His Ser Val Val Ser Ile Asp Ser Ala Ala Ala Leu Leu Pro
 35 40 45

Leu Lys Leu Val Leu Leu Pro
 50 55

<210> 567

<211> 51

<212> PRT

<213> Homo sapiens

<400> 567

Tyr Ser Asp Phe Asp Val Phe Cys Ser His Thr Tyr Gly Tyr Met Leu

5 10 15
 Ser His Cys Ser Gln Ser Ser Ser Pro Leu Leu Trp Pro Leu Gly Ile
 20 25 30
 Leu Thr Leu Ser Thr His Lys Met Ser Lys Leu Thr Leu Pro Pro Ile
 35 40 45
 Phe Arg Thr
 50

<210> 568
 <211> 75
 <212> PRT
 <213> Homo sapiens

<400> 568
 Lys Val Gly Glu Tyr Ile Leu Gln Ser Leu Leu Arg Ile Arg Lys Ile
 5 10 15
 Tyr Val Ala Phe Asn Ser Val Pro Ser Thr Cys Leu Leu Ala Ser Leu
 20 25 30
 Thr Glu Thr Pro Val Thr Thr Ile Leu Thr Ile Ile Ile Asn Leu Thr
 35 40 45
 Cys Phe Gln His Ala Glu Ser Ser Tyr Leu Phe Tyr Pro Leu Ala Asp
 50 55 60
 Phe Leu Leu Gln His Ile Ser Leu Gly Lys Leu
 65 70 75

<210> 569
 <211> 4809
 <212> DNA
 <213> Homo sapiens

<400> 569
 gcatccagag tgggtggactg gttacaggct atgaacctac actgatgcgg caccaccacc 60
 cagagtcacac rgggttatgtt gggtcacatt tactcttgct gtggtatggt ctataggttt 120
 ggacagatgt ccgataatcc tttttacatt ttggcatcct tgggtagctc gtcttgtagg 180
 aatggacttg cttcaaagtg gaggcaggca gatccttcag acgggtatat ggagccctgt 240
 tttcagttgc ttttctaatt ctctcttata gtttacctca aaatcttcct gaggtctcgc 300
 ttccctttta aatcccttgct tactttgcag catcactctg acactcccat tgattcctca 360
 gcacctactg actacacggg taggagtgcagggttagaat tcatgtttta ttcattctttg 420
 ggtctgtagc acccagcaaa gtgctcagta aatgcgcagt aattgatttg acctctgaac 480
 aaatacacac tgtactaaga atctacacac cgaaagacaa aaacaagaca aatttgagtg 540
 ctacaggtgt cagcgttggc atcacacatg tgcctgtgta ttccctctagg tggttaccag 600
 gagctctgcc actgcatgct cactagtgcagggttcgctc caccacccca gctgggtagc 660
 cgctgctctc acataagggg tccaattaaa attgccagga ataaattccc ccggactttg 720
 acttctcaag agctaagaag gtttgctgag tattctggca tgatgtttgg tgatcaaca 780
 actgctggcc aaaaatgatg agtatttccc cctcttgctg aagatgtgct ccatacaata 840
 gtccatcaca ttcattcatt atcagctgag aagtgtgcag aacaacatgt aatagataat 900
 atgattggct gcacacttcc agactgatga atgataatg tgatggacta ttgtatggag 960
 cacatcttca gcaagagggg gaaatactca tcattttatc tattacatgt tgttctgggt 1020

ttttttttt	tccaatgtcc	agcctaaact	ataaagtact	ttgagaacgc	acagtgagcc	1080
ataagcttgc	caataaagag	tcctctgtgg	tatggaactg	gcttatttca	tacacaatct	1140
gcaaacaatg	agggcactat	tggaaacata	ctgtgctgca	cagagcattt	acaccgctta	1200
tctttaatct	tccccagcaa	tccttgcttt	gtgcgcattt	atgatccttg	ctctcagaag	1260
tccacatact	tttccccaac	cgtaacaaat	tatttaactc	atctaagtga	tgtatgtccg	1320
cgcagctcga	aaacagtaat	tgtccttggg	aagaagtgag	tttaagagag	ctctagggca	1380
ctcatcacaa	ctccagccct	gccctccatg	tggtagcagc	tcctttggact	ggggctaagt	1440
gcttattctt	gtgcttcatt	cctggtaagc	tcaatttctt	taccttagga	taactttgct	1500
ggaaaagggc	tcagattcag	ccgaccattg	tggcctctgt	ggctgtcaca	gcttgtccct	1560
gacatgctat	gatgttgggt	ccccttctca	tccccttggg	atttcttctg	ctggcccaca	1620
gccagaacaa	ctaggccctt	tactccacca	tcctttgtt	ttcttttgtt	tcgttggtaa	1680
aaatcaatcc	ttctaccatc	catgcatagc	aattttctaa	aactgaattt	caagagcagt	1740
atctgaagaa	acaaacatga	tttggtcctt	tagtaaaaca	gaataaattt	taataaatca	1800
actttgaatg	agtgtgaaga	gttaagaaaa	agcacaaaa	tgagatcatc	agagcagctt	1860
ggcctcaaat	gacaggcagc	aggattctac	agggtttgag	ccttcctaag	tgaagctgtt	1920
tcctgcaggc	tcctgctcc	aagctcctag	ctaacagccc	cttctccac	gattggcaac	1980
aaagagcaaa	aataactttg	tacttgatgc	tgagtcagtg	taaaaagcca	taaaaaattc	2040
cctctaaatg	tcaaaatggt	tgcctccttt	gaggcttctc	tcctcctact	gggtctggat	2100
aaattagcac	tgggcttata	ttgagtcaca	gatctgggcc	ctgccacaga	gagcttctc	2160
ctagtgtgtg	atgctttttc	tccaaactat	tgatacaaaa	tgactggaa	tagaaatcaa	2220
cagaaaactg	tcaaagggtg	ggcatacaca	ttctcatgta	gatgtaaagc	tgtgcttaga	2280
attcctttgt	ggagtctgg	ttggtcttgg	ttttcttgg	gtttgattca	tttttttacg	2340
taaattacaa	aaaccctcca	catttcttca	tggattgtat	tagtccatgt	tctccagaga	2400
agcagaacga	gttggtatga	tgttttggaa	gagattatga	ggaaccggct	catgtgatga	2460
aggaggttga	gaggtcctgt	gctctgccat	ctgcaagctg	aagacctgga	aagctgaggg	2520
tgtggctcca	gtctgagctc	gaaggcccaa	gaaccagggg	aaccaacggt	gtagattcca	2580
ggttgaaggc	aggagaagat	ggatgtccca	gctcagcagg	caggcaggaa	gcaaatgggg	2640
taaattcctc	cttctccac	cttttgttcc	attcaggcct	tcaacagatt	ggatgagcgc	2700
ccccccaccc	ccacactagg	gagggccatc	tgctttactg	agtcggctga	gtcaagtgcc	2760
agcctcatcc	caaaacactc	tccagacaca	cgcagaaatg	tttcatctgg	gcaccctgtg	2820
gccagtcatg	ctgacacaca	gaactaacca	tgacatggat	tcttcttaaa	gcagtgatag	2880
gagcgacacg	aaacattttc	ataattttca	attattttta	atgaaaacta	tatctgatgg	2940
aattgtttaa	acctagtctg	gccacacatt	atttctgtgg	accgcccctc	cttcaatccc	3000
ttggacactg	atgactttat	gccagatta	cactggaggc	ctgtgctgat	tttctaacac	3060
atacctgcaa	ctgagctggc	aaaaagaaaa	ctaggcaagt	atgacagata	catgatgcac	3120
agggttaagt	caaaggaaag	aaaaacacca	actgcaggga	tgagggactc	acctcttag	3180
aagtttctac	ttgagcagct	agaagactac	aatgccactc	atcaaaacag	tgactcaggg	3240
ggagtatttg	ggataaagga	ggaatctgat	gttgagggtc	aaatttgaag	tgtctttaag	3300
acctacaggt	aacgagacag	ctggacaaac	acatggaact	caggacaaag	gctctaagga	3360
cagcacagca	gctgacatcc	tgtgtgacag	ccttgaaagc	agcaggcccc	ccgctcacat	3420
tttggaaggg	aaaatgggta	caatgttgtc	tgccactttg	gggccttctt	gggtcacatg	3480
cattttacat	ttatgcagtt	gatataattt	tgtttctgtg	gtcttttata	cattagacac	3540
catgattctc	aatcctttgt	tattttgtat	tacaaaaagc	tgaattatta	tttcaaatat	3600
gggcaaatta	gagccttcca	tattgccaag	gtgtatcaac	cacactgata	ycaygatctc	3660
tcttttgaat	tagttttcca	gttcacacct	accatttatt	tcatgattgg	tttcagactt	3720
gttcctcctg	gaaacactcc	ctaacaagca	cccttgccag	aatgaagaca	caccacacac	3780
atctacecca	ttactgcatg	tactcaagag	tcagctttta	tatgatctct	cccaagtgtc	3840
cctataatgg	ggatctttca	ctcaccctaa	agtgaggaca	aaatacttga	aagcatgagc	3900
ccagtgccctg	tagtgtgca	attaacctca	gaccaaggaa	gtgccgaacg	catctggctt	3960
ttagcgaagg	acctgacaaa	gtccttcagg	atgtttttgt	acatgagcta	gagaaatgta	4020
cctggagaac	agcttctact	gccagatgat	cttactcaaa	agatgcagat	taagcaaaat	4080
atcaacccaa	agggtgtcc	ctgatggccc	accagcccct	gtgcctggct	cgtttcttat	4140
gtttcctaga	tttggtttca	gacttgctcc	tcctgcagac	actccctaac	cagcatcctt	4200
gcagaaaact	ggtgaactag	aaaaggcctg	tgtgggtcac	gtggccaccc	aacaccacag	4260
cagtgtctaa	ggtatgcgtg	ggagcctgca	cagcaggagc	ggggtcttct	ggagaccgcg	4320
atgagatgca	aagggcagtg	gacaaggagc	caagggaggt	ggctctagtc	acgctgggtat	4380
ggtgcagct	tgaggatgct	gggcaagtcc	cgagccgtct	gccttcttag	taccacagtt	4440
accactgtct	gttaacctgc	gagttcaagt	gcttcacgtg	agacagctac	gagacaggcc	4500

```

cctggaaact ggaaaatgcy aagtaaatgt catgcacaat tggtgttcac attttatctc 4560
aatcactttt accaaatcag gctaaaccct gggatttcat aacgtcttgg gctgtacaaa 4620
ttgttccttg aaatgactca gagacatttt ctgaattggc ttccatcagc caagcatttc 4680
ttcagaactg gaaaaatgct ttaaatttgg ctttgtcatg attattaaaa cactctgtac 4740
attttttatt attgaaatta acacattgcc tactttttta aaattggaaa aagaaaaaaa 4800
aaaaaaaaa                                     4809

```

<210> 570

<211> 951

<212> DNA

<213> Homo sapiens

<400> 570

```

aaaattgaat attgagatac cattcttttag tgttaccttt tttaccacac tgtgtttctg 60
aaaatattgg aatttttattc atcttaaaaa ttggaccggg ccttatttac catctttaat 120
ccatttttagt actatgggtg agtacatgga attgaagtct ggcttaaaac ttcagaaaagt 180
tataatatcta ttttttttta tttttttgag acagagtctc gctgtgtcac ccaggctgga 240
gtgcgggtgcc acaatcttgg ctactgcaa cctctgagtc ccaggttcaa gcgatactca 300
tgccctcgcc tcttgagtag ctgggactac aggcgtgcac caccacatct ggctaattct 360
tttttgattt tttagtagag acgggggttc actgtggtct ccatctcctg acctcgtgat 420
ccgcctgcct cccaaagtgc tgggattaca ggcagtagcc accgcacaca gctgggactg 480
ggtaatttat aaagaaaaga ggtttaatga ctacagttc cgcaggtgtg gagaggcctc 540
aggaaaactta caatcatggt ggaaggcgaa ggggaagcaa ggcacgtctt acatggtggc 600
aggagagaac gagtgagggg ggagactgcc acaaaacttt tttttttgag acaagagtct 660
ggccctgttg cccaggctgg agtgcagtgg catgatctca gctcactgca acctctgcct 720
cacaggttca agcaattctc atgcctcagc ctccgcata gctgggacca caggtagtca 780
ccaccacacc tagctaattt ttgtagtttt agtagagatg ggggtctcact atgttgctca 840
ggctgggtcta aaactcctgg gctccagcaa tccgcctgcc ttggcctccc aaagtgtctg 900
ggttacaggc ataagccacc acatccagcc tgccacatac ttttaaacta t 951

```

<210> 571

<211> 819

<212> DNA

<213> Homo sapiens

<400> 571

```

cagcttaaaa atggttttctt gaaatcagtg attagcattc actcaccagt acccctacta 60
aggggtaggc actggtttgt actcctggga atacaggagt acaccagaat ttatttctgc 120
ttattgcttt tggtgcaaat gccgtggctt catctgagga attctagaat tcagaggggtg 180
tagccctcca ctctgctgtc ttgctatctg ctctcattgc atccgtttaa cctgcattct 240
gaaagatggt tctcagggtt ttccctgacg attttcttct tttctgatcc tgacaatggt 300
ttaaatcatt gtactgtggt tatcatttct ctgcatttat tttaccatc ttcctttgta 360
acttgctcta ttgtctttta atttctgcct gttctttatg gctttcaact tcataaataa 420
catgttttct caaatctctt tgtgaattcc agagagggcc aggcacggtg gctcacatct 480
gtaatccag cactttgggg aggctgagac ggggtggatca cttgaggtca ggagtttgag 540
accagcctgg ccaacatggt gaaatcccg ttcactaaaa atacaaaaat taccaggca 600
tggtggcggg cgctgtaat cccagggtact cgggaggctg agggaggaga atcgcttgaa 660
cctgggaggg tgagggagga gaatcgcttg aaccggggag gcagaggttg cagtgaaccg 720
agatcatggt gctgcactcc agcctggtca acagagcaag actctgcctc aaaaacaaac 780
aaataacaa acaaacaaac aaaacagaga gattttgct 819

```

<210> 572

<211> 203

<212> DNA

<213> Homo sapiens

<400> 572

```

tatagaatac tcaagctatg catcaagctt ggtaccgagc tcggatccac tatttacggc 60

```

cgccagtgtg ctggaattcg cccttagctc ggatccacta gtccagtgtg gtggaattcc 120
 attgtgttg gcccaacaca atggagccac cacatccagc ctgccacata cttttaaaact 180
 atcaggtctc atgagaactc atg 203

<210> 573

<211> 132

<212> PRT

<213> Homo sapiens

<400> 573

Met Val Glu Gly Glu Gly Glu Ala Arg His Val Leu His Gly Gly Arg
 5 10 15
 Arg Glu Arg Val Arg Gly Glu Thr Ala Thr Asn Phe Phe Phe Leu Arg
 20 25 30
 Gln Glu Ser Gly Pro Val Ala Gln Ala Gly Val Gln Trp His Asp Leu
 35 40 45
 Ser Ser Leu Gln Pro Leu Pro His Arg Phe Lys Gln Phe Ser Cys Leu
 50 55 60
 Ser Leu Pro His Ser Trp Asp His Arg Tyr Ala Pro Pro His Leu Ala
 65 70 75 80
 Asn Phe Cys Ser Phe Ser Arg Asp Gly Val Ser Leu Cys Cys Ser Gly
 85 90 95
 Trp Ser Lys Thr Pro Gly Leu Gln Gln Ser Ala Cys Leu Gly Leu Pro
 100 105 110
 Lys Cys Trp Gly Tyr Arg His Lys Pro Pro His Pro Ala Cys His Ile
 115 120 125
 Leu Leu Asn Tyr
 130

<210> 574

<211> 62

<212> PRT

<213> Homo sapiens

<400> 574

Met Thr His Ser Ser Ala Trp Leu Glu Arg Pro Gln Glu Thr Tyr Asn
 5 10 15
 His Gly Gly Arg Arg Arg Gly Ser Lys Ala Arg Leu Thr Trp Trp Gln
 20 25 30
 Glu Arg Thr Ser Glu Gly Gly Asp Cys His Lys Leu Phe Phe Phe Glu
 35 40 45
 Thr Arg Val Trp Pro Cys Cys Pro Gly Trp Ser Ala Val Ala
 50 55 60

<210> 575

<211> 76
 <212> PRT
 <213> Homo sapiens

<400> 575
 Met Val Lys Ser Arg Phe Thr Lys Asn Thr Lys Ile Thr Gln Ala Trp
 5 10 15
 Trp Arg Ala Pro Val Ile Pro Gly Thr Arg Glu Ala Glu Gly Gly Glu
 20 25 30
 Ser Leu Glu Pro Gly Arg Leu Arg Glu Glu Asn Arg Leu Asn Pro Gly
 35 40 45
 Gly Arg Gly Cys Ser Glu Pro Arg Ser Cys Cys Cys Thr Pro Ala Trp
 50 55 60
 Ser Thr Glu Gln Asp Ser Ala Ser Lys Thr Asn Lys
 65 70 75

<210> 576
 <211> 68
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (1)...(68)
 <223> Xaa = Any Amino Acid

<400> 576
 Met Leu Gly Lys Ser Arg Ala Val Cys Leu Pro Ser Thr Thr Val Thr
 5 10 15
 Thr Val Cys Tyr Leu Ala Ser Ser Ser Ala Ser Arg Glu Thr Ala Thr
 20 25 30
 Arg Gln Ala Pro Gly Asn Trp Lys Met Xaa Ser Lys Cys His Ala Gln
 35 40 45
 Leu Leu Phe Thr Phe Tyr Leu Asn His Phe Tyr Gln Ile Arg Leu Asn
 50 55 60
 Pro Gly Tyr Ser
 65

<210> 577
 <211> 57
 <212> PRT
 <213> Homo sapiens

<400> 577
 Met Tyr Leu Glu Asn Ser Phe Tyr Cys Gln Met Ile Leu Leu Lys Arg
 5 10 15
 Cys Arg Leu Ser Lys Ile Ser Thr Gln Arg Val Val Pro Asp Gly Pro

20 25 30

Pro Ala Pro Val Pro Gly Ser Phe Pro Met Phe Pro Arg Phe Gly Phe
 35 40 45

Arg Leu Ala Pro Pro Ala Asp Thr Pro
 50 55

<210> 578
 <211> 51
 <212> PRT
 <213> Homo sapiens

<400> 578
 Met Gln Leu Ile Tyr Leu Cys Phe Leu Gly Leu Leu Tyr Ile Arg His
 5 10 15

His Asp Ser Gln Ser Phe Val Ile Leu Tyr Tyr Lys Lys Leu Asn Tyr
 20 25 30

Tyr Phe Lys Tyr Gly Gln Ile Arg Ala Phe His Ile Ala Lys Val Tyr
 35 40 45

Gln Pro His
 50

<210> 579
 <211> 56
 <212> PRT
 <213> Homo sapiens

<400> 579
 Met His Phe Thr Phe Met Gln Leu Ile Tyr Leu Cys Phe Leu Gly Leu
 5 10 15

Leu Tyr Ile Arg His His Asp Ser Gln Ser Phe Val Ile Leu Tyr Tyr
 20 25 30

Lys Lys Leu Asn Tyr Tyr Phe Lys Tyr Gly Gln Ile Arg Ala Phe His
 35 40 45

Ile Ala Lys Val Tyr Gln Pro His
 50 55

<210> 580
 <211> 67
 <212> PRT
 <213> Homo sapiens

<400> 580
 Met Glu Leu Arg Thr Lys Ala Leu Arg Thr Ala Gln Gln Leu Thr Ser
 5 10 15

Cys Val Thr Ala Leu Lys Ala Ala Gly Pro Pro Leu Thr Phe Trp Lys
 20 25 30

Gly Lys Trp Val Gln Cys Cys Leu Pro Leu Trp Gly Leu Leu Gly Ser
 35 40 45

His Ala Phe Tyr Ile Tyr Ala Val Asp Ile Phe Met Phe Pro Gly Ser
 50 55 60

Phe Ile His
 65

<210> 581

<211> 77

<212> PRT

<213> Homo sapiens

<400> 581

Met Leu Glu Val Lys Phe Glu Val Ser Leu Arg Pro Thr Gly Asn Glu
 5 10 15

Thr Ala Gly Gln Thr His Gly Thr Gln Asp Lys Gly Ser Lys Asp Ser
 20 25 30

Thr Ala Ala Asp Ile Leu Cys Asp Ser Leu Glu Ser Ser Arg Pro Ala
 35 40 45

Ala His Ile Leu Glu Gly Lys Met Gly Thr Met Leu Ser Ala Thr Leu
 50 55 60

Gly Pro Ser Trp Val Thr Cys Ile Leu His Leu Cys Ser
 65 70 75

<210> 582

<211> 51

<212> PRT

<213> Homo sapiens

<400> 582

Met Leu Phe Leu Gln Thr Ile Asp Thr Lys Cys Thr Gly Ile Glu Ile
 5 10 15

Asn Arg Asn Trp Ser Lys Val Trp His Thr His Ser His Val Asp Val
 20 25 30

Lys Leu Cys Leu Glu Phe Leu Cys Gly Val Trp Phe Gly Leu Gly Phe
 35 40 45

Leu Gly Val
 50

<210> 583

<211> 60

<212> PRT

<213> Homo sapiens

<400> 583

214

Met Ser Thr Ser Asp Gly Phe Ala Pro Pro Pro Gln Leu Gly Ser Arg
 5 10 15

Cys Ser His Ile Arg Gly Pro Ile Lys Ile Ala Arg Asn Lys Phe Pro
 20 25 30

Arg Thr Leu Thr Ser Gln Glu Leu Arg Arg Phe Ala Glu Tyr Ser Gly
 35 40 45

Met Met Phe Gly Asp Gln Thr Thr Ala Gly Gln Lys
 50 55 60

<210> 584

<211> 76

<212> PRT

<213> Homo sapiens

<400> 584

Met Cys Leu Cys Ile Pro Leu Gly Gly Tyr Gln Glu Leu Cys His Cys
 5 10 15

Met Ser Thr Ser Asp Gly Phe Ala Pro Pro Pro Gln Leu Gly Ser Arg
 20 25 30

Cys Ser His Ile Arg Gly Pro Ile Lys Ile Ala Arg Asn Lys Phe Pro
 35 40 45

Arg Thr Leu Thr Ser Gln Glu Leu Arg Arg Phe Ala Glu Tyr Ser Gly
 50 55 60

Met Met Phe Gly Asp Gln Thr Thr Ala Gly Gln Lys
 65 70 75

<210> 585

<211> 50

<212> PRT

<213> Homo sapiens

<400> 585

Met Val Tyr Arg Phe Gly Gln Met Ser Asp Asn Pro Phe Tyr Ile Leu
 5 10 15

Ala Ser Leu Gly Ser Ser Ser Cys Arg Asn Gly Leu Ala Ser Lys Trp
 20 25 30

Arg Gln Ala Asp Pro Ser Asp Gly Tyr Met Glu Pro Cys Phe Gln Leu
 35 40 45

Leu Phe
 50

<210> 586

<211> 60

<212> PRT

<213> Homo sapiens

<400> 587

<400> 588

Leu Gln Phe Arg Gln Tyr Asn Lys Ser Val His Glu Val Asn Leu Lys
20 25 30

Gly Ala Cys Phe Thr Val Ala Gly Leu Pro Arg Ala Trp Thr Thr Gln
 35 40 45
 Tyr Ser Ile Ile Asp Lys Arg Ile Arg Gln Glu Ile Tyr Thr Cys Cys
 50 55 60
 Leu Ala Phe Val Val Ile Tyr Thr Asn Glu Asn Met Tyr Tyr Ser Tyr
 65 70 75 80
 Ile

<210> 589
 <211> 157
 <212> PRT
 <213> Homo sapiens

<400> 589
 Met Thr Met Cys Leu Cys Val Ala Pro Met Gly Arg Ala Thr Arg Met
 5 10 15
 Ser Val Thr Cys Asp Arg Leu His Ala Asn Ser Arg Val Arg Tyr Leu
 20 25 30
 Trp Cys Gln Lys Asp His Val Pro Gln Met Gln Asp Gln Asp Leu Glu
 35 40 45
 Met Glu Ser Met Lys Ala Leu Glu Lys Leu Val Lys Arg Arg His Pro
 50 55 60
 Pro Val Ile Phe Ala Ser Leu Val Gln Asn Val Thr Lys Met Pro Arg
 65 70 75 80
 Met Ser Gly Val Cys Val Ile Leu Thr Val Leu Lys Pro Thr Ser Ile
 85 90 95
 Pro Ser Ala Leu Leu Met Gly Asn Leu Met Ile Met His Ala Lys Ser
 100 105 110
 Lys Lys His Arg Val Arg Asn Arg Arg Lys Leu Lys Ser Cys Leu Trp
 115 120 125
 Val Asp Val Lys Ile Thr Gln Leu Gln Leu Leu Ser Leu Lys Met Gly
 130 135 140
 Ile Met Gln Glu Gln Ile Met Gln Arg Met Leu Thr Asn
 145 150 155

<210> 590
 <211> 347
 <212> PRT
 <213> Homo sapiens

<400> 590
 Met Leu Leu Ile Val Ala Arg Pro Val Lys Leu Ala Ala Phe Pro Thr
 5 10 15

Ser Leu Ser Asp Cys Gln Thr Pro Thr Gly Trp Asn Cys Ser Gly Tyr
 20 25 30
 Asp Asp Arg Glu Asn Asp Leu Phe Leu Cys Asp Thr Asn Thr Cys Lys
 35 40 45
 Phe Asp Gly Glu Cys Leu Arg Ile Gly Asp Thr Val Thr Cys Val Cys
 50 55 60
 Gln Phe Lys Cys Asn Asn Asp Tyr Val Pro Val Cys Gly Ser Asn Gly
 65 70 75 80
 Glu Ser Tyr Gln Asn Glu Cys Tyr Leu Arg Gln Ala Ala Cys Lys Gln
 85 90 95
 Gln Ser Glu Ile Leu Val Val Ser Glu Gly Ser Cys Ala Thr Asp Ala
 100 105 110
 Gly Ser Gly Ser Gly Asp Gly Val His Glu Gly Ser Gly Glu Thr Ser
 115 120 125
 Gln Lys Glu Thr Ser Thr Cys Asp Ile Cys Gln Phe Gly Ala Glu Cys
 130 135 140
 Asp Glu Asp Ala Glu Asp Val Trp Cys Val Cys Asn Ile Asp Cys Ser
 145 150 155 160
 Gln Thr Asn Phe Asn Pro Leu Cys Ala Ser Asp Gly Lys Ser Tyr Asp
 165 170 175
 Asn Ala Cys Gln Ile Lys Glu Ala Ser Cys Gln Lys Gln Glu Lys Ile
 180 185 190
 Glu Val Met Ser Leu Gly Arg Cys Gln Asp Asn Thr Thr Thr Thr Thr
 195 200 205
 Lys Ser Glu Asp Gly His Tyr Ala Arg Thr Asp Tyr Ala Glu Asn Ala
 210 215 220
 Asn Lys Leu Glu Glu Ser Ala Arg Glu His His Ile Pro Cys Pro Glu
 225 230 235 240
 His Tyr Asn Gly Phe Cys Met His Gly Lys Cys Glu His Ser Ile Asn
 245 250 255
 Met Gln Glu Pro Ser Cys Arg Cys Asp Ala Gly Tyr Thr Gly Gln His
 260 265 270
 Cys Glu Lys Lys Asp Tyr Ser Val Leu Tyr Val Val Pro Gly Pro Val
 275 280 285
 Arg Phe Gln Tyr Val Leu Ile Ala Ala Val Ile Gly Thr Ile Gln Ile
 290 295 300
 Ala Val Ile Cys Val Val Val Leu Cys Ile Thr Arg Lys Cys Pro Arg
 305 310 315 320

Ser Asn Arg Ile His Arg Gln Lys Gln Asn Thr Gly His Tyr Ser Ser
 325 330 335

Asp Asn Thr Thr Arg Ala Ser Thr Arg Leu Ile
 340 345

<210> 591
 <211> 565
 <212> DNA
 <213> Homo sapien

<400> 591
 actaaagcaa atgaacaagc tgacttgcta gtatcatctg cattcattga agcacaagaa 60
 cttcatgcct tgactcatgt aaatgcaata ggattaaaaa ataaatttga tatcacatgg 120
 aaacagacaa aaaatattgt acaacattgc acccagtgtc agattctaca cctggccact 180
 caggaagcaa gagttaatcc cagaggtcta tgtcctaata tgttatggca aatggatgtc 240
 atgcacgtac cttcatttgg aaaattgtca tttgtocatg tgacagttga tacttattca 300
 catttcatat gggcaacctg ccagacagga gaaagtactt cccatgttaa aagacattta 360
 ttatcttggtt ttcctgtcat gggagttcca gaaaaagtta aaacagacaa tgggccaggt 420
 tactgtagta aagcatttca aaaattctta aatcagtggg aaattacaca tacaatagga 480
 attctctata attccaagg acaggccata attgaaggaa ctaatagaac actcaaagct 540
 caattgggta aacaaaaaaa aaaaa 565

<210> 592
 <211> 188
 <212> PRT
 <213> Homo sapien

<400> 592
 Thr Lys Ala Asn Glu Gln Ala Asp Leu Leu Val Ser Ser Ala Phe Ile
 1 5 10 15
 Glu Ala Gln Glu Leu His Ala Leu Thr His Val Asn Ala Ile Gly Leu
 20 25 30
 Lys Asn Lys Phe Asp Ile Thr Trp Lys Gln Thr Lys Asn Ile Val Gln
 35 40 45
 His Cys Thr Gln Cys Gln Ile Leu His Leu Ala Thr Gln Glu Ala Arg
 50 55 60
 Val Asn Pro Arg Gly Leu Cys Pro Asn Val Leu Trp Gln Met Asp Val
 65 70 75 80
 Met His Val Pro Ser Phe Gly Lys Leu Ser Phe Val His Val Thr Val
 85 90 95
 Asp Thr Tyr Ser His Phe Ile Trp Ala Thr Cys Gln Thr Gly Glu Ser
 100 105 110
 Thr Ser His Val Lys Arg His Leu Leu Ser Cys Phe Pro Val Met Gly
 115 120 125
 Val Pro Glu Lys Val Lys Thr Asp Asn Gly Pro Gly Tyr Cys Ser Lys
 130 135 140
 Ala Phe Gln Lys Phe Leu Asn Gln Trp Lys Ile Thr His Thr Ile Gly
 145 150 155 160
 Ile Leu Tyr Asn Ser Gln Gly Gln Ala Ile Ile Glu Gly Thr Asn Arg
 165 170 175
 Thr Leu Lys Ala Gln Leu Val Lys Gln Lys Lys Lys
 180 185

<210> 593
 <211> 271

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(271)

<223> n = A,T,C or G

<400> 593

actttatggt	cnagtgcana	aanccnctg	gattgccacc	ntactctcag	ggctgtgant	60
tgtgcnccca	nagcaacctg	ggcacgcggg	gacagggggg	ccnacaattg	agggagcggg	120
gtccctagct	ggggtctata	catgncnggg	naagggcngc	tgagtnccat	nagcaaagga	180
nctagnatnt	gcgggggtgc	ggcctgggcc	taccctttna	agcatccntn	gatccactcc	240
angaanccng	gggtagncag	gtttnccaac	a			271

<210> 594

<211> 376

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(376)

<223> n = A,T,C or G

<400> 594

cctttggggg	nggggggaac	ctttaccatt	gtnccccctt	atttcatttg	gttnnggggtc	60
gcgccctcnn	gggccaacaa	agttatcgtn	nttgaagaga	anattttttt	ggnttngncc	120
cgattaagcg	ncaaatgtgt	agcaaaaangc	cgtgccactt	gtggcgtagc	tncgtcgggt	180
cgattcgacg	acaaggcgtn	gcgcgntanc	gttagtctcn	aatngaccn	gtggcatgag	240
cccacgangg	nttcgtgtcg	tcacatggnc	tctagacata	acgcncnccn	ttttttncag	300
agggggntgc	cgcccttagg	gagggnagggg	tggggacact	agccaancca	nantctnacc	360
ccattgaaga	aaaggn					376

<210> 595

<211> 242

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(242)

<223> n = A,T,C or G

<400> 595

agnctgctgn	tcgtnccctn	tatgtggctt	catnntgagg	acaanagtng	cactgaggct	60
tgnngnatgcc	aggcaaggnc	aagctggctc	aaaaagcatc	caccacctc	tgnaangggg	120
atgccangag	cangtgcacc	agtcccaact	angagnccn	ggcatgntac	atcttcttcc	180
accctnaaa	ntttgngcta	caangnccat	ttttcttttt	ctcttaaggg	ncnctnggct	240
tc						242

<210> 596

<211> 535

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(535)

<223> n = A,T,C or G

<400> 596

accagttgga	tactgctaaa	nagatatatta	tgcagcctca	tatgttaagt	cgtatatattt	60
gaaagctttt	taaatttttt	ctttaagaag	atttttagatg	cttatcactg	agtaccagag	120
ggatgtaggc	tgatgccctt	atcaacaaag	tcagggactg	tggcacacaa	ggattgacta	180
ctgcagacac	ggccacaatg	ctacctctag	agggcctgaa	tccccctgcc	ctctctggtg	240
gggagaaggg	ctggcagagc	cattagcatg	ggctccggcc	aatcctggcc	actttgacac	300
tcctggtgct	gacccagggg	cctggaggaa	gggatgaggt	gggcagtaga	gatgctcagg	360
gcagtggccc	ctttccatcc	acactggaac	tatttcagta	ttttaccacc	aattcagcca	420
ttcccttggtg	cgctggctga	acatcagccc	tgtctcaggt	ctcagtttcc	cctttgtaaa	480
gggaaagctc	tggattcagg	gagtgatgaa	gaggtcatca	tggctctgag	aattc	535

<210> 597

<211> 257

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(257)

<223> n = A,T,C or G

<400> 597

tttcnatacc	caaaantacc	ccatattang	accanacatt	tgtctnggaa	aaattaccat	60
tnntaant	ttgggccacc	tgagannaaa	tggtgtgaat	ncatgataag	atggancagn	120
atttctctta	agatnngatn	agaccccgtt	tttcacggaa	catatccaag	nacccaatag	180
gnaacaagcc	acgggnggag	tcacaaacat	atattcttta	ctctcataat	ccgtnnacaa	240
naactnttgn	acttgac					257

<210> 598

<211> 222

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(222)

<223> n = A,T,C or G

<400> 598

nntgntacc	gtcnaaactt	nncttggtac	ccgagctcgg	atccactagt	ccagtgtggt	60
ggaattccat	tgtgttgggc	tataagctgt	aatagtggag	ncgtgctngg	ttcattgcan	120
nagnccctcc	gcannacacn	ttggnacaac	ctgtgagnag	gcnataaatt	attcacataa	180
tcactactgc	atgaanctga	ctcaaacgca	tccacntaca	cc		222

<210> 599

<211> 238

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(238)

<223> n = A,T,C or G

<400> 599

gcatgacatc	ancgatgtnt	ttggnnacct	ganattngct	aaaactngng	natgccgggn	60
atgnagggtt	ggtantgatc	tatgcactca	catctcatgg	ggacgtttca	tgtggagtg	120
tcgacaangt	tgctgnancn	gagaagtgat	gatctcagtt	gaaaggggtca	tgtgaatata	180
cnttacactt	gaaaaagaag	cacattggga	atatcacgaa	acgnccacca	acatcctg	238

<210> 600

<211> 232

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(232)

<223> n = A,T,C or G

<400> 600

cgaactat	agactaccta	ggaaaattat	tttagtatca	gaagaatata	aggggtgtag	60
tactcatcag	agctaaatga	gagcgcttta	aaaatgttag	tttgtcttcc	gccatttcta	120
cagaaagctg	caatttcagg	ttttcaacct	aataggtgat	atttaanaaa	aaaaaaaagc	180
aatcgcaaat	agccccactg	cttttataaa	tcattttttc	cccaacacaa	tg	232

<210> 601

<211> 547

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(547)

<223> n = A,T,C or G

<400> 601

cattgtgttg	gggaaaaaat	gatttgtata	agcagtgggg	ctatttgcca	ttgctttttt	60
tttttcttaa	atatcaccta	ttaggttgaa	aacctgaaat	tgcagctttc	tgtagaaatg	120
gcggaagaca	aactaacatt	tttaaagcgc	tctcatttag	ctctgatgag	tactacaccc	180
ctnatattct	tctgatacta	aaataatttt	cctagtgtag	tctaaacttt	tttaaaaaga	240
catgtaatcc	gcggagttag	taactcaaaa	cgagtgcata	tnggaagtat	cgcagccggt	300
nctggatnaa	attcccagct	tgctngcttg	ctnagccggg	gggcggtnaa	aaaaacatct	360
gcagcccngg	ggnaaaaaacc	ttcgcatgtg	tcttacgtgt	ttacgttatt	ttatttccct	420
nnagcaaggc	nggganttgg	ggactcgaaa	tggtacagtt	gggctgggga	tcgcccttgc	480
tacataaaaag	ncgtccagaa	gagggacggt	tacaggcngg	ganctccaaa	ggtcagtcct	540
tgccatt						547

<210> 602

<211> 826

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(826)

<223> n = A,T,C or G

<400> 602

cggggggnt	tacgtctctc	tggacgcttt	tattgtacca	gggcgatccc	agcccaactg	60
taccattcga	gtccctactc	ctgccttgct	ctagggaaat	aaaataacgt	aaacacgtaa	120
gaacaatgag	aaagcggttt	cttccctagg	ctgcagattg	tcttcttcac	cgcccctgct	180
tagctagcta	gctagctggg	aatttaatcc	agaaacggct	tgcgatacct	cctagatgca	240

ctcgttttga	gttacaaact	ccgcgggatta	catgtctttt	taaaaaagtt	tagactacac	300
tagggaaaat	tatttttagta	tcagaagaat	atcagggggt	gtagtactca	tcagagctna	360
atgagagcgc	tttaaaaatg	ttagtttgtc	ttccgccatt	tctacagaaa	gctgcaattt	420
caggttttca	ncctaataag	tgatatntaa	gaaaaaaaaa	acaatcgcan	atagcccact	480
gctttttcaa	atcatttttc	tcttctaggt	atagcctgtc	aggtggccta	atgtattttt	540
gacatctcta	ggaattttta	tagaccagaa	atgggtgccca	gagatatgcc	tgactaatac	600
ttaagtgggg	atttatgtat	ttctcaanca	agtgtattaa	gcaaaactag	gcacgaatga	660
aatcaagatc	tttaggccag	aaatcatgaa	nanttttana	attattttan	gaatctgtgg	720
cttctcttct	taaaatngaa	aaaaaaattg	tttaaaccce	naaggtctga	atacccaagc	780
nccctgaacn	anagaacaan	gccggagcac	cccctcccaa	atcccc		826

<210> 603

<211> 817

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(817)

<223> n = A,T,C or G

<400> 603

nnangacttt	tgtggtntta	tacaattntt	ttttctattt	ctatgaagag	aaagccacag	60
agtctctaaa	taattctaaa	actcatcatg	actttcttgc	ctaaaagatc	ttgatttcaa	120
tcgtgcctag	ttttgcttta	atcacttgct	tgagaaatac	ataaatcccc	acttaagatt	180
agtgcaggca	tatctctggc	acccatttct	ggttctatta	aaattcctag	agatgtcaaa	240
aattacatta	ggccacctga	caggctatac	ctagaagaga	aaaaatgatt	tgtaaaagca	300
gtggggctat	ttgcgattgc	tttttttttt	tcttaaatac	cacctattag	gttgaaaacc	360
tgaaattgca	gctttctgta	gaaatggcgg	aagacaaact	aacattttta	aagcgctctc	420
atttagctct	gatgagtact	acaccctga	tattcttctg	atactaaaat	aattttccta	480
gtgtagtcta	aactttttta	aaaagacatg	taatccgagg	agtttgtaac	tcaaaacgag	540
tgcatctagg	aggtatcgca	agccgtttct	ggattaaatt	cccagctagc	ttgcttgctt	600
agcaggggag	ggnaaanaag	acatctgcag	cctagggaag	aaaacctttc	gcattgttct	660
tacgtgttta	cgttatttta	tttcctanaa	caaggcngaa	ttgggactcg	aatggttcag	720
ttgggggtgg	ggatccccctg	gtncataaaa	ngtcanaaag	anggtacagg	cggaacncca	780
agggtcgtcc	tgcatttana	ctcgggaattt	tggtgccc			817

<210> 604

<211> 694

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(694)

<223> n = A,T,C or G

<400> 604

cttttcaaat	cattttttnct	cttctaggta	tancctgtca	ggtggcctaa	tgtaattttt	60
gacatctcta	ngaattttta	tagaaccaga	aatgggtgcc	agagatatgc	ctgcactaat	120
cttaagtggg	gatttatgta	tttctcaagc	aagtgtattaa	agcaaaacta	ggcacgattg	180
aaatcaagat	cttttaggca	anaaagtcac	gatgagtttt	agaattattt	taggactctg	240
tggctttctc	ttcatagaaa	tagaaaaaaa	aattgtataa	aaccacaaaa	ggtcctgaat	300
agccaaagca	acactganca	aaaagaacan	agcagggaag	caacacacta	ccngaattca	360
aattatacta	ccagggtgta	gtaacccaaa	cagcattcta	ttggcataaa	atagacacca	420
agaccaatgg	ancagaataa	agaacccccac	aaataaatcc	atatatntac	cgccanctga	480
ttatcaataa	naaacaccaa	gaacatatnt	taagggaacnt	nctattcaat	aantagtgtc	540
ggnaaaaact	gggaaatcca	tatgcagaaa	naatgaaact	agacccttat	ccctcaccat	600

acgcaaannt caacttcgga atgggattac aaaacttaag acattccaac ccaagaaact 660
atnaaancta ctattaagaa aacagatcnc nccc 694

<210> 605
<211> 678
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(678)
<223> n = A,T,C or G

<400> 605
taaaaatcta gactacacta ggaaattatt ttantatcag aagaatatca ggggtgtagt 60
actcatcana gctaaatgag agcgctttaa aaatgttagt ttgtcttccg ccatttctac 120
agaaagctgc aatttcaggt tttcaaccta atagggtgata ttttaagaaa aaaaaaagca 180
atcgcaaata gccccactgc ttttacaat cattttttct cttctaggta tagcctgtca 240
ggtggcctaa tgtaattttt gacatctcta ggaattttta tagaaccaga aatgggtgcc 300
agagatatgc ctgcactaat cttaagtggg gatttatgta tttctcaagc aagtgattaa 360
agcaaaacta ggcacgattg aaatcaanat cttttaggca agaaagtcac gatgagttt 420
anaattattt taggactctg tggctttctc ttcatagaaa tagaaaaaaa aaattgtata 480
aaaaccacaa aaggtcctga atagcccaaa gcaacactga acaaaaangaa caaagcagga 540
agcaacacac taccggaatt caattatact accaaggtgt antaaccaaa acagcattct 600
attgggcata aaatagacca aagaccagtg ggaaacagaa taaagaancc caaaataaat 660
cctatattta cngccnc 678

<210> 606
<211> 263
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(263)
<223> n = A,T,C or G

<400> 606
gtggggctcng cancagecaa ctcagcttcc tttcgggctt tgtagcaga cggatcatcc 60
tctagtcac tggtntcaaa ttccattgtg tgggggccnc tcgcctcggc canagatctg 120
agtgancana cntgtcccca ctgaggtgcc ccacagcngn ttgtnttcag cangggctna 180
caactcgacc ggcagcngn ggctggcaga antgngcgcc tnnctattc ctacgcngtn 240
ngccgcagga aggangacag gcc 263

<210> 607
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 607
ccatgtgggt cccggttgct tt 22

<210> 608
<211> 22
<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 608

gataggggtg ctcaggggtt gg

22

<210> 609

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 609

gctggacagg gggcaaaagc tggggcagtg aaccatgtgc

40

<210> 610

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 610

ccttggtccag atagcccagt agctgac

27

<210> 611

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 611

gatagagaaa accgtccagg ccagtattgt gggaggctgg gagtgc

46

<210> 612

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 612

gcacatgggt cactgcccc a gcttttgccc cctgtccagc

40

<210> 613

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 613

gccgctcgag ttagaattcg ggggtggcca cgatggtg

38

<210> 614

<211> 53

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 614

cggcgggcat atgcatcacc atcaccatca catcataaac ggcgaggact gca

53

<210> 615

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 615

gcaactccag cctcccacaa tactggcctg gacggttttc tctatc

46

<210> 616

<211> 1350

<212> DNA

<213> Homo sapien

<400> 616

atgcatcacc	atcaccatca	catcataaac	ggcgaggact	gcagcccga	ctcgagccc	60
tggcaggcgg	cactggtcat	ggaaaacgaa	ttgttctgct	cgggcgtcct	ggtgcatccg	120
cagtgggtgc	tgtagccgc	acactgttc	cagaactcct	acaccatcgg	gctgggcctg	180
cacagtcttg	aggccgacca	agagccaggg	agccagatgg	tggaggccag	cctctccgta	240
cggcaccag	agtacaacag	acccttgctc	gctaacgacc	tcagtctcat	caagtggac	300
gaatccgtgt	cagagtctga	caccatccgg	agcatcagca	ttgcttcgca	gtgccctacc	360
gcggggaaact	cttgccctcg	ttctggctgg	ggtctgctgg	cgaacggcag	aatgcctacc	420
gtgctgcagt	gcgtgaacgt	gtcgggtgtg	tctgaggagg	tctgcagtaa	gctctatgac	480
ccgctgtacc	acccagcat	gttctgcgcc	ggcggagggc	aagaccagaa	ggactcctgc	540
aacggtgact	ctggggggcc	cctgatctgc	aacgggtact	tgcagggcct	tgtgtctttc	600
ggaaaagccc	cgtgtggcca	agttggcgtg	ccagggtgtc	acaccaacct	ctgcaaattc	660
actgagtga	tagagaaaac	cgtccaggcc	agtattgtgg	gaggctggga	gtgcgagaag	720
cattcccaac	cctggcaggt	gcttgtggcc	tctcgtggca	gggcagtctg	cggcgggtgt	780
ctggtgcacc	cccagtgggt	cctcacagct	gccactgca	tcaggaacaa	aagcgtgatc	840
ttgctgggtc	ggcacagcct	gtttcatcct	gaagacacag	gccaggattt	tcaggtcagc	900
cacagcttcc	cacaccgct	ctacgatatg	agcctcctga	agaatcgatt	cctcaggcca	960
ggtgatgact	ccagccacga	cctcatgctg	ctccgcctgt	cagagcctgc	cgagctcacg	1020
gatgctgtga	aggtcatgga	cctgcccacc	caggagccag	cactggggac	cacctgctac	1080
gcctcaggct	ggggcagcat	tgaaccagag	gagttcttga	cccaaagaa	acttcagtgt	1140
gtggacctcc	atgttatttc	caatgacgtg	tgtgcgcaag	ttaccctca	gaaggtgacc	1200
aagttcatgc	tgtgtgctgg	acgctggaca	gggggcaaaa	gctggggcag	tgaaccatgt	1260
gccctgcccg	aaaggccttc	cctgtacacc	aagggtgtgc	attaccgga	gtggatcaag	1320
gacaccatcg	tggccaaccc	cgaattctaa				1350

<210> 617

<211> 449

<212> PRT

<213> Homo sapien

<400> 617

```

Met His His His His His His Ile Ile Asn Gly Glu Asp Cys Ser Pro
 1          5          10          15
His Ser Gln Pro Trp Gln Ala Ala Leu Val Met Glu Asn Glu Leu Phe
          20          25          30
Cys Ser Gly Val Leu Val His Pro Gln Trp Val Leu Ser Ala Ala His
          35          40          45
Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu Gly Leu His Ser Leu Glu
          50          55          60
Ala Asp Gln Glu Pro Gly Ser Gln Met Val Glu Ala Ser Leu Ser Val
          65          70          75          80
Arg His Pro Glu Tyr Asn Arg Pro Leu Leu Ala Asn Asp Leu Met Leu
          85          90          95
Ile Lys Leu Asp Glu Ser Val Ser Glu Ser Asp Thr Ile Arg Ser Ile
          100          105          110
Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly Asn Ser Cys Leu Val Ser
          115          120          125
Gly Trp Gly Leu Leu Ala Asn Gly Arg Met Pro Thr Val Leu Gln Cys
          130          135          140
Val Asn Val Ser Val Val Ser Glu Glu Val Cys Ser Lys Leu Tyr Asp
          145          150          155          160
Pro Leu Tyr His Pro Ser Met Phe Cys Ala Gly Gly Gly Gln Asp Gln
          165          170          175
Lys Asp Ser Cys Asn Gly Asp Ser Gly Gly Pro Leu Ile Cys Asn Gly
          180          185          190
Tyr Leu Gln Gly Leu Val Ser Phe Gly Lys Ala Pro Cys Gly Gln Val
          195          200          205
Gly Val Pro Gly Val Tyr Thr Asn Leu Cys Lys Phe Thr Glu Trp Ile
          210          215          220
Glu Lys Thr Val Gln Ala Ser Ile Val Gly Gly Trp Glu Cys Glu Lys
          225          230          235          240
His Ser Gln Pro Trp Gln Val Leu Val Ala Ser Arg Gly Arg Ala Val
          245          250          255
Cys Gly Gly Val Leu Val His Pro Gln Trp Val Leu Thr Ala Ala His
          260          265          270
Cys Ile Arg Asn Lys Ser Val Ile Leu Leu Gly Arg His Ser Leu Phe
          275          280          285
His Pro Glu Asp Thr Gly Gln Val Phe Gln Val Ser His Ser Phe Pro
          290          295          300
His Pro Leu Tyr Asp Met Ser Leu Leu Lys Asn Arg Phe Leu Arg Pro
          305          310          315          320
Gly Asp Asp Ser Ser His Asp Leu Met Leu Leu Arg Leu Ser Glu Pro
          325          330          335
Ala Glu Leu Thr Asp Ala Val Lys Val Met Asp Leu Pro Thr Gln Glu
          340          345          350
Pro Ala Leu Gly Thr Thr Cys Tyr Ala Ser Gly Trp Gly Ser Ile Glu
          355          360          365
Pro Glu Glu Phe Leu Thr Pro Lys Lys Leu Gln Cys Val Asp Leu His
          370          375          380
Val Ile Ser Asn Asp Val Cys Ala Gln Val His Pro Gln Lys Val Thr
          385          390          395          400
Lys Phe Met Leu Cys Ala Gly Arg Trp Thr Gly Gly Lys Ser Trp Gly
          405          410          415
Ser Glu Pro Cys Ala Leu Pro Glu Arg Pro Ser Leu Tyr Thr Lys Val

```

420 425 430
 Val His Tyr Arg Lys Trp Ile Lys Asp Thr Ile Val Ala Asn Pro Glu
 435 440 445
 Phe

<210> 618
 <211> 3923
 <212> DNA
 <213> Homo sapien

<400> 618
 acagaagaaa tagcaagtgc cgagaagctg gcatcagaaa aacagagggg agatttgtgt 60
 ggctgcagcc gagggagacc aggaagatct gcatgggtgg aaggacctga tgatacagag 120
 gaattacaac acatatactt agtgtttcaa tgaacaccaa gataaataag tgaagagcta 180
 gtccgctgtg agtctcctca gtgacacagg gctggatcac catcgacggc actttctgag 240
 tactcagtgc agcaaagaaa gactacagac atctcaatgg caggggtgag aaataagaaa 300
 ggctgctgac ttaccatctt gaggccacac atctgctgaa atggagataa ttaacatcac 360
 tagaaacagc aagatgacaa tataatgtct aagtagtgac atgtttttgc acatttccag 420
 cccttttaaa tatccacaca cacaggaagc acaaaaggaa gcacagagat ccctgggaga 480
 aatgcccggc cgccatcttg ggtcatcgat gagcctcgcc ctgtgcctgg tcccgttgt 540
 gagggaagga cattagaaaa tgaattgatg tggttcctta aggatgggca ggaaaacaga 600
 tctgttgtg gatatttatt tgaacgggat tacagatttg aaatgaagtc acaaagttag 660
 cattaccaat gagaggaaaa cagacgagaa aatcttgatg gcttcacaag acatgcaaca 720
 aacaaaatgg aatactgtga tgacatgagg cagccaagct ggggaggaga taaccacggg 780
 gcagagggtc aggattctgg cctgtctgcc taaactgtgc gttcataacc aaatcatttc 840
 atatttctaa ccctcaaaac aaagctgttg taatatctga tctctacggt tccttctggg 900
 cccaacattc tccatatatc cagccacatc catttttaat atttagttcc cagatctgta 960
 ctgtgacctt tctacactgt agaataacat tactcatttt gttcaaagac ccttcgtgtt 1020
 gctgccta atgtagctga ctgtttttcc taaggagtgt tctggcccag gggatctgtg 1080
 aacaggctgg gaagcatctc aagatctttc cagggttata cttactagca cacagcatga 1140
 tcattacgga gtgaattatc taatcaacat catcctcagt gtctttgcc atactgaaat 1200
 tcatttccca cttttgtgcc cattotcaag acctcaaaat gtcattccat taatatcaca 1260
 ggattaactt ttttttttaa cctggaagaa ttcaatgtta catgcagcta tgggaattta 1320
 attacatatt ttgttttcca gtgcaaagat gactaagtcc tttatccctc ccctttgttt 1380
 gatttttttt ccagtataaa gttaaaatgc tttagcctgt actgaggctg tatacagcac 1440
 agcctctccc catccctcca gccttatctg tcatcaccat caaccctcc cataccacct 1500
 aaacaaaatc taacttgtaa ttccttgaac atgtcaggac atacattatt ccttctgcct 1560
 gagaagctct tccttgtctc ttaaatctag aatgatgtaa agttttgaat aagttgacta 1620
 tcttacttca tgcaaagaag ggacacatat gagattcatc atcacatgag acagcaaata 1680
 ctaaaagtgt aatttgatta taagagttaa gataaatata tgaaatgcaa gagccacaga 1740
 gggaaatgtt atggggcacg tttgtaagcc tgggatgtga agcaaaggca gggaacctca 1800
 tagtatctta tataatatac ttcatttctc tatctctatc acaatatcca acaagctttt 1860
 cacagaattc atgcagtga aatcccaaaa ggtaaccttt atccatttca tggtagtgc 1920
 gctttagaat tttggcaaat catactggtc acttatctca actttgagat gtgtttgtcc 1980
 ttgtagttaa ttgaaagaaa tagggcactc ttgtgagcca ctttagggtt cactcctggc 2040
 aataaagaat ttacaaagag ctactcagga ccagttgtta agagctctgt gtgtgtgtgt 2100
 gtgtgtgtgt gagtgtacat gccaaagtgt gcctctctct cttgacccat tatttcagac 2160
 ttaaaacaag catgttttca aatggcacta tgagctgcca atgatgtatc accaccatat 2220
 ctcatatttc tccagtaaat gtgataataa tgtcatctgt taacataaaa aaagtttgac 2280
 ttcacaaaag cagctggaaa tggacaacca caatatgcat aaatctaact cctaccatca 2340
 gctacacact gcttgacata tattgttaga agcacctcgc atttgtgggt tctcttaagc 2400
 aaaatacttg cattaggtct cagctggggc tgtgcatcag gcggtttgag aaatattcaa 2460
 ttctcagcag aagccagaat ttgaattccc tcatctttta ggaatcattt accaggtttg 2520
 gagaggattc agacagctca ggtgctttca ctaatgtctc tgaacttctg tccctctttg 2580
 tgttcatgga tagtccaata aataatgtta tctttgaact gatgctcata ggagagaata 2640
 taagaactct gagtgatatc aacattaggg attcaaagaa atattagatt taagctcaca 2700

ctgggtcaaaa	ggaaccaaga	tacaaagaac	tctgagctgt	catcgtcccc	atctctgtga	2760
gccacaacca	acagcaggac	ccaacgcatg	tctgagatcc	ttaaatacaag	gaaaccagt	2820
tcatgagttg	aattctccta	ttatggatgc	tagcttctgg	ccatctctgg	ctctcctctt	2880
gacacatatt	agcttctagc	ctttgcttcc	acgactttta	tcttttctcc	aacacatcgc	2940
ttaccaatcc	tctctctgct	ctgttgcttt	ggacttcccc	acaagaattt	caacgactct	3000
caagtctttt	cttccatccc	caccactaac	ctgaatgcct	agacccttat	ttttattaat	3060
ttccaataga	tgctgcctat	gggctatatt	gcttttagatg	aacattagat	atttaaagct	3120
caagagggttc	aaaatccaac	tcattatctt	ctctttcttt	cacctccctg	ctcctctccc	3180
tatattactg	attgcactga	acagcatggt	ccccaatgta	gccatgcaaa	tgagaaaccc	3240
agtggctcct	tgtggtacat	gcatgcaaga	ctgctgaagc	cagaaggatg	actgattacg	3300
cctcatgggt	ggaggggacc	actcctgggc	cttcgtgatt	gtcaggagca	agacctgaga	3360
tgctccctgc	cttcagtgtc	ctctgcatct	cccttttcta	atgaagatcc	atagaatttg	3420
ctacatttga	gaattccaat	taggaactca	catgttttat	ctgccctatc	aattttttaa	3480
acttgctgaa	aattaaagttt	tttcaaaatc	tgctcctgta	aattactttt	tcttacagt	3540
tcttggcata	ctatatcaac	tttgattcctt	tgttacaact	tttcttactc	ttttatcacc	3600
aaagtggcct	ttattctctt	tattattatt	attttctttt	actactatat	tacgttggtta	3660
ttattttggt	ctctatagta	tcaatttatt	tgatttagtt	tcaatttatt	tttattgctg	3720
acttttaaaa	taagtgattc	ggggggtggg	agaacagggg	agggagagca	ttaggacaaa	3780
tacctaattgc	atgtgggact	taaaacctag	atgatgggtt	gatagggtga	gcaaaccact	3840
atggcacacg	tatacctgtg	taacaaacct	acacattctg	cacatgtatc	ccagaacgta	3900
aagtaaaatt	taaaaaaaag	tga				3923

<210> 619

<211> 3674

<212> DNA

<213> Homo sapien

<400> 619

agaaagtttc	cttttttttt	tttaatggtg	aaaagatata	cacatattta	gaattagcca	60
gctgggctca	gttttagatta	ttccaatttt	gttggcaaca	tccagagcat	cgtaatcagg	120
agccaagtga	acatattcct	tcttctctcc	atcaggccaa	atcacggtgt	tgaccttggc	180
cacatcaatg	tcttagaact	tcttcacagc	ctgtttgatc	tggtgcttgt	tggttttaac	240
atccacaatg	aacacaagt	tggtgtgtgc	ttctatcttc	ttcgtggtga	ctcagtggtc	300
agcggaact	tgatgatagc	gtagtggtca	agcttgatc	tcctgggagc	gctcttccaa	360
agatatttgg	gctgcctcgg	gagttgcagc	gtcttgggcc	gccggaagg	gggtgacgta	420
cggatcttct	ttttttgtgt	ggctgtggac	acctttcaac	actgtcttct	tggtctttta	480
atccttcgct	ttggtttcgg	ctataggagg	ggcaggagct	tccttcttca	ctttcggcgc	540
catcttgtga	aaagggaaag	tttcctttct	aataccattt	tcacttctcc	cgaattttgt	600
ggatcggttc	ttggatatcta	ccccagattt	caggagtgtt	ggctggatct	taggggattgt	660
gaagtcttca	tttccctgtg	gtgagatctg	aggcatgatt	ttaaacagt	tgaggggaag	720
agatctccag	gcactttaat	agaatggaga	agcaggatgg	gatttgagag	gaaatctgat	780
tttgaaaaaa	ggagaactag	agttgagttc	gtaatttaact	agcaccttaa	aggtcattca	840
gcatgcccat	ctgcacagt	ggtgtaatca	ccctacagaa	caaaaacaaa	aaggcaatgg	900
agagggaagt	gtaaagcact	gtacatgttt	aactcattgt	tatgtaagct	agccgaaggc	960
ttcacagact	tgaattcatc	tcccaagtcc	tcttctgtga	ctggaaactc	tgctttaggt	1020
tgcttaaaac	ttgagaaaca	gaatattgct	tccccctgct	gccttcttga	gtacacttgc	1080
ctacacaaa	atgcacatcc	ttgtttgtgt	gtgtgtgtcc	atttgctgtg	acattcttgt	1140
gaaagtcaaa	gtttcccagc	tggtgacata	cacaagtttg	tttgggtgca	cctgtcagat	1200
gcataccctta	gacaggccct	ttgatactct	gggaagaca	ttggacttac	agtcggaacg	1260
aaaagaaaga	aatgtgatat	gtatagcgtg	cagtgtgttg	gagttttacc	tgtattgttt	1320
taatttcaac	aagcctgagg	actagccaca	aatgtaccca	gtttacaaat	gaggaaacag	1380
gtgcaaaaag	gttgttacct	gtcaaaggct	gtatgtggca	gagccaagat	ttgagcccag	1440
ttatgtctga	tgaacttagc	ctatgctctt	taaacttctg	aatgctgacc	attgaggata	1500
tctaaactta	gatcaattgc	attttccctc	caagactatt	tacttatcaa	tacaataata	1560
ccacctttac	caatctattg	ttttgatacg	agactcaaat	atgccagata	tatgtaaaag	1620
caacctacaa	gctctcta	catgctcacc	taaaagattc	ccgggatcta	ataggctcaa	1680
agaaacttct	tctagaaata	taaaagagaa	aattggatta	tgcaaaaatt	cattattaat	1740

```

ttttttcatc catcctttaa ttcagcaaac atttatctgt tgttgacttt atgcagtatg 1800
gccttttaag gattggggga cagggtgaaga acgggggtgcc agaatgcac ctcctactaa 1860
tgaggtcagt acacatttgc attttaaaat gccctgtcca gctgggcatg gtggatcatg 1920
cctgtaatct caacattgga aggccaaagg aggaggattg cttcagccca ggagttcaag 1980
accagcctgg gcaacataga aagaccccat ctctcaatca atcaatcaat gccctgtctt 2040
tgaaaataaa actctttaag aaaggtttaa tgggcagggt gtggtagctc atgcctataa 2100
tacagcactt tgggaggctg aggcaggagg atcactttag cccagaagtt caagaccagc 2160
ctgggcaaca agtgacacct catctcaatt ttttaataaa atgaatacat acataaggaa 2220
agataaaaag aaaagtttaa tgaaagaata cagtataaaa caaatctctt ggacctaaaa 2280
gtatttttgt tcaagccaaa tatttgtaat cacctctctg tgttgaggat acagaatata 2340
taagcccagg aaactgagca gaaagttcat gtactaacta atcaaccga ggcaaggcaa 2400
aaatgagact aactaatcaa tccgaggcaa ggggcaaatt agacggaacc tgactctggt 2460
ctattaagcg acaactttcc ctctgttgta ttttctttt attcaatgta aaaggataaa 2520
aactctctaa aactaaaaac aatgtttgtc aggagttaca aaccatgacc aactaattat 2580
ggggaatcat aaaatatgac tgtatgagat cttgatgggt taaaaagtgt acccactggt 2640
aatcacttta aacattaatg aacttaaaaa tgaatttacg gagattggaa tgtttctttc 2700
ctgttgtatt agttggctca ggctgccata acaaaatacc acagactggg aggcttaagt 2760
aacagaaatt catttctcac agttctgggg gctggaagtc cacgatcaag gtgcaggaaa 2820
ggcaggcttc attctgaggg cctctctctg gctcacatgt ggccaccctc ccactgcgtg 2880
ctcacatgac ctctttgtgc tcctggaaag aggtgtgtgg ggacagaggg aaagagaagg 2940
agagggaact ctctggtgtc tegtctttca aggaccctaa cctgggccac tttggcccag 3000
gcactgtggg gtgggggggt gtggctgctc tgcctctgag ggccaagata aagcaacaga 3060
aaaatgtcca aagctgtgca gcaaagaca gccaccgaac agggatctgc tcatcagtgt 3120
ggggacctcc aagtcggcca ccttgagggc aagcccccac agagcccatg caaggtggca 3180
gcagcagaag aaggaattg tccctgtcct tggcacattc ctcaccgacc tggatgatgt 3240
ggacactgag atgaatggta atgtggatga gaatatgatg gactcccaga aaaggagacc 3300
cagctgtcca ggtggctgca aatcattaca gccttcatcc tggggaggaa ctgggggcct 3360
ggttctgggt cagagagcag cccagtggag gtgagagcta cagcctgtcc tggcagctgg 3420
atccccagtc ccggtcaacc agtaatcaag gctgagcaga tcaggcttcc cggagctggt 3480
cttggaagc cagccctggg gtgagttggc tcctgctgtg gtactgagac aatattgtca 3540
taaattcaat gcgccttgt atccctttt cttttttatc tgtctacatc tataatcact 3600
atgcatacta gtctttgtta gtgtttctat tcmacttaat agagatatgt tatacttaaa 3660
aaaaaaaaaa aaaa 3674

```

<210> 620

<211> 2051

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(2051)

<223> n = A,T,C or G

<400> 620

```

ggaccagggg ctgaagtga cccccagcac agcacagctg ctctataaaa acgtggccag 60
actttttttt ttgaagcaag tcctgtttct tgttcgtcct gactagtccc atcagggccc 120
tggatcccaa gactcagcat ccaaggctcc ctccaggaat cctggcagct cagcatactt 180
tatcctgttt catctgagag caaaaatgta aaattggatg cacagaaaag tgactcaaag 240
tgcttaatga ctagaagaaa tctaggagca gcaagaagag caggacaaac aggccaggcg 300
gtgtcaggag ccagggtctc cagctggang gaacgtcaac cctgcagtgg gagcaggggc 360
cctttgcaca tcctaggcac agatggtaat gtgagaccca caggtaagct gggcttggtg 420
cctacccttc cccggattca gaaagaaacc aaacaaggag ctttgtgtgg aatgaaacct 480
cctttcctcc cagaagcact gctgactgtt tgggtgttgc catttgtggc agtgagccct 540
tgtttgttct gaggttgggc tggtttctcc tcttggccct gccctacaga tcataaagga 600
gaacagcaag acgtccccag caaacatcca cagatggcct tggaaataag tcaccttctt 660
caccctgcag gaatgccagt gaacatattg ctgacatctt ggagctcagt acctcatagt 720
gtaacggcgt cagtagatct gcctgtgctg ggaatttctg tactaccat tcctgagggg 780

```

cgatgcttct	gcagggcctg	tgacttgggt	cacaacttca	gacaccatca	tcttgcagca	840
gcaccgcacc	ctcactagcc	aggggtgttg	tgacttcctc	aaggccaagg	ccacattcaa	900
ggcttcggac	ttcattgatg	cgcttgtgct	gagcaagggt	gcttctccgg	gatcttaatt	960
caggaggtag	aatggagctt	gagatcaagt	gtctgatcaa	gcctcagtg	atgggcgctg	1020
ttcatcctct	ggtgctgaag	cagccaagag	acccaagtct	gcctggctgc	ctcttaggat	1080
atgacagcag	agccagtggc	ctctactaga	tcctgtacaa	cctcacaaaa	caccagaca	1140
tcgggagtgc	tgccagcctg	tgatgcaaga	gtcctaattc	tgaagacatt	gaatgacctg	1200
tcgttgtgct	gtttttacca	aaaaggatca	tgaggatcag	agaggaaaag	tcacttgccc	1260
aaagtccacac	agctgaacag	tggtggagtt	caactttgac	cgtgggctgt	ctggccccc	1320
aggtgtatgc	ttgcttctct	cccaagagac	tcctttctta	tcaggctcaa	atgaatgaaa	1380
ggaggatgtt	aaagacaacg	ccattattga	cgagatcact	cccaagcgga	ttggagattg	1440
tcccaatatt	tagacctata	gcaaggcctt	gggagaaatg	gtggtgcagc	aggagagcag	1500
gaacctaaacc	attgccatcc	taaggccctc	cattgtgtgg	agcaacgtgg	caccagcttt	1560
tcctgggttg	ggttgataat	ctaaatggat	gtagccgact	cattattgcg	gtatgtatag	1620
ggatgaagaa	gtaactgtaa	tgtagtggag	gaatagtaag	aaaattctta	gtgctggctt	1680
agcttaattg	atccaaaaac	ataaatgcta	ctttactatc	aattgaagca	tattatttca	1740
attattctgg	ttataatatg	gaggcaggat	gaaattgttt	ttattctttt	agaatttttt	1800
tttatcagga	aaacagaggt	aaagtgtctat	caattactat	ttaagagttc	tattttgaaa	1860
agtgagaatt	aaggattttt	cttttctttt	taaaaaaaac	ttttttaaaa	attaaaaata	1920
aaagaagcaa	aagtcttagg	aaaatgaagc	aagtagccct	gccactctat	gtacagtaat	1980
aacaatatct	gtcccagtta	ttatgtacaa	tattataaaa	aatgtcgag	acagtaaaaa	2040
aaaaaaaaa	a					2051

<210> 621

<211> 2841

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(2841)

<223> n = A,T,C or G

<400> 621

gcagagcaca	gcatagtg	tttaccaaat	catggccaga	ctgcttctgt	aagcaggccc	60
ctgatacctgt	tccacotcac	tggacaggac	ctcccaactg	gggcctccag	ctacccccac	120
cagcatccct	tggccaatgg	aaatttgaaa	tgttcctggg	acagagctcc	tggagagagg	180
ggcaggccac	cacctttgct	gtttgggtga	ctagccgttc	tggcctgcag	gctttggaga	240
gccaagctg	acaaggggta	gaagaggtgc	ctcagcacag	cacagccacg	ctacgaaaac	300
atggccagac	tcttgtttta	gtcagtcccc	gaacacattt	ctagtcagtg	ggtgaagtct	360
ttcaaccagg	gtctctggct	accttgaactg	ctgttctctg	gccagacagag	gtctcaggcc	420
tccttgagtc	agagctccc	gggggaggac	cagattgtca	tctttgctgt	ttgggtgacc	480
cagccatttc	agccttaggg	cttcagagtg	tctgaggtag	ccaggggctg	aagtgaacct	540
ccagcacagc	acagctgctg	tataaaaacg	tggccagact	ttttctttta	gcaagtccct	600
gttcttattc	ctcctgacta	ggttaagactt	ctcaacttgc	ctccagccac	atcttatttg	660
tgtgttcaga	ttggcaacag	gtttgtacct	cagtggtaca	gagctcccag	aggaaggggt	720
aggctatcat	cttccctgga	aaatacgagt	caattagggg	cttgagggga	ccccagcat	780
tccacagcag	cccttcagaa	aagtggccag	actctgtact	tgatgggcag	atcctccttg	840
cctgtgtctc	tagccagccc	accactggag	ctatcaagcc	agtagcaact	cagcagttcc	900
ttggacagag	cttccaggag	caaatgaaat	cctttctgcc	actgcctttg	cagtgaactg	960
cccttgctat	cctcagaaga	tatatcacgg	gagcaaaagac	cctaagtggc	atatcaaac	1020
ctccaataag	ctgcagttga	cccaaagaac	aagccaatcc	atctcccaca	ggttccacac	1080
acactccact	actcatcacc	agacagggaa	ccctggcttg	ggcccacagc	acagaccctc	1140
catcctgggc	cgattacact	gagtgattgc	taactcacat	gtctctggga	tggagcacc	1200
aggagacaag	caaagtgggtg	gagcagcaag	tcagtgatg	tggagcccag	agggcagggg	1260
gagctatctc	tctgggctcc	acttgccctt	gtgagacact	ttgtcccagc	actccttagt	1320
ctgcttgctc	ctcccagggc	cccagcctgg	ccacacctgc	ttacagggca	ctctcagatg	1380
cccataccat	agtttctgtg	ctagtggacc	gtaccatata	agtggagagc	tgcagcaagg	1440

tgccccntac	ggccacgcac	cagcctgcac	attacctctc	catactgcag	ccctttatat	1500
ggaaacttcc	tacatcactt	tgctgtgtgt	gtttacacag	gtggattttg	ctttacttgc	1560
actgacagca	cacaggaggg	cagcacacac	cccaaccac	atcaactgcc	attaaagaaa	1620
agaaatttca	gcccataatt	tcatgtccag	caaaatttagg	catcataagt	gaaggagaaa	1680
taagatcctt	ttcagacaag	caaagtctga	gggaattcaa	tatcaccaga	tctaccttac	1740
aagagctcct	gaaggaagca	ctaaatatgg	aaagaaaaaa	ccatcaccag	ccactacaaa	1800
aatgcagtga	agaacgcagt	gaattacgca	gtccagtgat	gctaaaaacc	aaccacatac	1860
gttaagtctg	caaaataaacc	agctgacagc	atgacgacag	gataaatcca	cacataccat	1920
tactaacctt	aaatgaaaat	gggctaaatg	ctcccattga	aagacatggg	gcaagctgga	1980
taaagaacca	agaccactg	gagtatgctg	tcttcaagaa	acccatctca	catgcggtgg	2040
catacatagg	ctcaaaataa	aggaatggag	aaaaatattt	caagcaaagt	gaaaacagaa	2100
aaaagcagg	gttgcactcc	tactttctga	caaaacagac	tatgcgaata	aagataaaaa	2160
agagaaggac	attacaaagg	tggtcctgac	ctttgatata	tctcattgct	tgataccaac	2220
ctgggctggt	ttaattgccc	aaanccaata	ggataatttg	ctgagggttg	ggagcttctc	2280
ccctgcagag	agtccctgat	ctcccaaaat	ttgggtgaga	tgtaagggtg	attttgctgt	2340
acaactcctt	ttctgaagtt	ttactcattt	ccaaaaagga	aggcaagttt	tcctgcttcc	2400
atgacgatgg	agagcaggca	tctcctttcc	tgagtttcag	cttgcttctg	acaggggaagg	2460
tgagtgtaa	ttttttccag	cttctaagat	ggcagagaac	gatcaccagc	ctgagcctta	2520
tttccaggta	agtagctgaa	ttagagtttt	gtcttaaaat	ttttccttaa	tgattaaaa	2580
gtaagattac	ccaccagctg	cttttaattt	ctcccttagc	attagaacac	tcagtaatca	2640
tatgaattgt	gcatttggtt	gttttgctta	actctttctg	tttggttatg	tttgggggtt	2700
tattgttggt	gtttcacttt	tctcccatct	cttcctgact	tggtcaaata	caaaggaatg	2760
ttcgaaattg	tggggagcaa	ggcatctgaa	atggctaaaa	ctcctgtggc	tgcaaaaaat	2820
agaaataaaa	aaaaaaaaaa	a				2841

<210> 622

<211> 3228

<212> DNA

<213> Homo sapien

<220>

<221> misc feature

<222> (1)...(3228)

<223> n = A,T,C or G

<400> 622

tccgccccat	tgacgcaaat	ggcggtaggc	gtgtacgggtg	ggagggtctat	ataagcagag	60
ctctcnggct	aactagagaa	cccactgctt	actggccttat	cgaaattaat	acgactcact	120
atagggagac	ccaagctggc	tagcgtttta	acttaagctt	ggtaccgagc	tcggatccac	180
tagtccagtg	tggtggaatt	ccattgtggt	gggcaggaaa	caagcaaaagt	ggtggagcag	240
caagtcagg	gatgtggagc	ccagagggtca	gggatggctg	tctctctagg	gtccacttgc	300
ccttgtgaga	cactttatcc	cagcacttta	ggaatactga	ggtcatacca	gccacatctt	360
atatgcaaga	ttgcccagca	gagatcaggt	ccgagagttc	cctttttaaa	aaaaggagac	420
ttgcttaata	aaagaagtct	agccacgttt	gtgtagagcg	gctgtgctgt	gctgggggtt	480
cacttttgag	agagttctcc	tctgagacct	gatctctgga	ggctgggcaa	tcttgcactt	540
gagatggggc	tggtctgatc	tcagcactcc	ttagtctgct	cgcctctccc	atggccccag	600
cctggccaca	cctgcttacg	gggcactctt	agatgccac	accataaact	ccatgctagt	660
ggactgtacc	atatcagtg	agagctgcag	caaggtggcc	cctagagcca	cgcaccagcc	720
tgacacattg	ctctccatac	ggcagccctt	tattttgaaa	cttcctaaat	cactttgctg	780
tgtgtgttta	caagggtgtg	ttttgcttta	cttgccctga	gagcacacgg	gagtgcagca	840
cacaccccaa	cccacatcaa	ctgccattaa	agaaaagaaa	tttcagccca	gaatttcagt	900
tccagcaaaa	ttaagcatca	taagtgaagg	agaaataaga	tccttttcag	acaagcaagt	960
gctgagggaa	tttggtatca	ccagatctac	cttacgagag	ctcctgaagg	aagcactaaa	1020
tatggaaaga	aaagatcatc	acctgctact	acaaaaacac	actgaagtac	acagtccaat	1080
gatgctaaaa	agcaagcaca	tatgtaagtc	tgcaaaataa	ccagctgaca	gcatgacgac	1140
aggataaaat	ccacacatac	cattactaac	cttaaatgta	aatgggctaa	atgctcccat	1200
tgaaagacac	ggggcaagct	gggtaaagaa	ccaagaccca	ctggagtatg	ccgtcttcaa	1260
gcaacccatc	tcacgtgcag	tgccatacat	aggctcaaaa	taaaggaatg	gagaaaaata	1320

tttcaagcaa	atggaaaaca	gaaaaaaggt	gttgcaactcc	cagtttctga	caaaacagac	1380
tctaccaata	aagataaaaa	aagagaagga	cattacaaag	gtggctcctga	cctttgataa	1440
atctcattat	tgcttgatac	caacctgggc	tatttgtatt	gcccaaacga	ataggataat	1500
ttgctgaggt	tgtggagctt	ctccccctca	cagagtccct	gatctccgaa	aatttggttg	1560
agatgtaagg	ttgattttgc	tgtacaactc	cttttttgaa	gttttactca	tttocaacaa	1620
ggaaggcaag	ttttcctgct	tccattgaca	aaggagagca	ggcacctcct	ttcctgagtt	1680
tcagcttgct	tctgacaggg	aaggagcttt	gagatttgaa	tactggcctg	ctgggttttg	1740
gacgtgcatt	gggcctgtgg	tcccatttgt	gttatttttc	tgggaaattt	cttccctttg	1800
gagtgaagaa	gcttacccaa	tgctgttacc	atcatcgtag	cttaaaagaa	ctccatttta	1860
agttcagga	ctccttgcca	gaagagaccg	tagccttgta	tcagatcata	aaggagaaga	1920
gcaagaggtc	cccggcaaac	atccacagat	ggccttgga	ataagtcacc	ttgtccacc	1980
tgagggaatg	ccagtgaact	tattgctgac	atcttgagc	tcagtaccct	catagtgtaa	2040
cggcgtcagc	agatctgcct	gtgctgggac	ttcctgtact	accatttcct	gaggggcgat	2100
gcttctgcag	ggcctgtgac	ttggtgcaca	acttcagaca	ccatcatctt	gcagcagcac	2160
cgcacctca	ctagccaggg	tgttgatgac	ttcctcaagg	ccaaggccac	attcaagget	2220
tcggacttca	ttgatgcgct	tgtgctgagc	aagggtggctt	ctccgggac	ttaattcagg	2280
aggtagaatg	gagcttgaga	tcaagtgtct	gatcaagcct	cagtgtatgg	gcgctgttca	2340
tcntctgggtg	ctgaagcagc	caagagaccc	aagtctgcct	ggctgcntct	taggatatga	2400
cagcagagcc	agtggcctct	actagatcct	gtacaacctc	acaaaacacc	cagacatcgg	2460
gagtgtgcct	agcctgtgat	gcaagagtcc	taatcctgaa	gacattgaat	gacctgtcat	2520
tctgctgttt	ttaccaaaaa	ggatcatgag	gatcagagag	gaaaagtcac	ttgcccaaa	2580
tcacacagct	gaacagtgg	ggagtccaac	tttgaccgtg	ggctgtctga	ccccaaggtg	2640
tatgcttgct	tctctcccaa	gagacaactt	tcttatcagg	ctcaaataaa	tgaaggagg	2700
atgttaaagg	taggatctct	gaagcctgtg	ccagtggaa	cgcagctcat	ggctggcacc	2760
tgtgttctca	ttcttacctc	attaagagta	aagtattattg	agtttattga	atttaagtat	2820
ctttagttag	atcatatatt	attagtaaga	actgggacca	aacagatttt	ctgactctaa	2880
aagagagatt	ttcacagaaa	cagatatata	cctgtaagta	tacagacacg	catacacaca	2940
tttctttact	gctcataaaa	attagtcctt	attagaatgt	gggatgtata	aatgtaagag	3000
aattttcatg	ttaaaattga	cagatacatt	tttaaatgt	cctaaaataa	atttaattat	3060
ttttntttta	gaattttcca	ttattaatgt	tatttttatg	agaaactata	taactttatt	3120
gataatacat	acaataaacc	tttgtttttc	aaattgaaaa	tacagtgtat	tttgcaata	3180
actaagtcct	aattttgtat	taaaatttta	aattttcaaa	aaaaaaaa		3228

<210> 623

<211> 4894

<212> DNA

<213> Homo sapiens

<400> 623

ctgcacgcgc	tggtccggg	tgacagccgc	gcgcctcggc	caggatctga	gtgatgagac	60
gtgtccccac	tgaggtgccc	cacagcagca	ggtgttgagc	atgggctgag	aagctggacc	120
ggcaccaaag	ggctggcaga	aatgggcgcc	tggtgtattc	ctaggcagtt	ggcggcagca	180
aggaggagag	gccgcagctt	ctggagcaga	gccgagacga	agcagttctg	gagtgcctga	240
acggcccccct	gagccctacc	cgcttgcccc	actatggctc	agaggctgtg	ggtgagccgc	300
ctgctgcggc	accggaaagc	ccagctcttg	ctggtcaacc	tgctaacctt	tggcctggag	360
gtgtgttttg	ccgcaggcat	cacctatgtg	ccgcctctgc	tgctggaagt	gggggtagag	420
gagaagtcca	tgaccatggt	gctgggtgag	tcactacatc	ctccttcctt	cctgttccag	480
atacatgcca	cctggcatgt	gggacaggag	tacctctgcc	ctgggagctg	cttgaggagg	540
gaggtggtct	gctgggaagg	cattgctggg	caggagggtg	accctgggct	gagggggcac	600
accaagagaa	aagagagaat	accaaggaca	taccacagtc	acctctggat	ccctggctcct	660
gcacagagcc	tggctcatag	gagacactgg	agaaatgtct	ctaacccttg	gctagccctt	720
ttataattta	tagcgattat	ctcatttaat	gcttacaacc	accatttgag	gtgatccatt	780
ttacagagaa	ggaagcagag	gcttttaaga	ggttaggtaa	gtcttagcca	aagccaaata	840
gcagctgaac	agtagagctg	ggactccatc	aaggctctcc	agccggagct	tgctcctacc	900
cctagacaaa	ggggtggact	cctgactctg	cagataaatt	ctacaaaagc	cacagaaggc	960
aagtagtaac	cattgtgtga	caaccctca	ccccaggaa	gaggggcccc	tgtgaggatt	1020
gcaggctctg	gagtcacact	gcttgttgaa	acgctgcctc	ttaccctccc	taggtctgag	1080

cctttgaata agtatcactt cttagtgtgt ccatgcotca gtttgtccat ctgaaaatgg 1140
gggcatctgt aatgcctgtg ttatgaggag taaattacag catccctgtg aagacgtagc 1200
acagtgtcga gtacggaatg ttatttccat ccttctcacg gagcttggtt ccccttcccc 1260
ttgcccttta cttgtcccag ccattgactc atactacttc ccttcttgca ggcattgggtc 1320
cagtgtctgg cctggtctgt gtcccgtccc taggtcagc cagtgaccac tggcgtggac 1380
gctatggccg ccgcccggcc ttcatctggg cactgtcctt gggcatcctg ctgagcctct 1440
ttctcatccc aaggccgggc tggctagcag ggctgtctgt cccggatccc aggccctgg 1500
agctggcact gctcatcctg ggctgtgggc tgctggactt ctgtggccag gtgtgcttca 1560
ctccactgga ggccctgtct tctgacctct tccgggaccc ggaccactgt cgccaggcct 1620
actctgtcta tgccttcatg atcagtcttg ggggtgcct gggctacctc ctgcttgcca 1680
ttgactggga caccagtgc ctggccccct acctgggcac ccaggaggag tgcctctttg 1740
gcctgtctac cctcatcttc ctcacctgcg tagcagccac actgctgggtg gctgaggagg 1800
cagcgtctgg ccccaccgag ccagcagaag ggctgtcggc cccctccttg tcgccccact 1860
gctgtccatg ccggggccgc ttggctttcc ggaacctggg cgccctgctt ccccggtgc 1920
accagctgtg ctgccgatg cccgcacccc tgcgccggct ctctgtggct gagctgtgca 1980
gctggatggc actcatgacc ttcacgtgtt tttacacgga ttctgtgggc gaggggctgt 2040
accagggcgt gccagagct gagccgggca ccgaggcccc gagacactat gatgaaggta 2100
aggccttggc agccagcaga ggctgggtgt ggagccgccc accagagacg acactcgggg 2160
ctgtgtctgg gctgtgtcct ctccatcctg gccccgactt ctctgtcagg aaagtgggga 2220
tggaccccat ctgcatacac ggcttctcat ggggtgtgaa catctctgct tgcggtttca 2280
ggaaggcctc tggctgtctt aggagtctga tcagagtctg tgccccagtt tgacagaagg 2340
aaaggcggag cttattcaaa gtctagaggg agtggaggag ttaaggctgg atttcagatc 2400
tgcctggttc cagccgcagt gtgccctctg ctccccaac gactttccaa ataatctcac 2460
cagcgccttc cagctcaggc gtcctagaag cgtcttgaag cctatggcca gctgtctttg 2520
tgttccctct caccgcctg tccctcacagc tgagactccc aggaaacctt cagactacct 2580
tcctctgcct tcagcaaggg gcgttgccca cattctctga gggtcagtgg aagaacctag 2640
actccattg ctagaggtag aaagggaag ggtgctgggg agcagggctg gtccacagca 2700
ggctctgtgc agcaggtaac tgtggttccg ccttctcatc tcctggagac tgctccgacc 2760
cttccctccc aggtctgtc tgatggcccc tctccctctg caggcgttcg gatgggcagc 2820
ctggggctgt tccgtcagtg cgccatctcc ctggtcttct ctctggctat ggaccggtg 2880
gtgcagcgat tcggcactcg agcagtctat ttggccagtg tggcagcttt ccctgtggct 2940
gccgtgcca catgcctgtc ccacagtgtg gccgtggtga cagcttcagc cgccctcacc 3000
gggttcacct tctcagccct gcagatcctg cctacacac tggcctccct ctaccaccgg 3060
gagaagcagg tgttcctgcc caaataccga ggggacactg gaggtgctag cagtgaggac 3120
agcctgatga ccaggttcc ctccctggag aagcctggag ctcccttccc taatggacac 3180
gtgggtggtg gaggcagtgg cctgtccca cctccaccgg cgtctgcgg ggcctctgcc 3240
tgtgatgtct ccgtacgtgt ggtggtgggt gagcccaccg aggccagggt ggttccgggc 3300
cggggcactt gcctggacct cgccatcctg gatagtgcct tcctgtgtc ccagggtggc 3360
ccatccctgt ttatgggctc cattgtccag ctcagccagt ctgtcactgc ctatatgggt 3420
tctgcccgag gcctgggtct ggtcgccatt tactttgcta cacaggtagt atttgacaag 3480
agcgaacttg ccaataactc agcgtagaaa acttccagca cattgggggt gagggcctgc 3540
ctcactgggt ccagctccc tgctcctgtt agcccatgg ggtgcccgg ctggccgcca 3600
gtttctgttg ctgccaaagt aatgtggctc tctgtgccca ccctgtgctg ctgagggtgcg 3660
tagctgcaca gctgggggct ggggcgtccc tctcctctct cccagctctc tagggctgcc 3720
tgactggagg ccttccaagg gggtttcagt ctggacttat acaggagggc cagaagggt 3780
ccatgcactg gaatgcgggg actctgcagg tggattaccc aggcctcagg ttaacagcta 3840
gcctcctagt tgagacacac ctagagaagg gtttttgga gctgaataaa ctcagtcacc 3900
tggtttccca tctctaagcc ccttaacctg cagcttcgtt taatgtagct cttgcatggg 3960
agtttctagg atgaaacact ccaccatggg atttgaacat atgaaagtta ttgtagggg 4020
aagagtctg aggggcaaca cacaagaacc agtccctc agccacagc actgtctttt 4080
tgctgatcca ccccctctt accttttata aggatgtggc ctgttggtcc ttctgttgcc 4140
atcacagaga cacaggcatt taaatattta acttatttat ttaacaaagt agaagggaat 4200
ccattgctag cttttctgtg ttggtgtcta atattgggt aggggtgggg atcccaaca 4260
atcaggtccc ctgagatagc tggctattgg gctgatcatt gccagaatct tcttctcctg 4320
gggtctggcc ccccaaatg cctaaccag gaccttgaa attctactca tcccaaatga 4380
taattccaaa tgctgttacc caaggttagg gtgttgaagg aaggtagagg gtggggcttc 4440
aggctcaac ggcttccta accaccctc tctcttggc ccagcctggt tccccacc 4500
tccactcccc tctactctct ctaggactgg gctgatgaag gcactgccc aaatttcccc 4560

```

tacccecaac tttccctac ccccaacttt cccaccagc tccacaaccc tgtttgagc 4620
tactgcagga ccagaagcac aaagtgcggt ttcccaagcc tttgtccatc tcagccccc 4680
gagtatatct gtgcttgggg aatctcacac agaaactcag gagcaccccc tgccctgagct 4740
aaggagggtc ttatctctca ggggggggtt aagtgccgtt tgcaataatg tcgtcttatt 4800
tatttagcgg ggtgaatatt ttatactgta agtgagcaat cagagtataa tgtttatggt 4860
gacaaaatta aaggctttct tatatgttta aaaa 4894

```

<210> 624

<211> 2904

<212> DNA

<213> Homo sapiens

<400> 624

```

gtctatgcct tcatgatcag tcttgggggc tgccctgggt acctcctgcc tgccattgac 60
tggaacacca gtgccctggc cccctacctg ggcacccagg aggagtgcct ctttggcctg 120
ctcaccctca tcttcctcac ctgcgtagca gccacactgc tggtggtgga ggaggcagcg 180
ctgggcccc cagagccagc agaagggtg tcggccccc ccttgctgcc cactgctgt 240
ccatgccggg ccgcttggc tttccggaac ctggcgccc tgctccccg gctgcaccag 300
ctgtgctgcc gcatgcccc caccctgcgc cggctcttcg tggctgagct gtgcagctgg 360
atggcactca tgacctcac gctgttttac acggatttcg tggcgaggg gctgtaccag 420
ggcgtgcccc gagctgagcc gggcaccgag gcccgagac actatgatga aggaaggcct 480
ctggctgctc taggagtctg atcagagtcg ttgcccagc ttgacagaag gaaaggcgga 540
gcttattcaa agtctagagg gagtggagga gttaaaggct gatttcagat ctgcctggtt 600
ccagcccgag tgtgccctct gctccccaa cgactttcca aataatctca ccagcgcctt 660
ccagctcagg cgtcctagaa gcgtcttgaa gcctatggcc agctgtcttt gtgttccctc 720
tcaccgcct gtccctcacag ctgagactcc caggaaacct tcagactacc ttctctgcc 780
ttcagcaagg ggcgttgccc acattctctg agggcgctcg gatgggcagc ctggggctgt 840
tctcgactg cgccatctcc ctggtcttct ctctggtcat ggaccgctg gtgcagcgat 900
tcggcactcg agcagtctat ttggccagtg tggcagcttt ccctgtggct gccggtgcca 960
catgcctgtc ccacagtgtg gccgtggtga cagcttcagc cgccctcacc gggttcacct 1020
tctcagccct gcagatcctg ccctacacac tggcctccct ctaccacggg gagaagcagg 1080
tgttcctgcc caaataaccga ggggacactg gaggtgctag cagtgaggac agcctgatga 1140
ccagcttcc tccagccctt aagcctggag ctccctccc taatggacac gtgggtgctg 1200
gagtcagtgg cctgtccca cctccaccg gcctctgcgg ggcctctgcc tgtgatgtct 1260
ccgtacgtgt ggtggtgggt gagcccaccg aggcagggt ggttccgggc cggggcatct 1320
gcctggacct cgccatcctg gatagtgcct tctgtgtgc ccagtgccc ccatccctgt 1380
ttatgggctc cattgtccag ctccagcagt ctgtcactgc ctatatggtg tctgcccag 1440
gcctgggtct ggtcgccatt tactttgcta cacaggtagt atttgacaag agcagcttgg 1500
ccaaatactc agcgtagaaa acttccagca cattgggggt gagggcctgc ctactgggt 1560
cccagctccc cgctcctgtt agcccatgg ggcctgcggg ctggccgcca gtttctgtt 1620
ctgcccagg aatgtggctc tctgtgcca ccctgtgctg ctgaggtgcg tagctgcaca 1680
gctgggggct gggcgctccc tctcctctct cccagctctc tagggctgcc tgactggagg 1740
ccttccaagg ggtttcagct ctggacttat acaggaggc cagaagggtt ccatgcactg 1800
gaatgcgggg actctgcagg tggattaccc aggcctcagg ttaacagcta gcctcctagt 1860
tgagacacac ctagagaagg gtttttggga gctgaataaa ctcagtcacc tggtttccca 1920
tctctaagcc ccttaacctg cagcttcgtt taatgtagct cttgcatggg agtttctagg 1980
atgaaacact cctccatggg atttgaacat atgaaagtta tttgtagggg aagagtcctg 2040
aggggaaca cacaagaacc aggtcccctc agcccacagc actgtctttt tgctgatcca 2100
ccccctctt accctttatc aggtgtggc ctgttggcc ttctgttgcc atcacagaga 2160
cacagcatt taaatattta acttatttat ttaacaaagt agaagggaat ccattgctag 2220
cttttctgtg ttggtgtcta atatttgggt aggggtgggg atccccaaca atcaggtccc 2280
ctgagatagc tggctcattg gctgatcatt gccagaatct tcttctcctg gggctctggc 2340
ccccaaatg cctaaccag gaccttgga attctactca tcccaaatga taattccaaa 2400
tgctgttacc caaggttagg gtgttgagg aaggtagagg gtgggcttc aggtctcaac 2460
ggcttcccta accaccctc ttctcttggc ccagcctggt tccccccact tccactcccc 2520
tctactctct ctaggactgg gctgatgaag gcactgccc aaatttccc taccccaac 2580
tttccctac ccccaacttt cccaccagc tccacaaccc tgtttgagc tactgcagga 2640

```

ccagaagcac	aaagtgcggt	ttcccaagcc	tttgtccatc	tcagccccc	gagtatatct	2700
gtgcttgggg	aatctcacac	agaaactcag	gagcaccccc	tgccctgagct	aagggaggtc	2760
ttatctctca	gggggggttt	aagtgcggtt	tgcaataatg	tcgtcttatt	tatttagcgg	2820
ggtgaatatt	ttatactgta	agtgcagcaat	cagagtataa	tgtttatggt	gacaaaatta	2880
aagcgtttct	tatatgttta	aaaa				2904

<210> 625

<211> 4034

<212> DNA

<213> Homo sapiens

<400> 625

aaccagcctg	cacgcgctgg	ctccgggtga	cagccgcgcg	cctcggccag	gatctgagtg	60
atgagacgtg	tccccactga	ggtgccccac	agcagcaggt	gttgagcatg	ggctgagaag	120
ctggaccggc	accaaaggcc	tggcagaaat	gggcgcctgg	ctgattccta	ggcagttggc	180
ggcagcaagg	aggagaggcc	gcagcttctg	gagcagagcc	gagacgaagc	agttctggag	240
tgccctgaacg	gccccctgag	ccctaccgcg	ctggcccact	atggtccaga	ggctgtgggt	300
gagccgcctg	ctgcggcacc	ggaaagccca	gctcttgctg	gtcaacctgc	taacctttgg	360
cctggagggtg	tgtttggccg	caggcatcac	ctatgtgccg	cctctgctgc	tggaagtggg	420
ggtagaggag	aagtctcatga	ccatggtgct	gggcattggt	ccagtgcctg	gcctggtctg	480
tgtcccgtctc	ctaggctcag	ccagtgaacca	ctggcgtgga	cgctatggcc	gccgcgggcc	540
cttcatctgg	gcactgtcct	tgggcatacct	gctgagcctc	tttctcatcc	caagggcccg	600
ctggctagca	gggctgctgt	gcccggatcc	caggcccctg	gagctggcac	tgctcatcct	660
gggcgtgggg	ctgctggact	tctgtggcca	ggtgtgcttc	actccactgg	aggccctgct	720
ctctgacctc	ttccggggacc	cggaccactg	tcgccaggcc	tactctgtct	atgccttcat	780
gatcagctctt	gggggctgcc	tgggctacct	cctgcctgcc	attgactggg	acaccagtgc	840
cctggccccc	tacctgggca	cccaggagga	gtgcctcttt	ggcctgctca	ccctcatctt	900
cctcacctgc	gtagcagcca	caactgctgt	ggctgaggag	gcagcgtg	gccccaccga	960
gccagcagaa	gggctgtcgg	ccccctcctt	gtcgcgccac	tgctgtccat	gccggggccc	1020
cttggctttc	cggaacctgg	gcgcctgct	tcccggctg	caccagctgt	gctgccgcat	1080
gccccgcacc	ctgcgcggcc	tcttcgtggc	tgagctgtgc	agctggatgg	caactcatgac	1140
cttcacgctg	ttttacacgg	atttcgtggg	cgaggggctg	taccagggcg	tgcccagagc	1200
tgagccgggc	accgaggccc	ggagacacta	tgatgaaggt	aaggccttgg	cagccagcag	1260
aggctgggtg	gggagccgcc	caccagagac	gacactcggg	gctgtgtctg	ggctgggtgc	1320
tctccatcct	ggccccgact	tctctgtcag	gaaagtgggg	atggaccca	tctgcataca	1380
cggcttctca	tggtgtgga	acatctctgc	ttgcggtttc	aggaaggcct	ctggctgtctc	1440
taggagtctg	atcagagtgc	ttgccccagt	ttgacagaag	gaaaggcgga	gcttattcaa	1500
agtctagagg	gagtggagga	gttaaggctg	gatttcagat	ctgcctgggt	ccagccgcag	1560
tgtgccctct	gctcccccaa	cgactttcca	aataatctca	ccagcgccct	ccagctcagg	1620
cgctctagaa	gcgtcttgaa	gcctatggcc	agctgtcttt	gtgttccctc	tcacccgcct	1680
gtcctcacag	ctgagactcc	caggaaacct	tcagactacc	ttcctctgcc	ttcagcaagg	1740
ggcgttgccc	acattctctg	agggctcagt	gaagaacctc	gactccatt	gctagaggtc	1800
gaaaggggaa	gggtgctggg	gagcagggt	ggtccacagc	aggtctcgtg	cagcaggtac	1860
ctgtgggttc	gccttctcat	ctccctgaga	ctgctccgac	ccttccctcc	caggctctgt	1920
ctgatggccc	ctctccctct	gcaggcgctc	ggatgggcag	cctggggctg	ttcctgcagt	1980
gcgccatctc	cctggtcttc	tctctggtca	tggaccggct	ggtgcagcga	ttcggcactc	2040
gagcagtcta	tttggccagt	gtggcagctt	tccctgtggc	tgccgggtgc	acatgcctgt	2100
cccacagtgt	ggccgtggtg	acagcttcag	ccgcctcac	cgggttcacc	ttctcagccc	2160
tgacagctct	gccctacaca	ctggcctccc	tctaccaccg	ggagaagcag	gtgttcctgc	2220
ccaaataccg	aggggacact	ggagggtgta	gcagtggaga	cagcctgatg	accagcttcc	2280
tgcaggcccc	taagcctgga	gctcccttcc	ctaattggaca	cgtgggtgct	ggaggcagtg	2340
gcctgtctcc	acctccaccc	gcgctctgcg	gggcctctgc	ctgtgatgtc	tcctgtacgtg	2400
tggtgggtgg	tgagcccacc	gaggccaggg	tggttccggg	ccggggcatc	tgccctggacc	2460
tcgccatcct	ggatagtgcc	ttcctgctgt	cccagggtgc	cccatccctg	tttatgggct	2520
ccattgtcca	gctcagccag	tctgtcactg	cctatatggt	gtctgccgca	ggcctgggtc	2580
tggtcgccat	ttactttgct	acacaggtag	tatttgacaa	gagcgacttg	gccaaatact	2640
cagcgtagaa	aacttccagc	acattggggg	ggagggcctg	cctcactggg	tcccagctcc	2700


```

ccgctcctgt tagcccatg gggctgccg gctggccgc agtttctgt gctgccaaag 2760
taatgtggct ctctgctgcc accctgtgct gctgaggtgc gtagctgcac agctgggggc 2820
tggggcgctcc ctctcctctc tcccagctct ctagggtgc ctgactggag gccttccaag 2880
gggggtttcag tctggactta tacagggagg ccagaagggc tccatgcaact ggaatgcggg 2940
gactctgcag gtggattacc caggctcagg gttaacagct agcctcctag ttgagacaca 3000
cctagagaag ggtttttggg agctgaataa actcagtcac ctggtttccc atctctaagc 3060
cccttaacct gcagcttcgt ttaatgtagc tcttgcatgg gagtttctag gatgaaacac 3120
tcctccatgg gatttgaaca tatgaaagt attttagagg gaagagtcct gaggggcaac 3180
acacaagaac caggctccct cagccacag cactgtcttt ttgctgatcc accccctct 3240
taccttttat caggatgtgc ctgttggtcc ttctgttgcc atcacagaga cacaggcatt 3300
taaataattta acttatttat ttaacaaagt agaagggaat ccattgctag cttttctgtg 3360
ttggtgtcta atatttgggt aggggtgggg atcccaaca atcaggctcc ctgagatagc 3420
tggtcattgg gctgatcatt gccagaatct tcttctcctg gggcttgccc ccccaaatg 3480
cctaaccag gaccttgaa attctactca tcccaaatga taattccaaa tgctgttacc 3540
caagggttagg gtgttgaagg aaggtagagg gtggggcttc aggtctcaac ggcttcccta 3600
accaccctc ttctcttggc ccagcctggt tccccccact tccactcccc tctactctct 3660
ctaggactgg gctgatgaag gcaactgccc aaatttcccc taccaccaac tttcccctac 3720
ccccaacttt cccaccagc tccacaacct tgtttggagc tactgcagga ccagaagcac 3780
aaagtgcggt ttcccaagcc tttgtccatc tcagccccc gagtatact gtgcttggg 3840
aatctcacac agaaactcag gagcaccccc tgcctgagct aaggagggtc ttatctctca 3900
gggggggttt agtgccgtt tgcaataatg tcgtcttatt tatttagcgg ggtgaatatt 3960
ttatactgta agtgagcaat cagagtataa tgtttatggt gacaaaatta aaggctttct 4020
tatatgttta aaaa 4034

```

<210> 626

<211> 6976

<212> DNA

<213> Homo sapiens

<400> 626

```

gaagctggac cggcaccaaa gggctggcag aaatgggcgc ctggctgatt cctaggcagt 60
tgccggcagc aaggaggaga ggccgcagct tctggagcag agccgagacg aagcagttct 120
ggagtgcctg aacggccccc tgagccctac ccgcctggcc cactatggtc cagaggctgt 180
gggtgacccg cctgctgcgg caccggaaa gcccagctctt gctgggtcaac ctgctaacct 240
ttggcctgga ggtgtgtttg gccgcaggca tcacctatgt gccgcctctg ctgctggaag 300
tgggggtaga ggagaagttc atgaccatgg tgctgggtga gtcactacat cctccttctc 360
tcctgttcca gatacatgcc acctggcatg tgggacagga gtacctctgc cctgggagct 420
gcttgagggg agagggtgtc tgctgggaag gcaattgctg gcaggagggt gaccctgggc 480
tgagggggca caccaagaga aagaagagaa taccaaggac ataccocagt cacctctgga 540
tcctgtgtcc tgcaagagc ctggctcata ggagacactg gagaaatgct cctaaccctt 600
ggctagccct ttataattt atagcgatta tctcatttaa tgcttacaac caccatttga 660
ggtgatccat ttacagaga aggaagcaga ggcttttaag aggttaggta agtcttagcc 720
aaagccaaat agcagctgaa cagtagagct gggactccat caaggtctcc cagccggagc 780
ttgtctctac ccctaggaca aggggtggac tcctgactct gcagataaat tctacaaaag 840
ccacagaagg caagtagtaa ccattgtgtg acaaccctc acccccagga agagggggcc 900
ctgtgaggat tgcaaggctc ggagtcacac tgcttgttga aacgctgcct cttaccctcc 960
ctagggtctg gcctttgaat aagtatcact tmttagttgc tccatgcctc agtttgtcca 1020
tctgaaaatg gggcatctg taatgcctgt gttatgagga gtaaattaca gcatccctgt 1080
gaagcagtag cacagtgtcg agtacggaat gttatttcca tccttctcac ggagcttgg 1140
tccccttccc cttgcccttt acttgtccca gccattgact catactactt cccttcttgc 1200
aggcattggt ccagtgtgg gcctgggtctg tgtcccgtc ctaggctcag ccagtacca 1260
ctggcgtgga cgctatggc gccgcccggc ctctcatctg gcaactgtct tgggcatcct 1320
gctgagcctc tttctcatcc caaggccgg ctggctagca gggctgctgt gcccggatec 1380
caggccctg gagctggcac tgctcatcct gggcgtgggg ctgctggact tctgtggcca 1440
ggtgtgcttc actccactgg aggcctgct ctctgacctc ttccgggacc cggaccactg 1500
tcgccaggcc tactctgtct atgccttcat gatcagctct gggggtgccc tgggctacct 1560
cctgctgccc attgactggg acaccagtgc cctggccccc tacctgggca cccaggagga 1620

```

gtgcctcttt ggcttgetca ccctcatctt cctcacctgc gtagcagcca cactgctggt 1680
ggctgaggag gcagcgctgg gccccaccga gccagcagaa gggctgtcgg cccctcctt 1740
gtcgcceccac tgctgtccat gccgggcccg cttggctttc cggaacctgg gcgccctgct 1800
tccccggctg caccagctgt gctgccgcac gccccgcacc ctgcgcgggc tcttcgtggc 1860
tgagctgtgc agctggatgg cactcatgac cttcacgctg ttttacacgg atttcgtggg 1920
cgaggggctg taccagggcg tgcccagagc tgagccgggc accgagggcc ggagacacta 1980
tgatgaaggt aaggccttgg cagccagcag aggctggtgt gggagccgcc caccagagac 2040
gacactcggg gctgtgtctg ggctggtgcc tctccatcct ggccccgact tctctgtcag 2100
gaaagtgggg atggacccca tctgcataca cggcttctca tgggtgtgga acatctctgc 2160
ttgcggtttc aggaaggcct ctggctgtct taggagtctg atcagagtgc ttgccccagt 2220
ttgacagaag gaaaggcgga gcttattcaa agtctagagg gagtggagga gtttaaggctg 2280
gatttcagat ctgcctggtt ccagccgcag tgtgccctct gctccccaa cgactttcca 2340
aataatctca ccagcgcctt ccagctcagg cgtcctagaa gcgtcttgaa gcctatggcc 2400
agctgtcttt gtgttccctc tcaccgcctt gtcctcacag ctgagactcc caggaaacct 2460
tcagactacc ttctctgccc ttcagcaagg ggcgttgccc acattctctg agggtcagt 2520
gaagaacct aactcccatt gctagaggta gaaaggggaa ggggtgctggg gaggagggct 2580
ggtccacagc aggtctcgtg cagcaggtac ctgtggttcc gccttctcat ctccctgaga 2640
ctgctccgac ccttccctcc caggctctgt ctgatggccc ctctccctct gcaggcgttc 2700
ggatgggagc cctggggctg ttctgtcagt gcgccatctc cctgggtctt tctctggtca 2760
tggaccggct ggtgcagcga ttccggcactc gagcagtcta ttggccagt gtggcagctt 2820
tccctgtggc tgccgggtgcc acatgcctgt cccacagtgt ggcctgtgtg acagcttcag 2880
ccgcccctac cgggttcacc ttctcagccc tgcagatcct gccctacaca ctggcctccc 2940
tctaccaccg ggagaagcag gtactcattg gccagtgggt ggagtcaggg tgggaggggt 3000
ggtctgggtt tttgggagge caactagctc agaacctggt atctggcaag caactttgga 3060
gaatgcttct ttgaatcaga gaagaagctt atcctagccc caggggccaga ggcttgggct 3120
gcagaacagt gtagattaga ttctgggaat gacttccctg ggtcaggact gtgtagcact 3180
tgaatggat attgcaggaa atgcaaaata cgtagtggg aatcccgaag ggtcaggcca 3240
gcaggagccc taggcttcta ggctggttgt tctatggaga ggcaaggcgc tgaatcagat 3300
gaccctggg ccattcagcc tcagcagacg ggagtgggaa tgggtccagcc ttagcaacac 3360
ctttcttcag ggagcagcaa cctgacttag cctgtatcct actctggtct ctgagatggg 3420
gcaggtcctt tctaccccc tttctttctg gcttattttt cttttctgtc taattccctt 3480
ttcttttctt gcatccctcc tttgcctcct tccctttctc ctcccccttc cccttccctt 3540
gtggcagata tctgagcttg acacctgacc cactcacttg ggcactgtgt aagttgtggg 3600
gacctccttc ttggttggcc ctacactaac cagcccctcc agggggccct ttcttggga 3660
agccacctaa cccagctagt gtggtcatcc ttgtccctc cactgacctc actgagctac 3720
aaacctgggt gctggactct gccttgaggg gcatgaagtt ggggtgtccc aaggaggag 3780
gagatgcagg actgctctca tagagctctc agactgtagg gaagacctgc cctgcgtct 3840
cgtagcactt gaggagagga gtaggtaagt tctgtactga gaggctggtt aactgagtag 3900
gtagctgcag gggtagagg tatggagggg aggggctaag gttttggtt ggggagcctg 3960
gtccctgaga ccctgttag cccactgata accttcttca gccttcaact tctgtcttgc 4020
ctgggctggg ggcagggggc tggcatcagc ggcaggcctt gagtatgtgc tgtcgtgcca 4080
gggaacgttc tggggctagc catcttctcc agatggagga gcatgtctgt cctcggacca 4140
ctccagactc caacctcagc ggacattcct ggggtggcag gcaggagga gaagtccctg 4200
gaggccccct cctaacagca gctgatggca gacttggcac tgcacgtgt ctgcctgttc 4260
ctttgccac ttgttgagct gcatgggtgag ccgtgggctt cctggtgtc aggtttgagc 4320
tctgccatgg ctcccacctc gcaaatgcag ccaactcaac tcttctggca tggggacaat 4380
gttgataag acctggcctt gtccttaaat aggaggtctt gggccatcaa gggcaggggt 4440
tggggggatg gtggtcgacc agtcaactct atctaagtca gacagcagga aggaagttag 4500
aagccttcaa cattagcaca gctggggctg ggggaggtgg gaagagggac attcctcctg 4560
cttgggtctt actgattct ccctgcccc aagggtggga caaggagct catggcagg 4620
cagctaccct agtggcatct gggaccccag agagcagag cttctctgca ccgggcaatg 4680
aggatttcca gatgtcggag tggagggcag gcaggaagga aggttaggag agcctgcgtg 4740
gggtttgggc catcaggggc cctgccttgg cttttgttcc tctgttctgt gcatctctta 4800
ccaccgtctt cattccccct gtgtcttttc cttaccttgg agctctgttc tctctgatct 4860
gtgatattga gtttgtctgc ctcttacctg ttctaagagg ctagaggaga cctagacttc 4920
tgggttcaca tttgtccccg cctaccccc ttacccttct cccactcctg aggaagggtc 4980
ctggttagac ttggaccaag tagggtctcc atcttctctc ctgctcctga ttctcatgaa 5040
gtcccattgc ccctgggatg gaggcaaggg tctgttctca cagctgggggt ggtgccagt 5100

```

ctgggtacac acctgtcctc ttcccccttt cttcaccctt ctgccttagg tgttctgccc 5160
caaataccga ggggacactg gaggtgctag cagtgaggac agcctgatga ccagcttccct 5220
gccaggccct aagcctggag ctcccttccc taatggacac gtgggtgctg gaggcagtgg 5280
cctgtcctcca cctccaccgg cgctctgctg ggcctctgcc tgtgatgtct ccgtacgtgt 5340
ggtggtgggt gagccaccgg aggccagggt ggttcggggc cggggcatct gcctggacct 5400
cgccatcctg gatagtgcct tcctgctgtc ccagggtggc ccatccctgt ttatgggctc 5460
cattgtccag ctccagccagt ctgtcactgc ctatatggtg tctgccgcag gcctgggtct 5520
ggtcgccatt tacttttgcta cacaggtagt atttgacaag agcgacttgg ccaaatactc 5580
agcgtagaaa acttccagca cattgggggtg gagggcctgc ctactgggtt cccagctccc 5640
cgctcctggt agcccatggt ggctgccggg ctggcccgcca gtttctgttg ctgccaaagt 5700
aatgtggctc tctgtgccca ccctgtgctg ctgaggtgctg tagctgcaca gctggggggt 5760
ggggcgctccc tctcctctct cccagctctc tagggctgcc tgactggagg ccttccaagg 5820
gggtttcagt ctggacttat acaggggagg cagaagggtt ccatgcactg gaatgcgggg 5880
actctgcagg tggattaccc aggtcagggt ttaacagcta gcctcctagt tgagacacac 5940
ctagagaagg gtttttggga gctgaataaa ctcagtcacc tggtttccca tctctaagcc 6000
ccttaacctg cagcttcggt taatgtagct cttgcatggg agtttctagg atgaaacact 6060
cctccatggg atttgaacat atgaaagtta tttgtagggg aagagtcctg aggggcaaca 6120
cacaagaacc aggtcccctc agcccacagc actgtctttt tgctgatcca cccccctctt 6180
accttttacc aggatgtggc ctgttgggtc ttctgttgcc atcacagaga cacaggcatt 6240
taaatattta acttatttat ttaacaaagt agaagggaat ccattgctag cttttctgtg 6300
ttggtgtcta atatttgggt aggttggggg atccccaaca atcagggtccc ctgagatagc 6360
tggtcattgg gctgatcatt gccagaatct tcttctcctg gggctctggc ccccaaaatg 6420
cctaaccag gaccttggaa attctactca tcccaaatga taattccaaa tgctgttacc 6480
caagggttag gtgttgaagg aaggtagagg gtggggcttc aggtctcaac ggcttcccta 6540
accaccctc ttctcttggc ccagcctggt tcccccaact tccactcccc tctactctct 6600
ctaggactgg gctgatgaag gcaactgccc aaatttcccc taccaccaac tttcccctac 6660
ccccaacttt ccccaaccgc tccacaacc tggttggagc tactgcagga ccagaagcac 6720
aaagtgcggt ttccaagcc tttgtccatc tcagccccc gagtatatct gtgcttgggg 6780
aatctcacac agaaactcag gagcaccccc tgcttagctt aagggaggtc ttatctctca 6840
gggggggttt aagtgcggtt tgcaataatg tcgtcttatt tathtagcgg ggtgaatatt 6900
ttatactgta agtgagcaat cagagtataa tgtttatggt gacaaaatta aaggctttct 6960
tatatgttta aaaaaa 6976

```

<210> 627

<211> 123

<212> PRT

<213> Homo sapiens

<400> 627

```

Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu Val Phe
          5              10              15

```

```

Ser Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg Ala Val
          20              25              30

```

```

Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala Thr Cys
          35              40              45

```

```

Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu Thr Gly
          50              55              60

```

```

Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala Ser Leu
          65              70              75              80

```

```

Tyr His Arg Glu Lys Gln Val Leu Ile Gly Gln Trp Val Glu Ser Gly
          85              90              95

```

239

Trp Glu Gly Trp Ser Gly Phe Leu Gly Gly Gln Leu Ala Gln Asn Leu
 100 105 110

Val Ser Gly Lys Gln Leu Trp Arg Met Leu Leu
 115 120

<210> 628

<211> 150

<212> PRT

<213> Homo sapiens

<400> 628

Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala
 5 10 15

Gln Leu Leu Leu Val Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu
 20 25 30

Ala Ala Gly Ile Thr Tyr Val Pro Pro Leu Leu Leu Glu Val Gly Val
 35 40 45

Glu Glu Lys Phe Met Thr Met Val Leu Gly Glu Ser Leu His Pro Pro
 50 55 60

Ser Phe Leu Phe Gln Ile His Ala Thr Trp His Val Gly Gln Glu Tyr
 65 70 75 80

Leu Cys Pro Gly Ser Cys Leu Glu Gly Glu Val Val Cys Trp Glu Gly
 85 90 95

Ile Ala Gly Gln Glu Gly Asp Pro Gly Leu Arg Gly His Thr Lys Arg
 100 105 110

Lys Lys Arg Ile Pro Arg Thr Tyr Pro Ser His Leu Trp Ile Pro Gly
 115 120 125

Pro Ala Gln Ser Leu Ala His Arg Arg His Trp Arg Asn Ala Pro Asn
 130 135 140

Leu Trp Leu Ala Leu Leu
 145 150

<210> 629

<211> 371

<212> PRT

<213> Homo sapiens

<400> 629

Met Leu Phe Pro Ser Phe Ser Arg Ser Leu Val Pro Leu Pro Leu Ala
 5 10 15

Leu Tyr Leu Ser Gln Pro Leu Thr His Thr Thr Ser Leu Leu Ala Gly
 20 25 30

Ile Gly Pro Val Leu Gly Leu Val Cys Val Pro Leu Leu Gly Ser Ala
 35 40 45

Ser Asp His Trp Arg Gly Arg Tyr Gly Arg Arg Arg Pro Phe Ile Trp
 50 55 60
 Ala Leu Ser Leu Gly Ile Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala
 65 70 75 80
 Gly Trp Leu Ala Gly Leu Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu
 85 90 95
 Ala Leu Leu Ile Leu Gly Val Gly Leu Leu Asp Phe Cys Gly Gln Val
 100 105 110
 Cys Phe Thr Pro Leu Glu Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro
 115 120 125
 Asp His Cys Arg Gln Ala Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu
 130 135 140
 Gly Gly Cys Leu Gly Tyr Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser
 145 150 155 160
 Ala Leu Ala Pro Tyr Leu Gly Thr Gln Glu Glu Cys Leu Phe Gly Leu
 165 170 175
 Leu Thr Leu Ile Phe Leu Thr Cys Val Ala Ala Thr Leu Leu Val Ala
 180 185 190
 Glu Glu Ala Ala Leu Gly Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala
 195 200 205
 Pro Ser Leu Ser Pro His Cys Cys Pro Cys Arg Ala Arg Leu Ala Phe
 210 215 220
 Arg Asn Leu Gly Ala Leu Leu Pro Arg Leu His Gln Leu Cys Cys Arg
 225 230 235 240
 Met Pro Arg Thr Leu Arg Arg Leu Phe Val Ala Glu Leu Cys Ser Trp
 245 250 255
 Met Ala Leu Met Thr Phe Thr Leu Phe Tyr Thr Asp Phe Val Gly Glu
 260 265 270
 Gly Leu Tyr Gln Gly Val Pro Arg Ala Glu Pro Gly Thr Glu Ala Arg
 275 280 285
 Arg His Tyr Asp Glu Gly Lys Ala Leu Ala Ala Ser Arg Gly Trp Cys
 290 295 300
 Gly Ser Arg Pro Pro Glu Thr Thr Leu Gly Ala Val Ser Gly Leu Val
 305 310 315 320
 Pro Leu His Pro Gly Pro Asp Phe Ser Val Arg Lys Val Gly Met Asp
 325 330 335
 Pro Ile Cys Ile His Gly Phe Ser Trp Val Trp Asn Ile Ser Ala Cys
 340 345 350

Gly Phe Arg Lys Ala Ser Gly Cys Ser Arg Ser Leu Ile Arg Val Val
 355 360 365

Ala Pro Val
 370

<210> 630
 <211> 2983
 <212> DNA
 <213> Homo sapiens

<400> 630

```

agagatagag tcttcctcctgg cattgcagga gagaatctga agggatgatg gatgcatcaa 60
aagagctgca agttctccac attgacttct tgaatcagga caacgccgtt tctcaccaca 120
catgggagtt ccaaacgagc agtctctgtg tccggcgagg acaggtgttt cacctgcggc 180
tgggtgctgaa ccagccccta caatcctacc accaactgaa actggaattc agcacagggc 240
cgaatcctag catcgccaaa cacaccctgg tgggtgctcga cccgaggacg ccctcagacc 300
actacaactg gcaggcaacc cttcaaaatg agtctggcaa agaggtcaca gtggctgtca 360
ccagttcccc caatgccatc ctgggcaagt accaactaaa cgtgaaaact ggaaaccaca 420
tccttaagtc tgaagaaaac atcctataacc ttctcttcaa cccatggtgt aaagaggaca 480
tggttttcat gcctgatgag gacgagcgca aagagtacat cctcaatgac acgggctgcc 540
attacgtggg ggctgccaga agtatcaaat gcaaaccctg gaactttggt cagtttgaga 600
aaaatgtcct ggactgctgc atttccctgc tgactgagag ctccctcaag cccacagata 660
ggagggaacc cgtgctgggtg tgcaaggcca tgtgtgctat gatgagcttt gagaaaggcc 720
agggcgtgct cattgggaat tggactgggg actatgaagg tggcacagcc ccatacaagt 780
ggacaggcag tgccccgatc ctgcagcagt actacaacac gaagcaggct gtgtgctttg 840
gccagtgtct ggtgtttgct gggatcctga ctacagtgtg gagagcgttg ggcattccag 900
cacgcagtgt gacaggcttc gattcagctc acgacacaga aaggaaacctc acggtggaca 960
cctatgtgaa tgagaatggc aagaaaatca ccagtatgac ccacgactct gtctggaatt 1020
tccatgtgtg gacggatgcc tggatgaagc gaccggatct gcccaagggc tacgacggct 1080
ggcaggctgt ggacgcaacg ccgcaggagc gaagccaggg tgtcttctgc tgtgggcat 1140
caccactgac cgctatccgc aaaggcgaca cttttattgt ctatgacacc agattcgtct 1200
tctcagaagt gaatgggtgac aggtcatctt ggttgggtgaa gatggtgaat gggcaggagg 1260
agttacacgt aatttcaatg gagaccacaa gcatcgggaa aaacatcagc accaaggcag 1320
tgggccaaga caggcggaga gatatacctt atgagtacaa gtatccagaa ggctcctctg 1380
aggagaggca ggtcatggat catgccttcc tccttctcag ttctgagagg gagcacagac 1440
gacctgtaaa agagaacttt cttcacatgt cggtaacaatc agatgatgtg ctgctgggaa 1500
actctgttaa tttcacctgt attcttaaaa ggaagaccgc tgccctacag aatgtcaaca 1560
tcttgggctc ctttgaacta cagttgtaca ctggcaagaa gatggcaaaa ctgtgtgacc 1620
tcaataagac ctgcagatc caaggtcaag tatcagaagt gactctgacc ttggactcca 1680
agacctacat caacagcctg gctatattag atgatgagcc agttatcaga ggtttcatca 1740
ttgcggaaat tgtggagtct aaggaaatca tggcctctga agtattcacg tctttccagt 1800
accctgagtt ctctatagag ttgcctaaca caggcagaat tggccagcta cttgtctgca 1860
attgtatctt caagaatacc ctggccatcc ctttgactga cgtcaagttc tctttggaaa 1920
gcctgggcat ctccctcacta cagacctctg accatgggac ggtgcagcct ggtgagacca 1980
tccaatccca aataaaatgc accccaataa aaactggacc caagaaattt atcgtcaagt 2040
taagtccaa acaagtgaag gagattaatg ctcagaagt tgttctcacc accaagtagc 2100
cttgtctgat gctgtggagc cttagttgag atttcagcat ttctacctt gtgcttagct 2160
ttcagattat ggatgattaa atttgatgac ttatatgagg gcagattcaa gagccagcag 2220
gtcaaaaagg ccaacacacac cataagcagc cagaccacac aggccaggctc ctgtgctatc 2280
acagggtcac ctcttttaca gttagaaaca ccagccgagg ccacagaatc ccatcccttt 2340
cctgagtcac ggcctcaaaa atcagggcca ccattgtctc aattcaaatc catagatttc 2400
gaagccacag agtctctccc tggagcagca gactatgggc agcccagtgc tgccacctgc 2460
tgacgacctt tgagaagctg ccatatcttc aggccatggg ttcaccagcc ctgaaggcac 2520
ctgtcaactg gagtgtcttc tcagcactgg gatgggcctg atagaagtgc attctcctcc 2580

```

```

tattgcctcc attctcctct ctctatccct gaaatccagg aagtcctctt cctgggtgctc 2640
caagcagttt gaagcccaat ctgcaaggac atttctcaag ggccatgtgg ttttgcagac 2700
aacctgtgcc tcaggcctga actcaccata gagacccatg tcagcaaacg gtgaccagca 2760
aatcctcttc ccttattcta aagctgcccc ttgggagact ccaggagaa ggcattgctt 2820
cctccctggg gtgaactctt tctttgggat tccatccact atcctggcaa ctcaaggctg 2880
cttctgttaa ctgaagcctg ctcttcttgg ttctgccctc cagagatttg ctcaaatgat 2940
caataagctt taaattaaac tctacttcaa gaaaaaaaaa ccg 2983

```

<210> 631

<211> 3064

<212> DNA

<213> Homo sapiens

<400> 631

```

aattctaaaa atgcttttgc aagcttgcag gcctgcaggt gcagcggccg ccagtgtgat 60
ggatatctgc agaattcggc ttgcgctcag ctggaattcc gcagagatag agtcttccct 120
ggcattgcag gagagaatct gaagggatga tggatgcac aaaagagctg caagttctcc 180
acattgactt cttgaatcag gacaacgcc tttctacca cacatgggag ttccaaacga 240
gcagtctgtg gttccggcga ggacaggtgt ttcacctgcg gctgggtgctg aaccagcccc 300
tacaatccta ccaccaactg aaactggaat tcagcacagg gccgaatcct agcatcgcca 360
aacacaccct ggtgggtgctc gacccgagga cgccctcaga ccactacaac tggcaggcaa 420
cccttcaaaa tgagtctggc aaagaggtca cagtggctgt caccagttcc cccaatgcca 480
tcctgggcaa gtaccaacta aacgtgaaaa ctggaaacca catccttaag tctgaagaaa 540
acatcctata ccttctcttc aaccatggt gttaaagagga catggttttc atgcctgatg 600
aggacgagcg caaagagtac atcctcaatg acacgggctg ccattacgtg ggggctgcca 660
gaagtatcaa atgcaaacc tggaaactttg gtcagtttga gaaaaatgtc ctggactget 720
gcatttccct gctgactgag agtccctca agcccacaga taggaggag cccgtgctgg 780
tgtgcagggc catgtgtgct atgatgagct ttgagaaagg ccagggcgtg ctcatggga 840
attggactgg tgacaccgaa ggtggcag cccatacaa gtggacaggc agtgccccga 900
tcctgcagca gtactacaac acgaagcagg ctgtgtgctt tggccagtgc tgggtgtttg 960
ctgggatcct gactacagt ctgagagcgt tgggcatccc agcacgcagt gtgacaggct 1020
tcgattcagc tcacgacaca gaaaggaacc tcacggtgga cacctatgtg aatgagaatg 1080
gcgagaaaat caccagtatg acccacgact ctgtctggaa tttccatgtg tggacggatg 1140
cctggatgaa ggcaccctac gacggctggc aggtgtgga cgcaacgcc caggagcgaa 1200
gccagggtgt cttctgctgt gggccatcac cactgaccgc catccgcaa ggtgacatct 1260
ttattgtctg tgacaccaga ttgtcttct cagaagtga tggtgacagg ctcatctggt 1320
tgggtgaagat ggtgaatggg caggaggagt tacacgtaat ttcaatggag accacaagca 1380
tcgggaaaaa catcagcacc aaggcagtg gccaagacag gcggagagat atcacctatg 1440
agtacaagta tcagaaggc tcctctgagg agaggcaggt catggatcat gccttccctc 1500
ttctcagttc tgagaggag cacagacagc ctgtaaaaga gaactttctt cacatgtcgg 1560
tacaatcaga tgatgtgctg ctgggaaact ctgttaattt caccgtgatt cttaaaagga 1620
agaccgctgc cctacagaat gtcaacatct tgggtcctt tgaactacag ttgtacactg 1680
gcaagaagat ggcaaaactg tgtgacctca ataagacctc gcagatccaa ggtcaagtat 1740
cagaagtga tctgaccttg gactccaaga cctacatcaa cagcctggct atattagatg 1800
atgagccagt tatcagaggt ttcatcattg cggaaattgt ggagtctaag gaaatcatgg 1860
cctctgaagt attcacgtca aaccagtacc ctgagttctc tatagagttg cctaacacag 1920
gcagaattgg ccagctactt gtctgcaatt gtatcttcaa gaataccctg gccatccctt 1980
tgactgacgt caagttctct ttggaaagcc tgggcatctc ctactacag acctctgacc 2040
atgggacggg gcagcctggg gagaccatcc aatcccaaat aaaatgcacc ccaataaaaa 2100
ctggacccaa gaaatttatc gtcaagttaa gttccaaaca agtgaaagag attaatgctc 2160
agaagattgt tctcatcacc aagtagcctt gtctgatgct gtggagcctt agttgagatt 2220
tcagcatttc ctaccttggt cttagctttc agattatgga tgattaaatt tgatgactta 2280
tatgagggca gattcaagag ccagcaggtc aaaaaggcca acacaacat aagcagccag 2340
accacaagg ccaggtcctg tgctatcaca gggtcacctc ttttacagtt agaaacacca 2400
gccgaggcca cagaatccca tccctttcct gagtcatggc ctcaaaaatc agggccacca 2460
ttgtctcaat tcaaatccat agatttcgaa gccacagagc tcttccctgg agcagcagac 2520
tatgggcagc ccagtgtgct cacctgctga cgacccttga gaagctgcca tatcttcagg 2580
ccatgggttc accagccctg aaggcacctg tcaactggag tgctctctca gcaactggat 2640

```

```

gggcctgata gaagtgcatt ctcctcctat tgcctccatt ctcctctctc tatccctgaa 2700
atccaggaag tccctctcct ggtgctccaa gcagtttgaa gcccaatctg caaggacatt 2760
tctcaagggc catgtggttt tgcagacaac cctgtcctca ggcctgaact caccatagag 2820
acccatgtca gcaaacgggtg accagcaaat cctcttcctt tattctaaag ctgccccttg 2880
ggagactcca gggagaaggc attgcttcct ccttggtgtg aactctttct ttggtattcc 2940
atccactatc ctggcaactc aaggtgtctt ctgttaactg aagcctgctc cttcttggtc 3000
tggcctccag agatttgctc aaatgatcaa taagctttaa attaaaccgg aatccgcgga 3060
attc                                     3064

```

<210> 632

<211> 684

<212> PRT

<213> Homo sapiens

<400> 632

```

Met Met Asp Ala Ser Lys Glu Leu Gln Val Leu His Ile Asp Phe Leu
                    5                      10                      15

```

```

Asn Gln Asp Asn Ala Val Ser His His Thr Trp Glu Phe Gln Thr Ser
                20                      25                      30

```

```

Ser Pro Val Phe Arg Arg Gly Gln Val Phe His Leu Arg Leu Val Leu
        35                      40                      45

```

```

Asn Gln Pro Leu Gln Ser Tyr His Gln Leu Lys Leu Glu Phe Ser Thr
        50                      55                      60

```

```

Gly Pro Asn Pro Ser Ile Ala Lys His Thr Leu Val Val Leu Asp Pro
        65                      70                      75                      80

```

```

Arg Thr Pro Ser Asp His Tyr Asn Trp Gln Ala Thr Leu Gln Asn Glu
                85                      90                      95

```

```

Ser Gly Lys Glu Val Thr Val Ala Val Thr Ser Ser Pro Asn Ala Ile
        100                      105                      110

```

```

Leu Gly Lys Tyr Gln Leu Asn Val Lys Thr Gly Asn His Ile Leu Lys
        115                      120                      125

```

```

Ser Glu Glu Asn Ile Leu Tyr Leu Leu Phe Asn Pro Trp Cys Lys Glu
        130                      135                      140

```

```

Asp Met Val Phe Met Pro Asp Glu Asp Glu Arg Lys Glu Tyr Ile Leu
        145                      150                      155                      160

```

```

Asn Asp Thr Gly Cys His Tyr Val Gly Ala Ala Arg Ser Ile Lys Cys
        165                      170                      175

```

```

Lys Pro Trp Asn Phe Gly Gln Phe Glu Lys Asn Val Leu Asp Cys Cys
        180                      185                      190

```

```

Ile Ser Leu Leu Thr Glu Ser Ser Leu Lys Pro Thr Asp Arg Arg Asp
        195                      200                      205

```

```

Pro Val Leu Val Cys Arg Ala Met Cys Ala Met Met Ser Phe Glu Lys
        210                      215                      220

```

```

Gly Gln Gly Val Leu Ile Gly Asn Trp Thr Gly Asp Tyr Glu Gly Gly

```


225		230		235		240
Thr Ala Pro Tyr Lys Trp Thr Gly Ser Ala Pro Ile Leu Gln Gln Tyr	245	250	255			
Tyr Asn Thr Lys Gln Ala Val Cys Phe Gly Gln Cys Trp Val Phe Ala	260	265	270			
Gly Ile Leu Thr Thr Val Leu Arg Ala Leu Gly Ile Pro Ala Arg Ser	275	280	285			
Val Thr Gly Phe Asp Ser Ala His Asp Thr Glu Arg Asn Leu Thr Val	290	295	300			
Asp Thr Tyr Val Asn Glu Asn Gly Lys Lys Ile Thr Ser Met Thr His	305	310	315	320		
Asp Ser Val Trp Asn Phe His Val Trp Thr Asp Ala Trp Met Lys Arg	325	330	335			
Pro Asp Leu Pro Lys Gly Tyr Asp Gly Trp Gln Ala Val Asp Ala Thr	340	345	350			
Pro Gln Glu Arg Ser Gln Gly Val Phe Cys Cys Gly Pro Ser Pro Leu	355	360	365			
Thr Ala Ile Arg Lys Gly Asp Ile Phe Ile Val Tyr Asp Thr Arg Phe	370	375	380			
Val Phe Ser Glu Val Asn Gly Asp Arg Leu Ile Trp Leu Val Lys Met	385	390	395	400		
Val Asn Gly Gln Glu Glu Leu His Val Ile Ser Met Glu Thr Thr Ser	405	410	415			
Ile Gly Lys Asn Ile Ser Thr Lys Ala Val Gly Gln Asp Arg Arg Arg	420	425	430			
Asp Ile Thr Tyr Glu Tyr Lys Tyr Pro Glu Gly Ser Ser Glu Glu Arg	435	440	445			
Gln Val Met Asp His Ala Phe Leu Leu Leu Ser Ser Glu Arg Glu His	450	455	460			
Arg Arg Pro Val Lys Glu Asn Phe Leu His Met Ser Val Gln Ser Asp	465	470	475	480		
Asp Val Leu Leu Gly Asn Ser Val Asn Phe Thr Val Ile Leu Lys Arg	485	490	495			
Lys Thr Ala Ala Leu Gln Asn Val Asn Ile Leu Gly Ser Phe Glu Leu	500	505	510			
Gln Leu Tyr Thr Gly Lys Lys Met Ala Lys Leu Cys Asp Leu Asn Lys	515	520	525			
Thr Ser Gln Ile Gln Gly Gln Val Ser Glu Val Thr Leu Thr Leu Asp	530	535	540			

245

Ser Lys Thr Tyr Ile Asn Ser Leu Ala Ile Leu Asp Asp Glu Pro Val
 545 550 555 560
 Ile Arg Gly Phe Ile Ile Ala Glu Ile Val Glu Ser Lys Glu Ile Met
 565 570 575

Ala Ser Glu Val Phe Thr Ser Phe Gln Tyr Pro Glu Phe Ser Ile Glu
 580 585 590

Leu Pro Asn Thr Gly Arg Ile Gly Gln Leu Leu Val Cys Asn Cys Ile
 595 600 605

Phe Lys Asn Thr Leu Ala Ile Pro Leu Thr Asp Val Lys Phe Ser Leu
 610 615 620

Glu Ser Leu Gly Ile Ser Ser Leu Gln Thr Ser Asp His Gly Thr Val
 625 630 635 640

Gln Pro Gly Glu Thr Ile Gln Ser Gln Ile Lys Cys Thr Pro Ile Lys
 645 650 655

Thr Gly Pro Lys Lys Phe Ile Val Lys Leu Ser Ser Lys Gln Val Lys
 660 665 670

Glu Ile Asn Ala Gln Lys Ile Val Leu Ile Thr Lys
 675 680

<210> 633

<211> 679

<212> PRT

<213> Homo sapiens

<400> 633

Met Met Asp Ala Ser Lys Glu Leu Gln Val Leu His Ile Asp Phe Leu
 5 10 15

Asn Gln Asp Asn Ala Val Ser His His Thr Trp Glu Phe Gln Thr Ser
 20 25 30

Ser Pro Val Phe Arg Arg Gly Gln Val Phe His Leu Arg Leu Val Leu
 35 40 45

Asn Gln Pro Leu Gln Ser Tyr His Gln Leu Lys Leu Glu Phe Ser Thr
 50 55 60

Gly Pro Asn Pro Ser Ile Ala Lys His Thr Leu Val Val Leu Asp Pro
 65 70 75 80

Arg Thr Pro Ser Asp His Tyr Asn Trp Gln Ala Thr Leu Gln Asn Glu
 85 90 95

Ser Gly Lys Glu Val Thr Val Ala Val Thr Ser Ser Pro Asn Ala Ile
 100 105 110

Leu Gly Lys Tyr Gln Leu Asn Val Lys Thr Gly Asn His Ile Leu Lys
 115 120 125

Ser Glu Glu Asn Ile Leu Tyr Leu Leu Phe Asn Pro Trp Cys Lys Glu
 130 135 140
 Asp Met Val Phe Met Pro Asp Glu Asp Glu Arg Lys Glu Tyr Ile Leu
 145 150 155 160
 Asn Asp Thr Gly Cys His Tyr Val Gly Ala Ala Arg Ser Ile Lys Cys
 165 170 175
 Lys Pro Trp Asn Phe Gly Gln Phe Glu Lys Asn Val Leu Asp Cys Cys
 180 185 190
 Ile Ser Leu Leu Thr Glu Ser Ser Leu Lys Pro Thr Asp Arg Arg Asp
 195 200 205
 Pro Val Leu Val Cys Arg Ala Met Cys Ala Met Met Ser Phe Glu Lys
 210 215 220
 Gly Gln Gly Val Leu Ile Gly Asn Trp Thr Gly Asp Tyr Glu Gly Gly
 225 230 235 240
 Thr Ala Pro Tyr Lys Trp Thr Gly Ser Ala Pro Ile Leu Gln Gln Tyr
 245 250 255
 Tyr Asn Thr Lys Gln Ala Val Cys Phe Gly Gln Cys Trp Val Phe Ala
 260 265 270
 Gly Ile Leu Thr Thr Val Leu Arg Ala Leu Gly Ile Pro Ala Arg Ser
 275 280 285
 Val Thr Gly Phe Asp Ser Ala His Asp Thr Glu Arg Asn Leu Thr Val
 290 295 300
 Asp Thr Tyr Val Asn Glu Asn Gly Glu Lys Ile Thr Ser Met Thr His
 305 310 315 320
 Asp Ser Val Trp Asn Phe His Val Trp Thr Asp Ala Trp Met Lys Arg
 325 330 335
 Pro Tyr Asp Gly Trp Gln Ala Val Asp Ala Thr Pro Gln Glu Arg Ser
 340 345 350
 Gln Gly Val Phe Cys Cys Gly Pro Ser Pro Leu Thr Ala Ile Arg Lys
 355 360 365
 Gly Asp Ile Phe Ile Val Tyr Asp Thr Arg Phe Val Phe Ser Glu Val
 370 375 380
 Asn Gly Asp Arg Leu Ile Trp Leu Val Lys Met Val Asn Gly Gln Glu
 385 390 395 400
 Glu Leu His Val Ile Ser Met Glu Thr Thr Ser Ile Gly Lys Asn Ile
 405 410 415
 Ser Thr Lys Ala Val Gly Gln Asp Arg Arg Arg Asp Ile Thr Tyr Glu
 420 425 430
 Tyr Lys Tyr Pro Glu Gly Ser Ser Glu Glu Arg Gln Val Met Asp His

435	440	445
Ala Phe Leu Leu Leu Ser Ser Glu Arg Glu His Arg Gln Pro Val Lys 450 455 460		
Glu Asn Phe Leu His Met Ser Val Gln Ser Asp Asp Val Leu Leu Gly 465 470 475 480		
Asn Ser Val Asn Phe Thr Val Ile Leu Lys Arg Lys Thr Ala Ala Leu 485 490 495		
Gln Asn Val Asn Ile Leu Gly Ser Phe Glu Leu Gln Leu Tyr Thr Gly 500 505 510		
Lys Lys Met Ala Lys Leu Cys Asp Leu Asn Lys Thr Ser Gln Ile Gln 515 520 525		
Gly Gln Val Ser Glu Val Thr Leu Thr Leu Asp Ser Lys Thr Tyr Ile 530 535 540		
Asn Ser Leu Ala Ile Leu Asp Asp Glu Pro Val Ile Arg Gly Phe Ile 545 550 555 560		
Ile Ala Glu Ile Val Glu Ser Lys Glu Ile Met Ala Ser Glu Val Phe 565 570 575		
Thr Ser Asn Gln Tyr Pro Glu Phe Ser Ile Glu Leu Pro Asn Thr Gly 580 585 590		
Arg Ile Gly Gln Leu Leu Val Cys Asn Cys Ile Phe Lys Asn Thr Leu 595 600 605		
Ala Ile Pro Leu Thr Asp Val Lys Phe Ser Leu Glu Ser Leu Gly Ile 610 615 620		
Ser Ser Leu Gln Thr Ser Asp His Gly Thr Val Gln Pro Gly Glu Thr 625 630 635 640		
Ile Gln Ser Gln Ile Lys Cys Thr Pro Ile Lys Thr Gly Pro Lys Lys 645 650 655		
Phe Ile Val Lys Leu Ser Ser Lys Gln Val Lys Glu Ile Asn Ala Gln 660 665 670		
Lys Ile Val Leu Ile Thr Lys 675		

<210> 634

<211> 5668

<212> DNA

<213> Homo sapiens

<400> 634

gtcacttagg aaaaggtgtc ctttcgggca gccgggctca gcatgaggaa cagaaggaat 60
gacactctgg acagcaccgc gaccctgtac tccagcgctg ctcggagcac agacttgtct 120
tacagtgaag gcgacttggt gaattttatt caagcaaatt ttaagaaacg agaatgtgtc 180

ttctttacca	aagattccaa	ggccacggag	aatgtgtgca	agtgtggcta	tgcccagagc	240
cagcacatgg	aaggcaccca	gatcaaccaa	agtggagaaat	ggaactacaa	gaaacacacc	300
aaggaatttc	ctaccgacgc	ctttggggat	attcagtttg	agacactggg	gaagaaaggg	360
aagtatatac	gtctgtcctg	cgacacggac	gcggaaatcc	tttacgagct	gctgacccag	420
cactggcacc	tgaaaacacc	caacctggtc	atttctgtga	ccgggggcgc	caagaacttc	480
gccttgaagc	cgcgcatgcg	caagatcttc	agccggctca	tctacatcgc	gcagtcctaa	540
ggtgcttgga	ttctcacggg	aggcacccat	tatggcctga	cgaagtacat	cggggaggtg	600
gtgagagata	acaccatcag	caggagtcca	gaggagaata	ttgtggccat	tggcatagca	660
gcttggggca	tggtctccaa	ccgggacacc	ctcatcagga	attgcatgac	tgagggctat	720
tttttagccc	agtaccttat	ggtgacttc	acaagggatc	cactgtatat	cctggacaac	780
aaccacacac	atttgctgct	cgtggacaat	ggtgtcatg	gacatcccac	tgctgaagca	840
aagctccgga	atcagctaga	gaagcatatc	tctgagcgca	ctattcaaga	ttccaactat	900
ggtggcaaga	tccccattgt	gtgttttgcc	caaggaggtg	gaaaagagac	tttgaaagcc	960
atcaatacct	ccatcaaaaa	taaaattcct	tgtgtggtgg	tggaaggctc	gggcccagtc	1020
gctgatgtga	tcgctagcct	ggtggaggtg	gaggatgccc	cgacatcttc	tgccgtcaag	1080
gagaagctgg	tgcgcttttt	accccgcacg	gtgtcccggc	tgtctgagga	ggagactgag	1140
agtgggatca	aatggctcaa	agaaattctc	gaatgttctc	acctattaac	agttattaaa	1200
atggaagaag	ctggggatga	aattgtgagc	aatgccatct	cctacgctct	atacaaagcc	1260
ttcagcacca	gtgagcaaga	caaggataac	tggaaatggg	agctgaagct	tctgctggag	1320
tggaaaccagc	tggacttagc	caatgatgag	attttcacca	atgaccgccg	atgggagctc	1380
gctgaccttc	aagaagtcac	gtttacggct	ctcataaagg	acagacccaa	gtttgtccgc	1440
ctctttcttg	agaatggctt	gaacctacgg	aagtttctca	cccatgatgt	cctcactgaa	1500
ctcttctcca	accacttcag	cacgcttggt	taccggaatc	tgcatatcgc	caagaattcc	1560
tataatgatg	ccctcctcac	gtttgtctgg	aaactgggtg	cgaacttccg	aagaggcttc	1620
cggaaggaag	acagaaatgg	ccgggacgag	atggacatag	aactccacga	cgtgtctcct	1680
attactcggc	accccctgca	agctctcttc	atctggggcca	ttcttcagaa	taagaaggaa	1740
ctctccaaag	tcattttgga	gcagaccagg	ggctgcactc	tggcagccct	gggagccagc	1800
aagcttctga	agactctggc	caaagtgaag	aacgacatca	atgctgctgg	ggagtccgag	1860
gagctggcta	atgagtacga	gaccgggct	gttgagctgt	tactgagtg	ttacagcagc	1920
gatgaagact	tggcagaaca	gctgctggtc	tattcctgtg	aagcttgggg	tggaaagcaac	1980
tgtctggagc	tggcgggtga	ggccacagac	cagcatttca	ccgcccagcc	tggggtccag	2040
aattttcttt	ctaagcaatg	gtatggagag	atttcccag	acaccaagaa	ctggaagatt	2100
atcctgtgtc	tgtttattat	acccttggtg	ggctgtggct	ttgtatcatt	taggaagaaa	2160
cctgtcgaca	agcacaagaa	gctgcttttg	tactatgtgg	cgttcttcac	ctcccccttc	2220
gtggtcttct	cctggaatgt	ggtcttctac	atcgcttcc	tcctgctgtt	tgccctacgtg	2280
ctgtccatgg	atttccattc	ggtgccacac	ccccccgagc	tggtcctgta	ctcgtgtggtc	2340
tttgcctctc	tctgtgatga	agtgaagacg	tggtagctaa	atggggtgaa	ttatttttact	2400
gacctgtgga	atgtgatgga	cacgctgggg	cttttttact	tcatagcagg	aattgtattt	2460
cggctccact	cttctaataa	aagctctttg	tattctggac	gagtcatttt	ctgtctggac	2520
tacattattt	tactctaaag	attgatccac	atttttactg	taagcagaaa	cttaggaccc	2580
aagattataa	tgctcgagag	gatgtgatc	gatgtgttct	tcttctgtgt	cctctttgag	2640
gtgtggatgg	tggccttttg	cgtggccagg	caagggatcc	ttaggcagaa	tgagcagcgc	2700
tggaggtgga	tattccgttc	ggtcatctac	gagccctacc	tggccatgtt	cggccagggtg	2760
cccagtgaag	tggatggtac	cacgtatgac	tttgccact	gcaccttcac	tgggaatgag	2820
tccaagccac	tgtgtgtgga	gctggatgag	cacaacctgc	cccggttccc	cgagtggatc	2880
accatcccc	tgggtgtcat	ctacatgtta	tccaccaaca	tcctgctggt	caacctgctg	2940
gtcgccatgt	ttggctacac	ggtgggcacc	gtccaggaga	acaatgacca	ggtctggaag	3000
ttccagaggt	acttctggt	gcaggagtac	tgacgcccgc	tcaatatccc	cttccccctc	3060
atcgtcttcg	cttacttcta	catggtgggt	aagaagtgtc	tcaagtgttg	ctgcaaggag	3120
aaaaacatgg	agtcttctgt	ctgctgtttc	aaaaatgaag	acaatgagac	tctggcatgg	3180
gaggtgtgca	tgaaggaaaa	ctacctgtgc	aagatcaaca	caaaagccaa	cgacacctca	3240
gaggaatga	ggcatcgatt	tagacaactg	gatacaaaagc	ttaatgatct	caagggtctt	3300
ctgaaagaga	ttgctaataa	aatcaataa	aactgtatga	aactctaag	gagaaaaatc	3360
taattatagc	aagatcatat	taaggaatgc	tgatgaacaa	ttttgctatc	gactactaaa	3420
tgagagattt	tcagaccctt	gggtacatgg	tggatgattt	taaatcacc	tagtgtgctg	3480
agaccttgag	aataaagtgt	gtgattgggt	tcatacttga	agacggatat	aaaggaagaa	3540
tatttctctt	atgtgtttct	ccagaatggt	gcctgtttct	ctctgtgtct	caatgcctgg	3600
gactggaggt	tgatagttta	agtgtgttct	taccgcctcc	tttttctttt	aatcttattt	3660

```

ttgatgaaca catatatagg agaacatcta tcctatgaat aagaacctgg tcatgcttta 3720
ctcctgtatt gttattttgt tcattttccaa ttgattctct acttttccct tttttgtatt 3780
atgtgactaa ttagttggca tattgttaaa agtctctcaa attaggccag attctaaaac 3840
atgctgcagc aagaggaccc cgctctcttc aggaaaagtg ttttcatttc tcaggatgct 3900
tcttacctgt cagaggagggt gacaaggcag tctcttgctc tcttggaactc accaggctcc 3960
tattgaagga accaccccca ttcctaaata tgtgaaaagt cgcccaaaat gcaaccttga 4020
aaggcactac tgactttgtt cttattggat actcctctta tttattattt ttccattaaa 4080
aataatagct ggctattata gaaaatttag accatacaga gatgtagaaa gaacataaat 4140
tgtccccatt accttaagggt aatcactgct aacaatttct ggatgggttt tcaagtctat 4200
tttttttcta tgtatgtctc aattctcttt caaaatttta cagaatgta tcatactaca 4260
tatatacttt ttatgtaagc tttttcactt agtattttat caaatatgtt tttattatat 4320
tcatagcctt cttaaacatt atatcaataa ttgcataata ggcaacctct agcgattacc 4380
ataattttgc tcattgaagg ctatctccag ttgatcattg ggatgagcat ctttgtgcat 4440
gaatcctatt gctgtatttg ggaaaatttt ccaagggttag attccaataa atatctattt 4500
attattaaat attaaaatat cgatttatta ttaaaacat ttataaggct ttttcataaa 4560
tgtatagcaa ataggaatta ttaacttgag cataagatat gagatacatg aacctgaact 4620
attaaaataa aatattatat ttaaccctag ttaagaaga agtcaatatg cttattttaa 4680
tattatggat ggtgggcaga tcacttgagg tcaggagttc gagaccagcc tggccaacat 4740
ggcaaaacca catctctact aaaaaataaa aaattagctg ggtgtggtgg tgcactcctg 4800
taatcccagc tactcagaag gctgaggtag aagaattgct ggaacctggg aggcggaggt 4860
tgcatggaac caagattgca ccactgcact ccagccgggg tgacagagtg agactccgac 4920
tgaaaataaa taaataaata aataaataaa taaataaata aatattatgg atggtgaagg 4980
gaatggtata gaattggaga gattatctta ctgaacacct gtagtcccag ctttctctgg 5040
aagtgtggtt atttgagcag gatgtgcaca aggcaattga aatgccata attagtttct 5100
cagctttgaa tacaactataa actcagtggc tgaaggagga aatttttagaa ggaagctact 5160
aaaagatcta atttgaaaaa ctacaaaagc attaaactaa aaagtttatt ttccttttgt 5220
ctgggcagta gtgaaaataa ctactcaca cattcactat gtttgcaagg aattaacaca 5280
aataaaaagat gcctttttac ttaaacgcca agacagaaaaa cttgcccaat actgagaagc 5340
aacttgcat agagagggaa ctgttaaatg ttttcaacc agttcatctg gtggatgttt 5400
ttgcaggtta ctctgagaat tttgcttatg aaaaatcatt atttttagtg tagttcaca 5460
taatgtattg aacatacttc taatcaaagg tgctatgtcc ttgtgtatgg tactaaatgt 5520
gtcctgtgta cttttgcaca actgagaatc ctgcggcttg gtttaatgag tgtgttcatt 5580
aaataaataa tggaggaatt gtcaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 5640
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 5668

```

<210> 635

<211> 1095

<212> PRT

<213> Homo sapiens

<400> 635

```

Met Arg Asn Arg Arg Asn Asp Thr Leu Asp Ser Thr Arg Thr Leu Tyr
          5                      10                      15

```

```

Ser Ser Ala Ser Arg Ser Thr Asp Leu Ser Tyr Ser Glu Ser Asp Leu
          20                      25                      30

```

```

Val Asn Phe Ile Gln Ala Asn Phe Lys Lys Arg Glu Cys Val Phe Phe
          35                      40                      45

```

```

Thr Lys Asp Ser Lys Ala Thr Glu Asn Val Cys Lys Cys Gly Tyr Ala
          50                      55                      60

```

```

Gln Ser Gln His Met Glu Gly Thr Gln Ile Asn Gln Ser Glu Lys Trp
          65                      70                      75                      80

```

```

Asn Tyr Lys Lys His Thr Lys Glu Phe Pro Thr Asp Ala Phe Gly Asp
          85                      90                      95

```

Ile Gln Phe Glu Thr Leu Gly Lys Lys Gly Lys Tyr Ile Arg Leu Ser
 100 105 110
 Cys Asp Thr Asp Ala Glu Ile Leu Tyr Glu Leu Leu Thr Gln His Trp
 115 120 125
 His Leu Lys Thr Pro Asn Leu Val Ile Ser Val Thr Gly Gly Ala Lys
 130 135 140
 Asn Phe Ala Leu Lys Pro Arg Met Arg Lys Ile Phe Ser Arg Leu Ile
 145 150 155 160
 Tyr Ile Ala Gln Ser Lys Gly Ala Trp Ile Leu Thr Gly Gly Thr His
 165 170 175
 Tyr Gly Leu Thr Lys Tyr Ile Gly Glu Val Val Arg Asp Asn Thr Ile
 180 185 190
 Ser Arg Ser Ser Glu Glu Asn Ile Val Ala Ile Gly Ile Ala Ala Trp
 195 200 205
 Gly Met Val Ser Asn Arg Asp Thr Leu Ile Arg Asn Cys Asp Ala Glu
 210 215 220
 Gly Tyr Phe Leu Ala Gln Tyr Leu Met Asp Asp Phe Thr Arg Asp Pro
 225 230 235 240
 Leu Tyr Ile Leu Asp Asn Asn His Thr His Leu Leu Leu Val Asp Asn
 245 250 255
 Gly Cys His Gly His Pro Thr Val Glu Ala Lys Leu Arg Asn Gln Leu
 260 265 270
 Glu Lys His Ile Ser Glu Arg Thr Ile Gln Asp Ser Asn Tyr Gly Gly
 275 280 285
 Lys Ile Pro Ile Val Cys Phe Ala Gln Gly Gly Gly Lys Glu Thr Leu
 290 295 300
 Lys Ala Ile Asn Thr Ser Ile Lys Asn Lys Ile Pro Cys Val Val Val
 305 310 315 320
 Glu Gly Ser Gly Arg Ile Ala Asp Val Ile Ala Ser Leu Val Glu Val
 325 330 335
 Glu Asp Ala Pro Thr Ser Ser Ala Val Lys Glu Lys Leu Val Arg Phe
 340 345 350
 Leu Pro Arg Thr Val Ser Arg Leu Ser Glu Glu Glu Thr Glu Ser Trp
 355 360 365
 Ile Lys Trp Leu Lys Glu Ile Leu Glu Cys Ser His Leu Leu Thr Val
 370 375 380
 Ile Lys Met Glu Glu Ala Gly Asp Glu Ile Val Ser Asn Ala Ile Ser
 385 390 395 400

Tyr Ala Leu Tyr Lys Ala Phe Ser Thr Ser Glu Gln Asp Lys Asp Asn
 405 410 415
 Trp Asn Gly Gln Leu Lys Leu Leu Leu Glu Trp Asn Gln Leu Asp Leu
 420 425 430
 Ala Asn Asp Glu Ile Phe Thr Asn Asp Arg Arg Trp Glu Ser Ala Asp
 435 440 445
 Leu Gln Glu Val Met Phe Thr Ala Leu Ile Lys¹ Asp Arg Pro Lys Phe
 450 455 460
 Val Arg Leu Phe Leu Glu Asn Gly Leu Asn Leu Arg Lys Phe Leu Thr
 465 470 475 480
 His Asp Val Leu Thr Glu Leu Phe Ser Asn His Phe Ser Thr Leu Val
 485 490 495
 Tyr Arg Asn Leu Gln Ile Ala Lys Asn Ser Tyr Asn Asp Ala Leu Leu
 500 505 510
 Thr Phe Val Trp Lys Leu Val Ala Asn Phe Arg Arg Gly Phe Arg Lys
 515 520 525
 Glu Asp Arg Asn Gly Arg Asp Glu Met Asp Ile Glu Leu His Asp Val
 530 535 540
 Ser Pro Ile Thr Arg His Pro Leu Gln Ala Leu Phe Ile Trp Ala Ile
 545 550 555 560
 Leu Gln Asn Lys Lys Glu Leu Ser Lys Val Ile Trp Glu Gln Thr Arg
 565 570 575
 Gly Cys Thr Leu Ala Ala Leu Gly Ala Ser Lys Leu Leu Lys Thr Leu
 580 585 590
 Ala Lys Val Lys Asn Asp Ile Asn Ala Ala Gly Glu Ser Glu Glu Leu
 595 600 605
 Ala Asn Glu Tyr Glu Thr Arg Ala Val Glu Leu Phe Thr Glu Cys Tyr
 610 615 620
 Ser Ser Asp Glu Asp Leu Ala Glu Gln Leu Leu Val Tyr Ser Cys Glu
 625 630 635 640
 Ala Trp Gly Gly Ser Asn Cys Leu Glu Leu Ala Val Glu Ala Thr Asp
 645 650 655
 Gln His Phe Thr Ala Gln Pro Gly Val Gln Asn Phe Leu Ser Lys Gln
 660 665 670
 Trp Tyr Gly Glu Ile Ser Arg Asp Thr Lys Asn Trp Lys Ile Ile Leu
 675 680 685
 Cys Leu Phe Ile Ile Pro Leu Val Gly Cys Gly Phe Val Ser Phe Arg
 690 695 700
 Lys Lys Pro Val Asp Lys His Lys Lys Leu Leu Trp Tyr Tyr Val Ala

705		710		715		720
Phe Phe Thr Ser	Pro Phe Val Val Phe	Ser Trp Asn Val Val	Phe Tyr			
	725	730	735			
Ile Ala Phe Leu	Leu Leu Phe Ala Tyr	Val Leu Leu Met Asp	Phe His			
	740	745	750			
Ser Val Pro His	Pro Pro Glu Leu Val	Leu Tyr Ser Leu Val	Phe Val			
	755	760	765			
Leu Phe Cys Asp	Glu Val Arg Gln Trp Tyr	Val Asn Gly Val Asn Tyr				
	770	775	780			
Phe Thr Asp Leu	Trp Asn Val Met Asp Thr	Leu Gly Leu Phe Tyr	Phe			
	785	790	795	800		
Ile Ala Gly Ile	Val Phe Arg Leu His	Ser Ser Asn Lys Ser	Ser Leu			
	805	810	815			
Tyr Ser Gly Arg	Val Ile Phe Cys Leu Asp	Tyr Ile Ile Phe Thr	Leu			
	820	825	830			
Arg Leu Ile His	Ile Phe Thr Val Ser Arg	Asn Leu Gly Pro Lys Ile				
	835	840	845			
Ile Met Leu Gln	Arg Met Leu Ile Asp Val	Phe Phe Phe Leu Phe Leu				
	850	855	860			
Phe Ala Val Trp	Met Val Ala Phe Gly Val	Ala Arg Gln Gly Ile Leu				
	865	870	875	880		
Arg Gln Asn Glu	Gln Arg Trp Arg Trp Ile	Phe Arg Ser Val Ile Tyr				
	885	890	895			
Glu Pro Tyr Leu	Ala Met Phe Gly Gln Val	Pro Ser Asp Val Asp Gly				
	900	905	910			
Thr Thr Tyr Asp	Phe Ala His Cys Thr Phe Thr	Gly Asn Glu Ser Lys				
	915	920	925			
Pro Leu Cys Val	Glu Leu Asp Glu His Asn Leu	Pro Arg Phe Pro Glu				
	930	935	940			
Trp Ile Thr Ile	Pro Leu Val Cys Ile Tyr Met	Leu Ser Thr Asn Ile				
	945	950	955	960		
Leu Leu Val Asn	Leu Leu Val Ala Met Phe Gly	Tyr Thr Val Gly Thr				
	965	970	975			
Val Gln Glu Asn	Asn Asp Gln Val Trp Lys Phe Gln	Arg Tyr Phe Leu				
	980	985	990			
Val Gln Glu Tyr	Cys Ser Arg Leu Asn Ile Pro Phe	Pro Phe Ile Val				
	995	1000	1005			
Phe Ala Tyr Phe	Tyr Met Val Val Lys Lys Cys	Phe Lys Cys Cys Cys				
	1010	1015	1020			

Lys Glu Lys Asn Met Glu Ser Ser Val Cys Cys Phe Lys Asn Glu Asp
 1025 1030 1035 1040
 Asn Glu Thr Leu Ala Trp Glu Gly Val Met Lys Glu Asn Tyr Leu Val
 1045 1050 1055
 Lys Ile Asn Thr Lys Ala Asn Asp Thr Ser Glu Glu Met Arg His Arg
 1060 1065 1070
 Phe Arg Gln Leu Asp Thr Lys Leu Asn Asp Leu Lys Gly Leu Leu Lys
 1075 1080 1085
 Glu Ile Ala Asn Lys Ile Lys
 1090 1095

<210> 636
 <211> 3639
 <212> DNA
 <213> Homo sapiens

<400> 636
 gattacgcaa gctatatttagg tgacactata gaatwctcag cttgcatcaa gcttgggtacc 60
 gagctcggat ccctagtaac ggccgccagt gtgctggaat tcgcccttgc agccggggctc 120
 agcatgagga acagaaggaa tgacactctg gacagcacc ggaccctgta ctccagcgcg 180
 tctcggagca cagacttgct ttacagtga agcgacttgg tgaattttat tcaagcaaat 240
 ttttaagaaac gagaatgtgt cttctttacc aaagattcca aggccacgga gaatgtgtgc 300
 aagtgtggct atgccagag ccagcacatg gaaggcacc agatcaacca aagtgagaaa 360
 tggaaactaca agaaacacac caagggaattt cctaccgacg cctttgggga tattcagttt 420
 gagacactgg ggaagaaagg gaagtatata cgtctgtcct gcgacacgga cgcggaaatc 480
 ctttacgagc tgctgaccca gcaactggcac ctgaaaacac ccaacctggt catttctgtg 540
 accggggggcg ccaagaactt cgccctgaag ccgcgcacgc gcaagatctt cagccgggctc 600
 atctacatcg cgcagctcaa aggtgcttgg attctcacgg gaggcaccca ttatggcctc 660
 atgaagtaca tcggggaggt ggtgagagat aacacccatca gcaggagttc agaggagaat 720
 attgtggcca ttggcatagc agcttggggc atgggtotcca accgggacac cctcatcagg 780
 aattgcatg ctgaggggcta ttttttagcc cagtacctta tggatgactt cacaagagat 840
 ccaactgtata tcttggaaca caaccacaca catttgctgc tcgtggacaa tggctgtcat 900
 ggacatccca ctgtcgaagc aaagctccgg aatcagctag agaagtatat ctctgagcgc 960
 actattcaag attccaacta tgggtggcaag atccccattg tgtgttttgc ccaaggaggt 1020
 ggaaaagaga ctttgaaagc catcaatacc tccatcaaaa ataaaattcc ttgtgtggtg 1080
 gtggaaggct cgggccagat cgctgatgtg atcgctagcc tgggtggaggt ggaggatgcc 1140
 ctgacatctt ctgccgtcaa ggagaagctg gtgcgctttt taccgccgac ggtgtcccg 1200
 ctgcctgagg aggagactga gagttggatc aaatggctca aagaaattct cgaatgttct 1260
 cacctattaa cagttattaa aatggaagaa gctggggatg aaattgtgag caatgccatc 1320
 tcctacgctc tatacaaagc cttcagcacc agtgagcaag acaaggataa ctggaatggg 1380
 cagctgaagc ttctgctgga gtggaaccag ctggacttag ccaatgatga gattttcacc 1440
 aatgaccgcc gatgggagtc tgctgacctt caagaagtca tgtttacggc tctcataaag 1500
 gacagaccga agtttgcgc cctctttctc gagaatggct tgaacctacg gaagtttctc 1560
 acccatgatg tctcactga actcttctcc aaccacttca gcacgcttgt gtaccggaat 1620
 ctgcagatcg ccaagaattc ctataatgat gccctctca cgtttgtctg gaaactggtt 1680
 gcgaacttcc gaagaggctt ccggaaggaa gacagaaatg gccgggacga gatggacata 1740
 gaactccacg acgtgtctcc tattactcgg caccctctgc aagctctctt catctgggcc 1800
 attcttcaga ataagaagga actctccaaa gtcatttggg agcagaccag gggctgcact 1860
 ctggcagccc tgggagccag caagcttctg aagactctgg ccaaagtga gaacgacatc 1920
 aatgctgtcg gggagtccga ggagctggct aatgagtacg agaccgggc tgttgagctg 1980
 ttacttgagt gttacagcag cgatgaagac ttggcagaac agetgctggt ctattcctgt 2040

```

gaagcttggg gtggaagcaa ctgtctggag ctggcggtgg aggccacaga ccagcatttc 2100
atcgcccagc ctggggtcca gaattttctt tctaagcaat ggtatggaga gatttcccga 2160
gacaccaaga actggaagat tatcctgtgt ctgtttatta tacccttggg gggctgtggc 2220
tttgtatcat ttaggaagaa acctgtcgac aagcacaaga agctgctttg gtactatgtg 2280
gcgttcttca cctccccctt cgtggtcttc tcctggaatg tggcttcta catcgccctc 2340
ctcctgctgt ttgcctacgt gctgctcatg gatttccatt cggtgccaca cccccccgag 2400
ctggctctgt actcgctggg ctttgcctc ttctgtgatg aagttagaca gtggtacgta 2460
aatggggtga attattttac tgacctgtgg aatgtgatgg acacgctggg gcttttttac 2520
ttcatagcag gaattgtatt tcggctccac tcttctaata aaagctcttt gtattctgga 2580
cgagtcattt tctgtctgga ctacattatt ttcactctaa gattgatcca catttttact 2640
gtaagcagaa acttaggacc caagattata atgctgcaga ggatgctgat cgatgtgttc 2700
ttcttctgt tctcttttgc gwggtggatg gtggcctttg gcgtggccag gcaagggatc 2760
cttaggcaga atgagcagcg ctggagggtg atattccgtt cggatcatcta cgagccctac 2820
ctggccatgt tcggccaggg gccacgtgac gtggatggta ccacgtatga ctttgccac 2880
tgcaccttca ctgggaatga gtccaagcca ctgtgtgtgg agctggatga gcacaacctg 2940
ccccggttcc ccgagtggat caccatcccc ctggtgtgca tctacatgtt atccaccaac 3000
atcctgctgg tcaacctgct ggtcgccatg tttggctaca cggtgggcac cgtccaggag 3060
aacaatgacc aggtctggaa gttccagagg tacttctctg tgcaggagta ctgcagccgc 3120
ctcaatatcc ccttcccctt catcgtcttc gcttacttct acatgggtggg gaagaagtgc 3180
ttcaagtgtt gctgcaagga gaaaaacatg gactcttctg tctgctgttt caaaaatgaa 3240
gacaatgaga ctctggcatg ggagggtgtc atgaaggaaa actaccttgt caagatcaac 3300
acaaaagcca acgacacctc agaggaaatg aggcacgat ttagacaact ggatacaag 3360
cttaatgata tcaagggtct tctgaaagag attgctaata aaatcaaata aaactgtatg 3420
aactctaata gagaaaaatc taattatagc aagatcatat taaggaaatgc tgatgaacaa 3480
ttttgctatc gactactaaa tgagagattt tcagaccctt gggatcatgg tggatgattt 3540
taaatacccc tagtgtgctg agaccttgag aataaagtgt gaaggcgcaa ttctgcagat 3600
atccatcaca ctggcgccg ctcgagcatg catctagag 3639

```

<210> 637

<211> 1095

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)...(1095)

<223> Xaa = Any Amino Acid

<400> 637

```

Met Arg Asn Arg Arg Asn Asp Thr Leu Asp Ser Thr Arg Thr Leu Tyr
          5              10              15

```

```

Ser Ser Ala Ser Arg Ser Thr Asp Leu Ser Tyr Ser Glu Ser Asp Leu
          20              25              30

```

```

Val Asn Phe Ile Gln Ala Asn Phe Lys Lys Arg Glu Cys Val Phe Phe
          35              40              45

```

```

Thr Lys Asp Ser Lys Ala Thr Glu Asn Val Cys Lys Cys Gly Tyr Ala
          50              55              60

```

```

Gln Ser Gln His Met Glu Gly Thr Gln Ile Asn Gln Ser Glu Lys Trp
          65              70              75              80

```

```

Asn Tyr Lys Lys His Thr Lys Glu Phe Pro Thr Asp Ala Phe Gly Asp
          85              90              95

```

```

Ile Gln Phe Glu Thr Leu Gly Lys Lys Gly Lys Tyr Ile Arg Leu Ser

```

255

100	105	110
Cys Asp Thr Asp Ala Glu Ile Leu Tyr Glu Leu Leu Thr Gln His Trp 115 120 125		
His Leu Lys Thr Pro Asn Leu Val Ile Ser Val Thr Gly Gly Ala Lys 130 135 140		
Asn Phe Ala Leu Lys Pro Arg Met Arg Lys Ile Phe Ser Arg Leu Ile 145 150 155 160		
Tyr Ile Ala Gln Ser Lys Gly Ala Trp Ile Leu Thr Gly Gly Thr His 165 170 175		
Tyr Gly Leu Met Lys Tyr Ile Gly Glu Val Val Arg Asp Asn Thr Ile 180 185 190		
Ser Arg Ser Ser Glu Glu Asn Ile Val Ala Ile Gly Ile Ala Ala Trp 195 200 205		
Gly Met Val Ser Asn Arg Asp Thr Leu Ile Arg Asn Cys Asp Ala Glu 210 215 220		
Gly Tyr Phe Leu Ala Gln Tyr Leu Met Asp Asp Phe Thr Arg Asp Pro 225 230 235 240		
Leu Tyr Ile Leu Asp Asn Asn His Thr His Leu Leu Leu Val Asp Asn 245 250 255		
Gly Cys His Gly His Pro Thr Val Glu Ala Lys Leu Arg Asn Gln Leu 260 265 270		
Glu Lys Tyr Ile Ser Glu Arg Thr Ile Gln Asp Ser Asn Tyr Gly Gly 275 280 285		
Lys Ile Pro Ile Val Cys Phe Ala Gln Gly Gly Gly Lys Glu Thr Leu 290 295 300		
Lys Ala Ile Asn Thr Ser Ile Lys Asn Lys Ile Pro Cys Val Val Val 305 310 315 320		
Glu Gly Ser Gly Gln Ile Ala Asp Val Ile Ala Ser Leu Val Glu Val 325 330 335		
Glu Asp Ala Leu Thr Ser Ser Ala Val Lys Glu Lys Leu Val Arg Phe 340 345 350		
Leu Pro Arg Thr Val Ser Arg Leu Pro Glu Glu Glu Thr Glu Ser Trp 355 360 365		
Ile Lys Trp Leu Lys Glu Ile Leu Glu Cys Ser His Leu Leu Thr Val 370 375 380		
Ile Lys Met Glu Glu Ala Gly Asp Glu Ile Val Ser Asn Ala Ile Ser 385 390 395 400		
Tyr Ala Leu Tyr Lys Ala Phe Ser Thr Ser Glu Gln Asp Lys Asp Asn 405 410 415		

Trp Asn Gly Gln Leu Lys Leu Leu Leu Glu Trp Asn Gln Leu Asp Leu
 420 425 430
 Ala Asn Asp Glu Ile Phe Thr Asn Asp Arg Arg Trp Glu Ser Ala Asp
 435 440 445
 Leu Gln Glu Val Met Phe Thr Ala Leu Ile Lys Asp Arg Pro Lys Phe
 450 455 460
 Val Arg Leu Phe Leu Glu Asn Gly Leu Asn Leu Arg Lys Phe Leu Thr
 465 470 475 480
 His Asp Val Leu Thr Glu Leu Phe Ser Asn His Phe Ser Thr Leu Val
 485 490 495
 Tyr Arg Asn Leu Gln Ile Ala Lys Asn Ser Tyr Asn Asp Ala Leu Leu
 500 505 510
 Thr Phe Val Trp Lys Leu Val Ala Asn Phe Arg Arg Gly Phe Arg Lys
 515 520 525
 Glu Asp Arg Asn Gly Arg Asp Glu Met Asp Ile Glu Leu His Asp Val
 530 535 540
 Ser Pro Ile Thr Arg His Pro Leu Gln Ala Leu Phe Ile Trp Ala Ile
 545 550 555 560
 Leu Gln Asn Lys Lys Glu Leu Ser Lys Val Ile Trp Glu Gln Thr Arg
 565 570 575
 Gly Cys Thr Leu Ala Ala Leu Gly Ala Ser Lys Leu Leu Lys Thr Leu
 580 585 590
 Ala Lys Val Lys Asn Asp Ile Asn Ala Ala Gly Glu Ser Glu Glu Leu
 595 600 605
 Ala Asn Glu Tyr Glu Thr Arg Ala Val Glu Leu Phe Thr Glu Cys Tyr
 610 615 620
 Ser Ser Asp Glu Asp Leu Ala Glu Gln Leu Leu Val Tyr Ser Cys Glu
 625 630 635 640
 Ala Trp Gly Gly Ser Asn Cys Leu Glu Leu Ala Val Glu Ala Thr Asp
 645 650 655
 Gln His Phe Ile Ala Gln Pro Gly Val Gln Asn Phe Leu Ser Lys Gln
 660 665 670
 Trp Tyr Gly Glu Ile Ser Arg Asp Thr Lys Asn Trp Lys Ile Ile Leu
 675 680 685
 Cys Leu Phe Ile Ile Pro Leu Val Gly Cys Gly Phe Val Ser Phe Arg
 690 695 700
 Lys Lys Pro Val Asp Lys His Lys Lys Leu Leu Trp Tyr Tyr Val Ala
 705 710 715 720

Phe Phe Thr Ser Pro Phe Val Val Phe Ser Trp Asn Val Val Phe Tyr
 725 730 735
 Ile Ala Phe Leu Leu Leu Phe Ala Tyr Val Leu Leu Met Asp Phe His
 740 745 750
 Ser Val Pro His Pro Pro Glu Leu Val Leu Tyr Ser Leu Val Phe Val
 755 760 765
 Leu Phe Cys Asp Glu Val Arg Gln Trp Tyr Val Asn Gly Val Asn Tyr
 770 775 780
 Phe Thr Asp Leu Trp Asn Val Met Asp Thr Leu Gly Leu Phe Tyr Phe
 785 790 795 800
 Ile Ala Gly Ile Val Phe Arg Leu His Ser Ser Asn Lys Ser Ser Leu
 805 810 815
 Tyr Ser Gly Arg Val Ile Phe Cys Leu Asp Tyr Ile Ile Phe Thr Leu
 820 825 830
 Arg Leu Ile His Ile Phe Thr Val Ser Arg Asn Leu Gly Pro Lys Ile
 835 840 845
 Ile Met Leu Gln Arg Met Leu Ile Asp Val Phe Phe Phe Leu Phe Leu
 850 855 860
 Phe Ala Xaa Trp Met Val Ala Phe Gly Val Ala Arg Gln Gly Ile Leu
 865 870 875 880
 Arg Gln Asn Glu Gln Arg Trp Arg Trp Ile Phe Arg Ser Val Ile Tyr
 885 890 895
 Glu Pro Tyr Leu Ala Met Phe Gly Gln Val Pro Ser Asp Val Asp Gly
 900 905 910
 Thr Thr Tyr Asp Phe Ala His Cys Thr Phe Thr Gly Asn Glu Ser Lys
 915 920 925
 Pro Leu Cys Val Glu Leu Asp Glu His Asn Leu Pro Arg Phe Pro Glu
 930 935 940
 Trp Ile Thr Ile Pro Leu Val Cys Ile Tyr Met Leu Ser Thr Asn Ile
 945 950 955 960
 Leu Leu Val Asn Leu Leu Val Ala Met Phe Gly Tyr Thr Val Gly Thr
 965 970 975
 Val Gln Glu Asn Asn Asp Gln Val Trp Lys Phe Gln Arg Tyr Phe Leu
 980 985 990
 Val Gln Glu Tyr Cys Ser Arg Leu Asn Ile Pro Phe Pro Phe Ile Val
 995 1000 1005
 Phe Ala Tyr Phe Tyr Met Val Val Lys Lys Cys Phe Lys Cys Cys Cys
 1010 1015 1020
 Lys Glu Lys Asn Met Glu Ser Ser Val Cys Cys Phe Lys Asn Glu Asp

1025	1030	1035	1040
Asn Glu Thr Leu Ala Trp Glu Gly Val Met Lys Glu Asn Tyr Leu Val			
1045	1050	1055	
Lys Ile Asn Thr Lys Ala Asn Asp Thr Ser Glu Glu Met Arg His Arg			
1060	1065	1070	
Phe Arg Gln Leu Asp Thr Lys Leu Asn Asp Leu Lys Gly Leu Leu Lys			
1075	1080	1085	
Glu Ile Ala Asn Lys Ile Lys			
1090	1095		

<210> 638
 <211> 15
 <212> PRT
 <213> Homo sapiens

<400> 638
 Arg Met Pro Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser
 5 10 15

<210> 639
 <211> 45
 <212> DNA
 <213> Homo sapiens

<400> 639
 agaatgccta ccgtgctgca gtgcgtgaac gtgtcggtagg tgtct 45

<210> 640
 <211> 45
 <212> DNA
 <213> Homo sapiens

<400> 640
 gagccaggga gccagatggt ggaggccagc ctctccgtac ggcac 45

<210> 641
 <211> 45
 <212> DNA
 <213> Homo sapiens

<400> 641
 gaggccgacc aagagccagg gagccagatg gtggaggcca gcctc 45

<210> 642
 <211> 45
 <212> DNA
 <213> Homo sapiens

<400> 642
 ggctgcaca gtcttgaggc cgaccaagag ccaggaggacc agatg 45

<210> 643
<211> 45
<212> DNA
<213> Homo sapiens

<400> 643
tacaccatcg ggctgggcct gcacagtctt gaggccgacc aagag

45

<210> 644
<211> 42
<212> DNA
<213> Homo sapiens

<400> 644
ttccagaact cctacaccat cgggctgggc ctgcacagtc tt

42

<210> 645
<211> 45
<212> DNA
<213> Homo sapiens

<400> 645
ctgtcagccg cacactgttt ccagaactcc tacaccatcg ggctg

45

<210> 646
<211> 45
<212> DNA
<213> Homo sapiens

<400> 646
catccgcagt ggggtgctgtc agccgcacac tgtttccaga actcc

45

<210> 647
<211> 45
<212> DNA
<213> Homo sapiens

<400> 647
tcgggcgtcc tgggtgcatcc gcagtgggtg ctgtcagccg cacac

45

<210> 648
<211> 45
<212> DNA
<213> Homo sapiens

<400> 648
aacgaattgt tctgctcggg cgtcctggtg catccgcagt ggggtg

45

<210> 649
<211> 45
<212> DNA
<213> Homo sapiens

<400> 649
gcactggtca tggaaaacga attgttctgc tcgggcgtcc tgggtg

45

<210> 650
<211> 51

<212> DNA
<213> Homo sapiens

<400> 650
tcgcagccct ggcaggcggc actggtcatg gaaaacgaat tggtctgctc g 51

<210> 651
<211> 45
<212> DNA
<213> Homo sapiens

<400> 651
atcagcattg cttcgcagtg ccctaccgcg gggaactctt gcctc 45

<210> 652
<211> 45
<212> DNA
<213> Homo sapiens

<400> 652
tccgtgtccg agtctgacac catccggagc atcagcattg cttcg 45

<210> 653
<211> 45
<212> DNA
<213> Homo sapiens

<400> 653
atcaagttgg acgaatccgt gtccgagtct gacaccatcc ggagc 45

<210> 654
<211> 45
<212> DNA
<213> Homo sapiens

<400> 654
aacgacctca tgctcatcaa gttggacgaa tccgtgtccg agtct 45

<210> 655
<211> 45
<212> DNA
<213> Homo sapiens

<400> 655
agacccttgc tcgctaacga cctcatgctc atcaagttgg acgaa 45

<210> 656
<211> 15
<212> PRT
<213> Homo sapiens

<400> 656
Glu Pro Gly Ser Gln Met Val Glu Ala Ser Leu Ser Val Arg His
5 10 15

<210> 657
<211> 15

<212> PRT

<213> Homo sapiens

<400> 657

Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val Glu Ala Ser Leu
5 10 15

<210> 658

<211> 15

<212> PRT

<213> Homo sapiens

<400> 658

Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met
5 10 15

<210> 659

<211> 15

<212> PRT

<213> Homo sapiens

<400> 659

Tyr Thr Ile Gly Leu Gly Leu His Ser Leu Glu Ala Asp Gln Glu
5 10 15

<210> 660

<211> 14

<212> PRT

<213> Homo sapiens

<400> 660

Phe Gln Asn Ser Tyr Thr Ile Gly Leu Gly Leu His Ser Leu
5 10

<210> 661

<211> 15

<212> PRT

<213> Homo sapiens

<400> 661

Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu
5 10 15

<210> 662

<211> 15

<212> PRT

<213> Homo sapiens

<400> 662

His Pro Gln Trp Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser
5 10 15

<210> 663
<211> 15
<212> PRT
<213> Homo sapiens

<400> 663
Ser Gly Val Leu Val His Pro Gln Trp Val Leu Ser Ala Ala His
5 10 15

<210> 664
<211> 15
<212> PRT
<213> Homo sapiens

<400> 664
Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp Val
5 10 15

<210> 665
<211> 15
<212> PRT
<213> Homo sapiens

<400> 665
Ala Leu Val Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val
5 10 15

<210> 666
<211> 17
<212> PRT
<213> Homo sapiens

<400> 666
Ser Gln Pro Trp Gln Ala Ala Leu Val Met Glu Asn Glu Leu Phe Cys
5 10 15

Ser

<210> 667
<211> 15
<212> PRT
<213> Homo sapiens

<400> 667
Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly Asn Ser Cys Leu
5 10 15

<210> 668
<211> 15
<212> PRT
<213> Homo sapiens

<400> 668

Ser Val Ser Glu Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser
5 10 15

<210> 669

<211> 15

<212> PRT

<213> Homo sapiens

<400> 669

Ile Lys Leu Asp Glu Ser Val Ser Glu Ser Asp Thr Ile Arg Ser
5 10 15

<210> 670

<211> 15

<212> PRT

<213> Homo sapiens

<400> 670

Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser
5 10 15

<210> 671

<211> 15

<212> PRT

<213> Homo sapiens

<400> 671

Arg Pro Leu Leu Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu
5 10 15

<210> 672

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 672

ggaccagcat atgaggaaca gaaggaatga cactc

35

<210> 673

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 673

ccgctcgagt ccacccaag cttcacagg

29

```
<210> 675
<211> 652
<212> PRT
<213> Homo sapiens
```

```

<400> 675
Met Arg Asn Arg Arg Asn Asp Thr Leu Asp Ser Thr Arg Thr Leu Tyr
          5                      10                      15

Ser Ser Ala Ser Arg Ser Thr Asp Leu Ser Tyr Ser Glu Ser Asp Leu
          20                      25                      30

Val Asn Phe Ile Gln Ala Asn Phe Lys Lys Arg Glu Cys Val Phe Phe
          35                      40                      45

Thr Lys Asp Ser Lys Ala Thr Glu Asn Val Cys Lys Cys Gly Tyr Ala
          50                      55                      60

```

Gln Ser Gln His Met Glu Gly Thr Gln Ile Asn Gln Ser Glu Lys Trp
 65 70 75 80
 Asn Tyr Lys Lys His Thr Lys Glu Phe Pro Thr Asp Ala Phe Gly Asp
 85 90 95
 Ile Gln Phe Glu Thr Leu Gly Lys Lys Gly Lys Tyr Ile Arg Leu Ser
 100 105 110
 Cys Asp Thr Asp Ala Glu Ile Leu Tyr Glu Leu Leu Thr Gln His Trp
 115 120 125
 His Leu Lys Thr Pro Asn Leu Val Ile Ser Val Thr Gly Gly Ala Lys
 130 135 140
 Asn Phe Ala Leu Lys Pro Arg Met Arg Lys Ile Phe Ser Arg Leu Ile
 145 150 155 160
 Tyr Ile Ala Gln Ser Lys Gly Ala Trp Ile Leu Thr Gly Gly Thr His
 165 170 175
 Tyr Gly Leu Met Lys Tyr Ile Gly Glu Val Val Arg Asp Asn Thr Ile
 180 185 190
 Ser Arg Ser Ser Glu Glu Asn Ile Val Ala Ile Gly Ile Ala Ala Trp
 195 200 205
 Gly Met Val Ser Asn Arg Asp Thr Leu Ile Arg Asn Cys Asp Ala Glu
 210 215 220
 Gly Tyr Phe Leu Ala Gln Tyr Leu Met Asp Asp Phe Thr Arg Asp Pro
 225 230 235 240
 Leu Tyr Ile Leu Asp Asn Asn His Thr His Leu Leu Leu Val Asp Asn
 245 250 255
 Gly Cys His Gly His Pro Thr Val Glu Ala Lys Leu Arg Asn Gln Leu
 260 265 270
 Glu Lys Tyr Ile Ser Glu Arg Thr Ile Gln Asp Ser Asn Tyr Gly Gly
 275 280 285
 Lys Ile Pro Ile Val Cys Phe Ala Gln Gly Gly Gly Lys Glu Thr Leu
 290 295 300
 Lys Ala Ile Asn Thr Ser Ile Lys Asn Lys Ile Pro Cys Val Val Val
 305 310 315 320
 Glu Gly Ser Gly Gln Ile Ala Asp Val Ile Ala Ser Leu Val Glu Val
 325 330 335
 Glu Asp Ala Leu Thr Ser Ser Ala Val Lys Glu Lys Leu Val Arg Phe
 340 345 350
 Leu Pro Arg Thr Val Ser Arg Leu Pro Glu Glu Glu Thr Glu Ser Trp
 355 360 365
 Ile Lys Trp Leu Lys Glu Ile Leu Glu Cys Ser His Leu Leu Thr Val

370	375	380
Ile Lys Met Glu Glu Ala Gly Asp Glu Ile Val Ser Asn Ala Ile Ser		
385	390	395 400
Tyr Ala Leu Tyr Lys Ala Phe Ser Thr Ser Glu Gln Asp Lys Asp Asn		
	405	410 415
Trp Asn Gly Gln Leu Lys Leu Leu Leu Glu Trp Asn Gln Leu Asp Leu		
	420	425 430
Ala Asn Asp Glu Ile Phe Thr Asn Asp Arg Arg Trp Glu Ser Ala Asp		
	435	440 445
Leu Gln Glu Val Met Phe Thr Ala Leu Ile Lys Asp Arg Pro Lys Phe		
	450	455 460
Val Arg Leu Phe Leu Glu Asn Gly Leu Asn Leu Arg Lys Phe Leu Thr		
	465	470 475 480
His Asp Val Leu Thr Glu Leu Phe Ser Asn His Phe Ser Thr Leu Val		
	485	490 495
Tyr Arg Asn Leu Gln Ile Ala Lys Asn Ser Tyr Asn Asp Ala Leu Leu		
	500	505 510
Thr Phe Val Trp Lys Leu Val Ala Asn Phe Arg Arg Gly Phe Arg Lys		
	515	520 525
Glu Asp Arg Asn Gly Arg Asp Glu Met Asp Ile Glu Leu His Asp Val		
	530	535 540
Ser Pro Ile Thr Arg His Pro Leu Gln Ala Leu Phe Ile Trp Ala Ile		
	545	550 555 560
Leu Gln Asn Lys Lys Glu Leu Ser Lys Val Ile Trp Glu Gln Thr Arg		
	565	570 575
Gly Cys Thr Leu Ala Ala Leu Gly Ala Ser Lys Leu Leu Lys Thr Leu		
	580	585 590
Ala Lys Val Lys Asn Asp Ile Asn Ala Ala Gly Glu Ser Glu Glu Leu		
	595	600 605
Ala Asn Glu Tyr Glu Thr Arg Ala Val Glu Leu Phe Thr Glu Cys Tyr		
	610	615 620
Ser Ser Asp Glu Asp Leu Ala Glu Gln Leu Leu Val Tyr Ser Cys Glu		
	625	630 635 640
Ala Trp Gly Gly Leu Glu His His His His His His		
	645	650

<210> 676

<211> 132

<212> PRT

<213> Homo sapien

<400> 676

```

Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe
1           5           10           15
Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser
          20           25           30
Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly
      35           40           45
Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val
    50           55           60
Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val
65           70           75           80
Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
      85           90           95
Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp
    100          105          110
Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu
      115          120          125
Gly Pro Pro Ala
    130

```

<210> 677

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 677

ggggaattca tgatccggga gaaatttgcc cactgc

36

<210> 678

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 678

gggctcgagt caggagtttg agaccagcct ggc

33

<210> 679

<211> 675

<212> DNA

<213> Homo sapiens

<400> 679

```

atgcatcacc atcaccatca cacggccgcg tccgataact tccagctgtc ccagggtggg 60
cagggattcg ccattccgat cgggcaggcg atggcgatcg cgggccagat caagcttccc 120

```



```

accgttcata tcgggcctac cgccttcctc ggcttgggtg ttgtcgacaa caacggcaac 180
ggcgacacgag tccaacgcgt ggtcgggagc gtcgccggcg caagtctcgg catctccacc 240
ggcgacgtga tcaccgcggt cgacggcgct ccgatcaact cggccaccgc gatggcggac 300
gcgcttaacg ggcatcatcc cggtgacgtc atctcgggtg cctggcaaac caagtcgggc 360
ggcacgcgta cagggaaact gacattggcc gagggacccc cggccgaatt catgatccgg 420
gagaaatttg cccactgcac cgtgctaacc attgcacaca gattgaacac cattattgac 480
agcgacaaga taatggtttt agattcagga agactgaaag aatatgatga gccgtatggt 540
ttgctgcaaa ataaagagag cctattttac aagatgggtg aacaactggg caaggcagaa 600
gccgtgccc tcactgaaac agcaaaacag agatgggggt tcaccatggt gccagggtg 660
gtctcaaact cctga 675

```

<210> 680

<211> 291

<212> DNA

<213> Homo sapiens

<400> 680

```

atgggggatcc gggagaaatt tgcccactgc accgtgctaa ccattgcaca cagattgaac 60
accattattg acagcgacaa gataatgggt ttagattcag gaagactgaa agaatatgat 120
gagccgtatg ttttgcgtga aaataaagag agcctatttt acaagatggt gcaacaactg 180
ggcaaggcag aagccgctgc cctcactgaa acagcaaaac agagatgggg ttccaccatg 240
ttggccaggc tgggtctcaa ctcctctcag caccaccacc accaccactg a 291

```

<210> 681

<211> 1074

<212> DNA

<213> Homo sapiens

<400> 681

```

atgtcagcca ttgagaggggt gtcagaggca atcgtcagca tccgaagaat ccagaccttt 60
ttgctacttg atgagatata acagcgcaac cgtcagctgc cgtcagatgg taaaaagatg 120
gtgcatgtgc aggattttac tgcttttttg gataaggcat cagagacccc aactctacaa 180
ggcctttcct ttactgtcag acctggcgaa ttgtagctg ttgctggccc cgtgggagca 240
gggaagtcac caagttaag tgccgtgctc ggggaattgg cccaagtca cgggctgggc 300
agcgtgcatg gaagaattgc ctatgtgtct cagcagccct ggggtttctc gggaactctg 360
aggagtaata ttttattttg gaagaaatac gaaaaggaa gatatgaaa agtcataaag 420
gcttggtgctc tgaaaaagga ttacagctg ttggaggatg gtgatctgac tgtgatagga 480
gatcggggaa ccacgtgag tggagggcag aaagcacggg taaaccttgc aagagcagtg 540
tatcaagatg ctgacatcta tctcctggac gatcctctca gtgcagtaga tgcggaagtt 600
agcagacact tgttcgaaact gtgtatttgt caaattttgc atgagaagat cacaatttta 660
gtgactcatc agttgcagta cctcaaagct gcaagtcaga ttctgatatt gaaagatggt 720
aaaatgggtg agaaggggac ttacactgag ttctctaaaat ctggtataga ttttggtccc 780
cttttaaga aggataatga ggaaagtga caacctccag ttccaggaac tcccacacta 840
aggaatcgta ccttctcaga gtcttcgggt tggctctaac aatcttctag accctccttg 900
aaagatgggt ctctggagag ccaagataca gagaatgtcc cagttacact atcagaggag 960
aaccgttctg aaggaaaagt tggttttcag gcctataaga attacttcag agctgggtgct 1020
cactggattg tcttcatttt ctttattctc gagcaccacc accaccacca ctga 1074

```

<210> 682

<211> 224

<212> PRT

<213> Homo sapiens

<400> 682

```

Met His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu
          5                      10                      15

```

```

Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala

```

20	25	30
Ile Ala Gly Gln Ile Lys Leu Pro Thr Val His Ile Gly Pro Thr Ala		
35	40	45
Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val		
50	55	60
Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr		
65	70	75
Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr		
85	90	95
Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser		
100	105	110
Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr		
115	120	125
Leu Ala Glu Gly Pro Pro Ala Glu Phe Met Ile Arg Glu Lys Phe Ala		
130	135	140
His Cys Thr Val Leu Thr Ile Ala His Arg Leu Asn Thr Ile Ile Asp		
145	150	155
Ser Asp Lys Ile Met Val Leu Asp Ser Gly Arg Leu Lys Glu Tyr Asp		
165	170	175
Glu Pro Tyr Val Leu Leu Gln Asn Lys Glu Ser Leu Phe Tyr Lys Met		
180	185	190
Val Gln Gln Leu Gly Lys Ala Glu Ala Ala Ala Leu Thr Glu Thr Ala		
195	200	205
Lys Gln Arg Trp Gly Phe Thr Met Leu Ala Arg Leu Val Ser Asn Ser		
210	215	220

<210> 683

<211> 357

<212> PRT

<213> Homo sapiens

<400> 683

Met Ser Ala Ile Glu Arg Val Ser Glu Ala Ile Val Ser Ile Arg Arg		
5	10	15
Ile Gln Thr Phe Leu Leu Leu Asp Glu Ile Ser Gln Arg Asn Arg Gln		
20	25	30
Leu Pro Ser Asp Gly Lys Lys Met Val His Val Gln Asp Phe Thr Ala		
35	40	45
Phe Trp Asp Lys Ala Ser Glu Thr Pro Thr Leu Gln Gly Leu Ser Phe		

270

50	55	60
Thr Val Arg Pro Gly Glu Leu Leu Ala Val Val Gly Pro Val Gly Ala		
65	70	75 80
Gly Lys Ser Ser Leu Leu Ser Ala Val Leu Gly Glu Leu Ala Pro Ser		
	85	90 95
His Gly Leu Val Ser Val His Gly Arg Ile Ala Tyr Val Ser Gln Gln		
	100	105 110
Pro Trp Val Phe Ser Gly Thr Leu Arg Ser Asn Ile Leu Phe Gly Lys		
	115	120 125
Lys Tyr Glu Lys Glu Arg Tyr Glu Lys Val Ile Lys Ala Cys Ala Leu		
	130	135 140
Lys Lys Asp Leu Gln Leu Leu Glu Asp Gly Asp Leu Thr Val Ile Gly		
	145	150 155 160
Asp Arg Gly Thr Thr Leu Ser Gly Gly Gln Lys Ala Arg Val Asn Leu		
	165	170 175
Ala Arg Ala Val Tyr Gln Asp Ala Asp Ile Tyr Leu Leu Asp Asp Pro		
	180	185 190
Leu Ser Ala Val Asp Ala Glu Val Ser Arg His Leu Phe Glu Leu Cys		
	195	200 205
Ile Cys Gln Ile Leu His Glu Lys Ile Thr Ile Leu Val Thr His Gln		
	210	215 220
Leu Gln Tyr Leu Lys Ala Ala Ser Gln Ile Leu Ile Leu Lys Asp Gly		
	225	230 235 240
Lys Met Val Gln Lys Gly Thr Tyr Thr Glu Phe Leu Lys Ser Gly Ile		
	245	250 255
Asp Phe Gly Ser Leu Leu Lys Lys Asp Asn Glu Glu Ser Glu Gln Pro		
	260	265 270
Pro Val Pro Gly Thr Pro Thr Leu Arg Asn Arg Thr Phe Ser Glu Ser		
	275	280 285
Ser Val Trp Ser Gln Gln Ser Ser Arg Pro Ser Leu Lys Asp Gly Ala		
	290	295 300
Leu Glu Ser Gln Asp Thr Glu Asn Val Pro Val Thr Leu Ser Glu Glu		
	305	310 315 320
Asn Arg Ser Glu Gly Lys Val Gly Phe Gln Ala Tyr Lys Asn Tyr Phe		
	325	330 335
Arg Ala Gly Ala His Trp Ile Val Phe Ile Phe Leu Ile Leu Glu His		
	340	345 350
His His His His His		
	355	

<210> 684
<211> 96
<212> PRT
<213> Homo sapiens

<400> 684
Met Gly Ile Arg Glu Lys Phe Ala His Cys Thr Val Leu Thr Ile Ala
 5 10 15
His Arg Leu Asn Thr Ile Ile Asp Ser Asp Lys Ile Met Val Leu Asp
 20 25 30
Ser Gly Arg Leu Lys Glu Tyr Asp Glu Pro Tyr Val Leu Leu Gln Asn
 35 40 45
Lys Glu Ser Leu Phe Tyr Lys Met Val Gln Gln Leu Gly Lys Ala Glu
 50 55 60
Ala Ala Ala Leu Thr Glu Thr Ala Lys Gln Arg Trp Gly Phe Thr Met
 65 70 75 80
Leu Ala Arg Leu Val Ser Asn Ser Leu Glu His His His His His His
 85 90 95

<210> 685
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 685
cgcccatggg gatccgggag aaatttgccc actgc 35

<210> 686
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 686
cgcctcgagg gagtttgaga ccagcctggc caaca 35

<210> 687
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 687

gcatggacca tatgtcagcc attgagaggg tgtcagag

38

<210> 688

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 688

ccgctcgaga ataaggaaaa tgaagacaat ccag

34

<210> 689

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 689

gttgaattca tgcacgggcc ccaggtg

27

<210> 690

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 690

cccctcgagt cactatgggc tgcctcttga

30

<210> 691

<211> 915

<212> DNA

<213> Homo sapiens

<400> 691

atgcatcacc atcaccatca cacggccgcg tccgataact tccagctgtc ccagggtggg 60
 cagggtattcg ccattccgat cgggcaggcg atggcgatcg cgggccagat caagcttccc 120
 accgttcata tcgggcctac cgccttctct ggcttggttg ttgtcgacaa caacggcaac 180
 ggcgacacgag tccaacgcgt ggtcgggagc gctccggcgg caagtctcgg catctccacc 240
 ggcgacgtga tcaccgcggt cgacggcggt ccgatcaact cggccaccgc gatggcggac 300
 gcgcttaacg ggcacatccc cggtgacgtc atctcggtga cctggcgaac caagtcgggc 360
 ggcacgcgta cagggaacgt gacattggcc gagggacccc cggccgaatt catgcacggg 420
 ccccaggtgc tggcacgctg ctccgagtgt gcttgtcctg ccttggctgc cacctctgcg 480
 ggggtgcgtc tggagggggg ggaccggcca ccaaccttac ccagtcaagg aagtggatgg 540
 ccatgttccc acagcctgag tggctgccac ctgatggctg atggagcaaa ggccttagga 600
 aaagcagatg gcccttgccc ctaccttttt gttagaagaa ctgatgttcc atgtcctgca 660
 gcgagtgagg ttggtggtg tgccccagc tcctggcgcg ccctcgacaga ggtgactggt 720

```
<210> 692
<211> 304
<212> PRT
<213> Homo sapiens
```

<400> 692																	
Met	His	His	His	His	His	His	Thr	Ala	Ala	Ser	Asp	Asn	Phe	Gln	Leu		
			5						10					15			
Ser	Gln	Gly	Gly	Gln	Gly	Phe	Ala	Ile	Pro	Ile	Gly	Gln	Ala	Met	Ala		
			20					25					30				
Ile	Ala	Gly	Gln	Ile	Lys	Leu	Pro	Thr	Val	His	Ile	Gly	Pro	Thr	Ala		
		35					40					45					
Phe	Leu	Gly	Leu	Gly	Val	Val	Asp	Asn	Asn	Gly	Asn	Gly	Ala	Arg	Val		
	50					55					60						
Gln	Arg	Val	Val	Gly	Ser	Ala	Pro	Ala	Ala	Ser	Leu	Gly	Ile	Ser	Thr		
65					70					75					80		
Gly	Asp	Val	Ile	Thr	Ala	Val	Asp	Gly	Ala	Pro	Ile	Asn	Ser	Ala	Thr		
				85					90					95			
Ala	Met	Ala	Asp	Ala	Leu	Asn	Gly	His	His	Pro	Gly	Asp	Val	Ile	Ser		
			100					105					110				
Val	Thr	Trp	Gln	Thr	Lys	Ser	Gly	Gly	Thr	Arg	Thr	Gly	Asn	Val	Thr		
		115					120					125					
Leu	Ala	Glu	Gly	Pro	Pro	Ala	Glu	Phe	Met	His	Gly	Pro	Gln	Val	Leu		
	130					135					140						
Ala	Arg	Cys	Ser	Glu	Cys	Ala	Cys	Pro	Ala	Leu	Ala	Ala	Thr	Ser	Ala		
145					150					155					160		
Gly	Val	Arg	Leu	Glu	Gly	Val	Asp	Arg	Pro	Pro	Thr	Leu	Pro	Ser	Gln		
				165					170					175			
Gly	Ser	Gly	Trp	Pro	Cys	Ser	His	Ser	Leu	Ser	Gly	Cys	His	Leu	Met		
			180					185					190				
Ala	Asp	Gly	Ala	Lys	Ala	Leu	Gly	Lys	Ala	Asp	Gly	Pro	Trp	Pro	Tyr		
		195					200					205					
Leu	Phe	Val	Arg	Arg	Thr	Asp	Val	Pro	Cys	Pro	Ala	Ala	Ser	Glu	Val		
	210					215					220						
Gly	Gly	Cys	Ala	Pro	Ser	Ser	Trp	Arg	Ala	Leu	Ala	Glu	Val	Thr	Gly		
225					230					235					240		
Cys	Ser	Leu	Gly	Pro	Leu	Gly	Leu	Ala	Gln	His	Ala	Gln	Ala	Ser	Val		
				245					250					255			

274

Leu Leu Leu Cys Tyr Lys Trp Ser His Ile Gly Glu Thr Ser Ser His
 260 265 270

Leu Arg Ser Lys Val Tyr Ala Ala Phe Gly Gly Ser Ser Pro Cys Leu
 275 280 285

Lys Gly Leu Met Ser Leu Trp Ala Ser Trp Leu Ser Arg Gly Arg Pro
 290 295 300

<210> 693
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 693
 cgaagtcacg tggaggccag cctc

24

<210> 694
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 694
 cctgaccgaa ttcattaact ggcctggac

29

<210> 695
 <211> 166
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (1)...(166)
 <223> Xaa = Any Amino Acid

<400> 695
 Met Gly His His His His His Val Glu Ala Ser Leu Ser Val Arg
 1 5 10 15
 His Pro Glu Tyr Asn Arg Pro Leu Leu Ala Asn Asp Leu Met Leu Ile
 20 25 30
 Lys Leu Asp Glu Ser Val Ser Glu Ser Asp Thr Ile Arg Ser Ile Ser
 35 40 45
 Ile Ala Ser Gln Cys Pro Thr Ala Gly Asn Ser Cys Leu Val Ser Gly
 50 55 60
 Trp Gly Leu Leu Ala Asn Gly Arg Met Pro Thr Val Leu Gln Cys Val
 65 70 75 80
 Asn Val Ser Val Val Ser Glu Glu Val Cys Ser Lys Leu Tyr Asp Pro

85										90					95				
Leu	Tyr	His	Pro	Ser	Met	Phe	Cys	Ala	Gly	Gly	Gly	Gln	Xaa	Gln	Xaa				
100								105					110						
Asp	Ser	Cys	Asn	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Ile	Cys	Asn	Gly	Tyr				
115								120					125						
Leu	Gln	Gly	Leu	Val	Ser	Phe	Gly	Lys	Ala	Pro	Cys	Gly	Gln	Val	Gly				
130								135					140						
Val	Pro	Gly	Val	Tyr	Thr	Asn	Leu	Cys	Lys	Phe	Thr	Glu	Trp	Ile	Glu				
145								150					155						
Lys	Thr	Val	Gln	Ala	Ser														
165																			

```
<210> 696
<211> 504
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> misc_feature
<222> (1)...(504)
<223> n = A,T,C or G
```

[illegible]

```
<210> 697
<211> 21
<212> DNA
<213> Artificial Sequence
```

<220>
<223> PCR primer

<400> 697
ctcagggttc cggagccgcg g 21

```
<210> 698
<211> 35
<212> DNA
<213> Artificial Sequence
```

<220>
<223> PCR primer

<400> 698
ctatagaatt cattaccaa aagctgggct ccaagc 35

<210> 699

<211> 241
 <212> PRT
 <213> Homo sapiens

<400> 699

```

Met Gln His His His His His His Leu Arg Val Pro Glu Pro Arg Pro
 1           5           10           15
Gly Glu Ala Lys Ala Glu Gly Ala Ala Pro Pro Thr Pro Ser Lys Pro
           20           25           30
Leu Thr Ser Phe Leu Ile Gln Asp Ile Leu Arg Asp Gly Ala Gln Arg
 35           40           45
Gln Gly Gly Arg Thr Ser Ser Gln Arg Gln Arg Asp Pro Glu Pro Glu
 50           55           60
Pro Glu Pro Glu Pro Glu Gly Gly Arg Ser Arg Ala Gly Ala Gln Asn
 65           70           75           80
Asp Gln Leu Ser Thr Gly Pro Arg Ala Ala Pro Glu Glu Ala Glu Thr
           85           90           95
Leu Ala Glu Thr Glu Pro Glu Arg His Leu Gly Ser Tyr Leu Leu Asp
 100           105           110
Ser Glu Asn Thr Ser Gly Ala Leu Pro Arg Leu Pro Gln Thr Pro Lys
 115           120           125
Gln Pro Gln Lys Arg Ser Arg Ala Ala Phe Ser His Thr Gln Val Ile
 130           135           140
Glu Leu Glu Arg Lys Phe Ser His Gln Lys Tyr Leu Ser Ala Pro Glu
 145           150           155           160
Arg Ala His Leu Ala Lys Asn Leu Lys Leu Thr Glu Thr Gln Val Lys
           165           170           175
Ile Trp Phe Gln Asn Arg Arg Tyr Lys Thr Lys Arg Lys Gln Leu Ser
 180           185           190
Ser Glu Leu Gly Asp Leu Glu Lys His Ser Ser Leu Pro Ala Leu Lys
 195           200           205
Glu Glu Ala Phe Ser Arg Ala Ser Leu Val Ser Val Tyr Asn Ser Tyr
 210           215           220
Pro Tyr Tyr Pro Tyr Leu Tyr Cys Val Gly Ser Trp Ser Pro Ala Phe
 225           230           235           240
Trp

```

<210> 700
 <211> 729
 <212> DNA
 <213> Homo sapiens

<400> 700

```

atgcagcatc accaccatca ccacctcagg gttccggagc cgcggcccgg ggaggcgaaa      60
gcgagggggg cgcgcgccgc gaccccgctc aagccgctca cgtccttcct catccaggac      120
atcctgcggg acggcgcgca gcggaaggc ggccgcacga gcagccagag acagcgcgac      180
ccggagccgg agccagagcc agagccagag ggaggacgca gccgcgccgg ggcgcagaac      240
gaccagctga gcaccggggc ccgcgcgcgg ccgatgagg ccgagacgct ggcagagacc      300
gagccagaaa ggcacttggg gtcttatctg ttggactctg aaaacacttc aggcgcctt      360
ccaaggcttc ccaaaccgcc taagcagccg cagaagcgct cccgagctgc cttctccac      420
actcaggtga tcgagttgga gaggaagttc agccatcaga agtacctgtc ggcccctgaa      480
cgggcccacc tggccaagaa cctcaagctc acggagaccc aagtgaagat atggttccag      540
aacagacgct ataagactaa gcgaaagcag ctctcctcgg agctgggaga cttggagaag      600
cactcctttt tgccggccct gaaagaggag gccttctccc ggcctcctc ggtctccgtg      660
tataacagct atccttacta ccctacactg cactgcgtgg gcagctggag cccagctttt      720
tggtaatga                                     729

```

277

<210> 701
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 701
 ctactaagcg ctggagtgag ggatcag

27

<210> 702
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 702
 catcgagaat tcactactct ctgactagat gtc

33

<210> 703
 <211> 161
 <212> PRT
 <213> Homo sapiens

<400> 703
 Met Gln His His His His His His Ala Gly Val Arg Asp Gln Gly Gln
 1 5 10 15
 Gly Ala Arg Trp Pro His Thr Gly Lys Arg Gly Pro Leu Leu Gln Gly
 20 25 30
 Leu Thr Trp Ala Thr Gly Gly His Cys Phe Ser Ser Glu Glu Ser Gly
 35 40 45
 Ala Val Asp Gly Ala Gly Gln Lys Lys Asp Arg Ala Trp Leu Arg Cys
 50 55 60
 Pro Glu Ala Val Ala Gly Phe Pro Leu Gly Ser Asp Cys Arg Glu Gly
 65 70 75 80
 Gly Arg Gln Gly Cys Gly Gly Ser Asp Asp Glu Asp Asp Leu Gly Val
 85 90 95
 Ala Pro Gly Leu Ala Pro Ala Trp Ala Leu Thr Gln Pro Pro Ser Gln
 100 105 110
 Ser Pro Gly Pro Gln Ser Leu Pro Ser Thr Pro Ser Ser Ile Trp Pro
 115 120 125
 Gln Trp Val Ile Leu Ile Thr Glu Leu Thr Ile Pro Ser Pro Ala His
 130 135 140
 Gly Pro Pro Trp Leu Pro Asn Ala Leu Glu Arg Gly His Leu Val Arg
 145 150 155 160
 Glu

<210> 704
 <211> 489
 <212> DNA
 <213> Homo sapiens

<400> 704

atgcagcatc	accaccatca	ccacgctgga	gtgagggatc	aggggcaggg	cgcgagatgg	60
cctcacacag	ggaagagagg	gcccctcctg	cagggcctca	cctgggccac	aggaggacac	120
tgtttttcct	ctgaggagtc	aggagctgtg	gatggtgctg	gacagaagaa	ggacagggcc	180
tggctcaggt	gtccagaggc	tgctgctggc	ttccctttgg	gatcagactg	cagggagggga	240
ggcgggcagg	gttggtgggg	gagtgacgat	gaggatgacc	tgggggtggc	tccaggcctt	300
gcccctgcct	gggccctcac	ccagcctccc	tcacagtctc	ctggccctca	gtctctcccc	360
tccactccat	cctccatctg	gcctcagtgg	gtcattctga	tactgaact	gaccataccc	420
agccctgccc	acggccctcc	atggctcccc	aatgccttgg	agaggggaca	tctagtcaga	480
gagtagtga						489

<210> 705

<211> 132

<212> PRT

<213> Homo sapiens

<400> 705

Thr	Ala	Ala	Ser	Asp	Asn	Phe	Gln	Leu	Ser	Gln	Gly	Gly	Gln	Gly	Phe
1				5					10					15	
Ala	Ile	Pro	Ile	Gly	Gln	Ala	Met	Ala	Ile	Ala	Gly	Gln	Ile	Arg	Ser
			20					25					30		
Gly	Gly	Gly	Ser	Pro	Thr	Val	His	Ile	Gly	Pro	Thr	Ala	Phe	Leu	Gly
			35				40					45			
Leu	Gly	Val	Val	Asp	Asn	Asn	Gly	Asn	Gly	Ala	Arg	Val	Gln	Arg	Val
	50				55					60					
Val	Gly	Ser	Ala	Pro	Ala	Ala	Ser	Leu	Gly	Ile	Ser	Thr	Gly	Asp	Val
65					70				75					80	
Ile	Thr	Ala	Val	Asp	Gly	Ala	Pro	Ile	Asn	Ser	Ala	Thr	Ala	Met	Ala
			85					90					95		
Asp	Ala	Leu	Asn	Gly	His	His	Pro	Gly	Asp	Val	Ile	Ser	Val	Asn	Trp
			100					105					110		
Gln	Thr	Lys	Ser	Gly	Gly	Thr	Arg	Thr	Gly	Asn	Val	Thr	Leu	Ala	Glu
			115				120					125			
Gly	Pro	Pro	Ala												
			130												

<210> 706

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 706

ggggaattca tcacctatgt gccgcctctg c

31

<210> 707

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 707
gggctcgagt cactcgccca cgaaatccgt gtaaaacagc

40

<210> 708
<211> 1203
<212> DNA
<213> Homo sapiens

<400> 708
atgcatcacc atcaccatca cacggccgcg tccgataact tccagctgtc ccagggtggg 60
cagggattcg ccattccgat cgggcaggcg atggcgatcg cgggccagat caagcttccc 120
accgttcata tcgggcctac cgccttcctc ggcttgggtg ttgtcgacaa caacggcaac 180
ggcgcacgag tccaacgcgt ggtcgggagc gctccggcgg caagtctcgg catctccacc 240
ggcgcagtgat tcaccgcggt cgacggcgct ccgatcaact cggccaccgc gatggcggac 300
gcggttaacg ggcacatcc cgtgacgtc atctcgggtga cctggcaaac caagtccggc 360
ggcgcgcgtg cagggaacgt gacattggcc gagggacccc cggccgaatt catcacctat 420
gtgccgcctc tgctgctgga agtgggggta gaggagaagt tcatgaccat ggtgctgggc 480
attggtccag tgcctggcct ggtctgtgtc ccgctcctag gctcagccag tgaccactgg 540
cgtggacgct atggccgccc cggcccttc atctgggcac tgccttggg catcctgctg 600
agcctctttc tcatcccaag ggccgctgg ctagcagggc tgctgtgccc ggatcccagg 660
cccttgagc tggcactgct catcctgggc gtggggctgc tggacttctg tggccagggtg 720
tgcttcactc cactggaggc cctgctctct gacctcttcc gggaccgcga ccaactgtcg 780
caggcctact ctgtctatgc cttcatgatc agtcttgggg gctgcctggg ctacctcctg 840
cctgccattg actgggacac cagtgccttg gccccctacc tgggcaccca ggaggagtgc 900
ctctttggcc tgctcaccct catcttctc acctgcgtag cagccacact gctggtggct 960
gaggaggcag cgctgggccc caccgagcca gcagaagggc tgcgggccc ctcttgtcg 1020
ccccactgct gtccatgccg ggcccgttg gctttccgga acctgggcgc cctgcttccc 1080
cggctgcacc agctgtgctg ccgcatgccc cgcacctgc gccggctctt cgtggctgag 1140
ctgtgcagct ggatggcact catgaccttc acgctgtttt acacggattt cgtgggcgag 1200
tga 1203

<210> 709
<211> 400
<212> PRT
<213> Homo sapiens

<400> 709
Met His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu
5 10 15
Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala
20 25 30
Ile Ala Gly Gln Ile Lys Leu Pro Thr Val His Ile Gly Pro Thr Ala
35 40 45
Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val
50 55 60
Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr
65 70 75 80
Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr
85 90 95
Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser

280

100	105	110
Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr		
115	120	125
Leu Ala Glu Gly Pro Pro Ala Glu Phe Ile Thr Tyr Val Pro Pro Leu		
130	135	140
Leu Leu Glu Val Gly Val Glu Glu Lys Phe Met Thr Met Val Leu Gly		
145	150	155
Ile Gly Pro Val Leu Gly Leu Val Cys Val Pro Leu Leu Gly Ser Ala		
165	170	175
Ser Asp His Trp Arg Gly Arg Tyr Gly Arg Arg Arg Pro Phe Ile Trp		
180	185	190
Ala Leu Ser Leu Gly Ile Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala		
195	200	205
Gly Trp Leu Ala Gly Leu Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu		
210	215	220
Ala Leu Leu Ile Leu Gly Val Gly Leu Leu Asp Phe Cys Gly Gln Val		
225	230	235
Cys Phe Thr Pro Leu Glu Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro		
245	250	255
Asp His Cys Arg Gln Ala Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu		
260	265	270
Gly Gly Cys Leu Gly Tyr Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser		
275	280	285
Ala Leu Ala Pro Tyr Leu Gly Thr Gln Glu Glu Cys Leu Phe Gly Leu		
290	295	300
Leu Thr Leu Ile Phe Leu Thr Cys Val Ala Ala Thr Leu Leu Val Ala		
305	310	315
Glu Glu Ala Ala Leu Gly Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala		
325	330	335
Pro Ser Leu Ser Pro His Cys Cys Pro Cys Arg Ala Arg Leu Ala Phe		
340	345	350
Arg Asn Leu Gly Ala Leu Leu Pro Arg Leu His Gln Leu Cys Cys Arg		
355	360	365
Met Pro Arg Thr Leu Arg Arg Leu Phe Val Ala Glu Leu Cys Ser Trp		
370	375	380
Met Ala Leu Met Thr Phe Thr Leu Phe Tyr Thr Asp Phe Val Gly Glu		
385	390	395
		400

<210> 710
<211> 20
<212> PRT
<213> Homo sapiens

<400> 710
Leu Leu Pro Pro Pro Ala Leu Cys Gly Ala Ser Ala Cys Asp Val
 5 10 15

Ser Val Arg Val
 20

<210> 711
<211> 60
<212> DNA
<213> Homo sapiens

<400> 711
ctgctccac ctccaccgc gctctgcggg gcctctgcct gtgatgtctc cgtacgtgtg 60

<210> 712
<211> 10
<212> PRT
<213> Homo sapiens

<400> 712
Ala Ser Ala Cys Asp Val Ser Val Arg Val
 5 10

<210> 713
<211> 30
<212> DNA
<213> Homo sapiens

<400> 713
gcctctgcct gtgatgtctc cgtacgtgtg 30

<210> 714
<211> 9
<212> PRT
<213> Homo sapiens

<400> 714
Ala Ser Ala Cys Asp Val Ser Val Arg
 1 5

<210> 715
<211> 9
<212> PRT
<213> Homo sapiens

<400> 715
Ser Ala Cys Asp Val Ser Val Arg Val
 5

<210> 716
<211> 27

<212> DNA

<213> Homo sapiens

<400> 716

tctgcctgtg atgtctccgt acgtgtg

27

<210> 717

<211> 19

<212> PRT

<213> Homo sapiens

<400> 717

Gly Ile Gly Pro Val Leu Gly Leu Val Cys Val Pro Leu Leu Gly Ser
5 10 15

Ala Ser Asp

<210> 718

<211> 19

<212> PRT

<213> Homo sapiens

<400> 718

Val Pro Pro Leu Leu Leu Glu Val Gly Val Glu Glu Lys Phe Met Thr
5 10 15

Met Val Leu

<210> 719

<211> 19

<212> PRT

<213> Homo sapiens

<400> 719

Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala
5 10 15

Gln Leu Leu

<210> 720

<211> 57

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(57)

<223> n = A,T,C or G

<400> 720

ggnathggnc cngtnytnng nytngtntgy gtnccnytny tnggnwsngc nwsngay 57

<210> 721
<211> 57
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(57)
<223> n = A,T,C or G

<400> 721
gtncncncny tnytnytnga rgtnggngtn gargaraart tyatgacnat ggtnytn 57

<210> 722
<211> 57
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(57)
<223> n = A,T,C or G

<400> 722
atggtncarm gnytntgggt nwsnmgnytn ytnmgncaym gnaargcnca rytntn 57

<210> 723
<211> 9
<212> PRT
<213> Homo sapiens

<400> 723
Val Leu Gln Cys Val Asn Val Ser Val
1 5

<210> 724
<211> 9
<212> PRT
<213> Homo sapiens

<400> 724
Arg Met Pro Thr Val Leu Gln Cys Val
1 5

<210> 725
<211> 9
<212> PRT
<213> Homo sapiens

<400> 725
Asn Leu Cys Lys Phe Thr Glu Trp Ile
1 5

<210> 726
<211> 9
<212> PRT

<213> Homo sapiens

<400> 726

Met Leu Ile Lys Leu Asp Glu Ser Val

1 5

<210> 727

<211> 9

<212> PRT

<213> Homo sapiens

<400> 727

Leu Leu Ala Asn Asp Leu Met Leu Ile

1 5

<210> 728

<211> 10

<212> PRT

<213> Homo sapiens

<400> 728

Leu Leu Ala Asn Gly Arg Met Pro Thr Val

1 5 10

<210> 729

<211> 10

<212> PRT

<213> Homo sapiens

<400> 729

Leu Met Leu Ile Lys Leu Asp Glu Ser Val

1 5 10

<210> 730

<211> 10

<212> PRT

<213> Homo sapiens

<400> 730

Val Leu Gln Cys Val Asn Val Ser Val Val

1 5 10

<210> 731

<211> 10

<212> PRT

<213> Homo sapiens

<400> 731

Gly Leu Leu Ala Asn Gly Arg Met Pro Thr

1 5 10

<210> 732

<211> 10

<212> PRT

<213> Homo sapiens

<400> 732

Thr Val Leu Gln Cys Val Asn Val Ser Val

285

1 5 10

<210> 733

<211> 9

<212> PRT

<213> Homo sapiens

<400> 733

Gly Val Leu Val His Pro Gln Trp Val

1 5

<210> 734

<211> 9

<212> PRT

<213> Homo sapiens

<400> 734

Val Leu Val His Pro Gln Trp Val Leu

1 5

<210> 735

<211> 1195

<212> DNA

<213> Homo sapiens

<400> 735

```

ccgagactca cggccaagct aaggcgaaga gtgggtggct gaagccatac tattttatag 60
aattaatgga aagcagaaaa gacatcacaa accaagaaga actttggaaa atgaagccta 120
ggagaaatgt agaagaagac gattatttgc ataaggacac gggagagacc agcatgctaa 180
aaagacctgt gcttttgcac ttgcacccaa cagcccatgc tgatgaattt gactgccctt 240
cagaacttca gcacacacag gaactctttc cacagtggca cttgcccaatt aaaatagctg 300
ctattatagc atctctgact tttctttaca ctcttctgag ggaagtaatt caccctttag 360
caacttccca tcaacaatat ttttataaaa ttccaatcct ggcatcaac aaagtcttgc 420
caatgggttc catcaacttc ttggcattgg tttacctgcc aggtgtgata gcagcaattg 480
tccaacttca taatggaacc aagtataaga agtttccaca ttggttggat aagtggatgt 540
taacaagaaa gcagtttggg cttctcagtt tcttttttgc tgtactgcat gcaatttata 600
gtctgtctta cccaatgagg cgatcctaca gatacaagtt gctaaactgg gcatatcaac 660
aggtccaaca aaataaagaa gatgcctgga ttgagcatga tgtttggaga atggagattt 720
atgtgtctct ggaatttgtg ggattggcaa tactggctct gttggctgtg acatctattc 780
catctgtgag tgactctttg acatggagag aatttacta tattcagagc aagctaggaa 840
ttgtttccct tctactgggc acaatacacg cattgatttt tgcctggaat aagtggatag 900
atataaaaca atttgtatgg tatacacctc caacttttat gatagctgtt ttccttccaa 960
ttgttgcctt gatattttaa agcatactat tcctgccatg cttgaggaag aagatactga 1020
agattagaca tggttgggaa gacgtcacca aaattaacaa aactgagata tgttcccagt 1080
tgtagaatta ctgtttacac acatttttgt tcaatattga tatattttat caccaacatt 1140
tcaagtttgt atttgttaat aaaatgatta ttcaaggaaa aaaaaaaaaa aaaaa 1195

```

<210> 736

<211> 339

<212> PRT

<213> Homo sapiens

<400> 736

Met Glu Ser Arg Lys Asp Ile Thr Asn Gln Glu Glu Leu Trp Lys Met

5

10

15

Lys Pro Arg Arg Asn Leu Glu Glu Asp Asp Tyr Leu His Lys Asp Thr
 20 25 30
 Gly Glu Thr Ser Met Leu Lys Arg Pro Val Leu Leu His Leu His Gln
 35 40 45
 Thr Ala His Ala Asp Glu Phe Asp Cys Pro Ser Glu Leu Gln His Thr
 50 55 60
 Gln Glu Leu Phe Pro Gln Trp His Leu Pro Ile Lys Ile Ala Ala Ile
 65 70 75 80
 Ile Ala Ser Leu Thr Phe Leu Tyr Thr Leu Leu Arg Glu Val Ile His
 85 90 95
 Pro Leu Ala Thr Ser His Gln Gln Tyr Phe Tyr Lys Ile Pro Ile Leu
 100 105 110
 Val Ile Asn Lys Val Leu Pro Met Val Ser Ile Thr Leu Leu Ala Leu
 115 120 125
 Val Tyr Leu Pro Gly Val Ile Ala Ala Ile Val Gln Leu His Asn Gly
 130 135 140
 Thr Lys Tyr Lys Lys Phe Pro His Trp Leu Asp Lys Trp Met Leu Thr
 145 150 155 160
 Arg Lys Gln Phe Gly Leu Leu Ser Phe Phe Phe Ala Val Leu His Ala
 165 170 175
 Ile Tyr Ser Leu Ser Tyr Pro Met Arg Arg Ser Tyr Arg Tyr Lys Leu
 180 185 190
 Leu Asn Trp Ala Tyr Gln Gln Val Gln Gln Asn Lys Glu Asp Ala Trp
 195 200 205
 Ile Glu His Asp Val Trp Arg Met Glu Ile Tyr Val Ser Leu Gly Ile
 210 215 220
 Val Gly Leu Ala Ile Leu Ala Leu Leu Ala Val Thr Ser Ile Pro Ser
 225 230 235 240
 Val Ser Asp Ser Leu Thr Trp Arg Glu Phe His Tyr Ile Gln Ser Lys
 245 250 255
 Leu Gly Ile Val Ser Leu Leu Leu Gly Thr Ile His Ala Leu Ile Phe
 260 265 270
 Ala Trp Asn Lys Trp Ile Asp Ile Lys Gln Phe Val Trp Tyr Thr Pro
 275 280 285
 Pro Thr Phe Met Ile Ala Val Phe Leu Pro Ile Val Val Leu Ile Phe
 290 295 300
 Lys Ser Ile Leu Phe Leu Pro Cys Leu Arg Lys Lys Ile Leu Lys Ile
 305 310 315 320
 Arg His Gly Trp Glu Asp Val Thr Lys Ile Asn Lys Thr Glu Ile Cys

325

330

335

Ser Gln Leu

<210> 737

<211> 2172

<212> DNA

<213> Homo sapiens

<400> 737

```
aaaattgaat attgagatac cattctttag tgttaccttt tttaccaca tgtgtttctg 60
aaaatattgg aattttattc atcttaaaaa ttggaccggg ccttatttac catctttaat 120
ccatttttagt actatgggtg agtacatgga attgaagtct ggcttaaata ttcagaaagt 180
tatatatcta ttttatttta tttttttgag acagagtctc gctgtgtcac ccaggctgga 240
gtgcgggtgcc acaatcttgg ctactgcaa cctctgagtc ccaggttcaa gcgatactca 300
tgcctcggcc tcctgagtag ctgggactac aggcgtgcac caccacatct ggctaattct 360
tttttgtatt tttagtagag acgggggttc actgtggtct ccactctctg acctcgtgat 420
ccgcctgcct cccaaagtgc tgggattaca ggcatgagcc accgcacaca gctgggactg 480
ggtaatttat aaagaaaaga ggtttaatga ctcacagttc cgcatggctg gagaggcctc 540
aggaaactta caatcatggt ggaaggcgaa ggggaagcaa ggcacgtctt acatgggtggc 600
aggagagaac gagtgagggg ggagactgcc acaaactttt tttttttgag acaagagtct 660
ggccctggtg cccaggctgg agtgagtg catgatctca gctcactgca acctctgcct 720
cacaggttca agcaattctc atgcctcagc ctcccgcata gctgggacca caggatgca 780
ccaccacacc tagctaattt ttgtagtttt agtagagatg gggctctact atgttgctca 840
ggctggctca aaactcctgg gctccagcaa tccgcctgcc ttggcctccc aaagtgtg 900
ggttacaggc ataagccacc acatccagcc tgccacatac ttttaacta tcaggtctca 960
tgagaactca tgcactatca caagaatagc atggggaaaa tcccccccat aatccaatca 1020
cctcccacca ggtctcctcc gacacgtggg attgggtggg gacacagagc caaacctat 1080
cagatgctgc aggggctggg gacactgaga ccactcagac ctggtgtctc tgtactctt 1140
ctgggctctg totgtctcca ggacctccct ccccttccat ggtatagaag gaaagtgtg 1200
taagggtcaa attgcacagg aactccttaa gacatacatc atccactcag cagttttagg 1260
ttcgcagcaa aatggagtgg aaggaacaga aatttcctgt gcaccctcc ccgctgtctc 1320
cgccatatcg gcatcctgca tccagagtgg tggactgggt acaggctatg aacctacact 1380
gatgcggcac caccacccag agtccacggg ttatgttggg tcacatttac tcttgctgtg 1440
gtatggtcta taggtttgga cagatgtccg ataactcctt ttacattttg gcatccttgg 1500
gtagctcgtc ttgtaggaat ggacttgctt caaagtggag gcaggcagat ccttcagacg 1560
ggtatatgga gccctgtttt cagttgcttt tctaattctc tcttatcggt tacctcaaaa 1620
tcttctgag gtctcgcttc cttttaaaat ccttgtctac tttgcagcat cactctgaca 1680
ctccattgat tcctcagcac ctactgacta cacggttagg agtgcaaggg tagaattcat 1740
gttttattca tctttgggtc tgtagcacc agcaaagtgc tcagtaaatg cgagtaatt 1800
gatttgacct ctgaacaaat acacactgta ctaagaatct acacaccgaa agacaaaaac 1860
aagacaaatt tgagtgttac aggtgtcacg cttggcatca cacatgtgcc tgtgtattcc 1920
tctaggtggg taccaggagc tctgccactg catgtccact agtgacgggt tcgctccacc 1980
acccagctg ggtagccgct gctctcacat aaggggtcca attaaaattg ccaggaataa 2040
attccccggg actttgactt ctcaagagct aagaagggtt gctgagtatt ctggcatgat 2100
gtttggtgat caaacaactg ctggccaaaa atgatgagta tttccccctc ttgctgaaga 2160
tgtgtccat ac 2172
```

<210> 738

<211> 2455

<212> DNA

<213> Homo sapiens

<400> 738

```
cagcttaaaa atggtttctt gaaatcagtg attagcattc actcaccagt acccctacta 60
aggggtaggc actggtttgt actcctggga atacaggagt acaccagaat ttatttctgc 120
```

```

ttattgcttt tgttgcaaat gccgtggctt catctgagga attctagaat tcagaggggtg 180
tagccctcca ctctgctgtc ttgctatctg ctctcattgc atccgtttta cctgcattct 240
gaaagatgtt tctcaggttt ttccttgacg attttcttct tttctgattc tgacaatgtt 300
ttaaatcatt gtactgtggt tatcatttct ctgcatttat tttaccatc ttcctttgta 360
acttgtccta ttgtctttta atttctgcct gttctttatg gctttcaact tcataaataa 420
catgttttct caaatctctt tgtgaattcc agagagggcc aggcacggtg gctcacatct 480
gtaatcccag cactttgggg aggctgagac ggggtgatca cttgaggtca ggagtttgag 540
accagcctgg ccaacatggt gaaatcccgt ttcactaaaa atacaaaaat taccaggga 600
tggtggcggg cgcctgtaat ccaggtact cgggaggtg agggaggaga atcgcttgaa 660
cctgggaggg tgagggagga gaatcgctt aaccgggag gcagaggtt cagtgaaccg 720
agatcatgtt gctgcactcc agcctggtca acagagcaag actctgcctc aaaaacaaac 780
aaataaacia aaaaacaaac aaaacagaga gattttgctg caatgtacaa ggagcaattt 840
gctcctttta aaaaataatt ttggccagg gacagtggct cacacctgta atccagcac 900
tttgggaagc caaggtgggt ggatcattt aggtcaggag tttgagatca gcctggccaa 960
catggtgaaa cactatctct attaaaaata caaaaatgtg ctcatgtgtg tgggtgcacat 1020
ctgtaatctc agcctcccgc atagctggga ccacaggtat gcaccaccac acctagctaa 1080
ttttttagt ttttagtag atggggtctc actatgttgc tcaggctggt ctaaaactcc 1140
tgggctccag caatccgcct gccttggcct cccaaagtgc tggggttaca ggcataagcc 1200
accacatcca gcctgccaca tacttttaaa ctatcaggtc tcatgagaac tcatgcacta 1260
tcacaagaat agcatgggga aaatccccc cataatccaa tcacctccca ccaggtctcc 1320
tccgacacgt gggattgggt ggggacacag agccaaaccg tatcagatgc tgcaggggct 1380
ggggacactg agaccactca gacctggtgt ctctgtcact cttctgggct ctgtctgtct 1440
ccaggacctc cctccccttc catggtatag aaggaaagt ctgttaagggt caaattgcac 1500
aggaactcct taagacatac atcatccact cagcagttt aggttcgcag caaatggag 1560
tggaaggaac agaaatttcc tgtgcacccc tccccgtgt ctccgccata tcggcatcct 1620
gcatccagag tgggtgactg gttacaggct atgaacctac actgatgagg caccaccacc 1680
cagagtcac aggttatgtt ggttcacatt tactcttgc gtggtatggt ctataggttt 1740
ggacagatgt cggataatcc tttttacatt ttggcatcct tgggtagctc gtctttagg 1800
aatggacttg cttcaaagtg gaggcaggca gatccttcag acgggtatat ggagccctgt 1860
tttcagttgc ttttctaatt ctctcttct gtttacctca aaatcttct gaggtctcgc 1920
ttccttttaa aatccttgc tactttgcag catcactctg aactccatt gattcctcag 1980
cacctactga ctacacggtt aggagtgc aa gggtagaatt catgttttat tcatctttg 2040
gtctgtagca ccagcaaaag tgctcagtaa atgcgcagta attgatttga cctctgaaca 2100
aatacacact gtactaagaa tctacacacc gaaagacaaa aacaagacaa atttgagtgc 2160
tacaggtgtc acgtttgca tcacacatgt gctgtgtat tctctagggt ggttaccagg 2220
agctctgcca ctgcatgtcc actagtgc ggttcgctcc accaccccag ctgggtagcc 2280
gctgctctca cataaggggt ccaattaaaa ttgccaggaa taaattcccc cggactttga 2340
cttctcaaga gctaagaagg tttgctgagt attctggcat gatgtttggt gatcaaaaa 2400
ctgctggcca aaaatgatga gtatttcccc ctcttgctga agatgtgctc catac 2455

```

<210> 739

<211> 2455

<212> DNA

<213> Homo sapiens

<400> 739

```

cagcttaaaa atggtttctt gaaatcagt attagcattc actcaccagt accctacta 60
aggggtaggc actggtttgt actcctggga atacaggagt acaccagaat ttatttctgc 120
ttattgcttt tgttgcaaat gccgtggctt catctgagga attctagaat tcagaggggtg 180
tagccctcca ctctgctgtc ttgctatctg ctctcattgc atccgtttta cctgcattct 240
gaaagatgtt tctcaggttt ttccttgacg attttcttct tttctgattc tgacaatgtt 300
ttaaatcatt gtactgtggt tatcatttct ctgcatttat tttaccatc ttcctttgta 360
acttgtccta ttgtctttta atttctgcct gttctttatg gctttcaact tcataaataa 420
catgttttct caaatctctt tgtgaattcc agagagggcc aggcacggtg gctcacatct 480
gtaatcccag cactttgggg aggctgagac ggggtgatca cttgaggtca ggagtttgag 540
accagcctgg ccaacatggt gaaatcccgt ttcactaaaa atacaaaaat taccaggga 600
tggtggcggg ccgctgtaat ccaggtact cgggaggtg agggaggaga atcgcttgaa 660
cctgggaggg tgagggagga gaatcgctt aaccgggag gcagaggtt cagtgaaccg 720

```

```

agatcatgtt gctgcactcc agcctgggtca acagagcaag actctgcctc aaaaacaaac 780
aaataaacia acaaaacaaac aaaacagaga gatcttgctg caatgtacaa ggagcaattt 840
gctcctttaa aaaaataatt tttggccagg cacagtggct cacacctgta atcccagcac 900
tttgggaagc caaggtgggt ggatcatttg aggtcaggag tttgagatca gcctggccaa 960
catggtgaaa cactatctct attaaaaata caaaaatgtg ctgagtgtgg tgggtgcacat 1020
ctgtaatctc agcctcccgc atagctggga ccacaggtat gcaccaccac acctagctaa 1080
ttttttagt tttagtagag atgggtctc actatgttg tcaggctggg ctaaaactcc 1140
tgggtccag caatccgct gccttggcct cccaaagtgc tggggttaca ggcataagcc 1200
accacatcca gcctgccaca tacttttaaa ctatcaggtc tcatgagaac tcatgacta 1260
tcacaagaat agcatgggga aaatccccc cataatcaa tcacctcca ccaggtctcc 1320
tccgacacgt gggattgggt ggggacacag agccaaaccg tatcagatgc tgcaggggct 1380
ggggacactg agaccactca gacctggtgt ctctgtcact cttctgggct ctgtctgtct 1440
ccaggacctc cctccccttc catggtatag aaggaaagtg ctgtaagggt caaattgcac 1500
aggaactcct taagacatac atcatccact cagcagtttt aggttcgcag caaaatggag 1560
tggaaggaaac agaaatttcc tgtgcacccc tcccgcgtgt ctccgccata tcggcatcct 1620
gcatccagag tgggtggactg gttacaggct atgaacctac actgatgcgg caccaccacc 1680
cagagtcacac aggttatgtt ggttcacatt tactcttct gtggtatggt ctataggttt 1740
ggacagatgt ccgataatcc tttttacatt ttggcatcct tgggtagctc gtctttagg 1800
aatggacttg cttcaaaagt gaggcaggca gatccttcag acgggtatat ggagccctgt 1860
tttcagttgc ttttctaatt ctctcttctc gtttacctca aaatcttctc gaggtctcgc 1920
ttccttttaa aatccttgc tactttgcag catcactctg acactccatt gattcctcag 1980
cacctactga ctacacgggt aggagtgcac gggtagaatt catgttttat tcatctttgg 2040
gtctgtagca cccagcaaag tgcctagtaa atgcgcagta attgatttga cctctgaaca 2100
aatacacact gtactaagaa tctacacacc gaaagacaaa aacaagacaa atttgagtgc 2160
tacaggtgtc acgcttggca tcacacatgt gcctgtgtat tcctctaggt ggttaccagg 2220
agctctgcca ctgcatgtcc actagtgcag ggttcgctcc accaccccag ctgggtagcc 2280
gctgctctca cataaggggt ccaattaaaa ttgccaggaa taaattcccc cggactttga 2340
cttctcaaga gctaagaagg tttgctgagt attctggcat gatgtttggt gatcaacaa 2400
ctgctggcca aaaatgatga gtatttcccc ctcttgcgtga agatgtgctc catac 2455

```

<210> 740

<211> 62

<212> PRT

<213> Homo sapiens

<400> 740

```

Met Thr His Ser Ser Ala Trp Leu Glu Arg Pro Gln Glu Thr Tyr Asn
              5                      10                      15

```

```

His Gly Gly Arg Arg Arg Gly Ser Lys Ala Arg Leu Thr Trp Trp Gln
      20                      25                      30

```

```

Glu Arg Thr Ser Glu Gly Gly Asp Cys His Lys Leu Phe Phe Phe Glu
      35                      40                      45

```

```

Thr Arg Val Trp Pro Cys Cys Pro Gly Trp Ser Ala Val Ala
      50                      55                      60

```

<210> 741

<211> 135

<212> PRT

<213> Homo sapiens

<400> 741

```

Met Val Glu Gly Glu Gly Glu Ala Arg His Val Leu His Gly Gly Arg
              5                      10                      15

```

290

Arg Glu Arg Val Arg Gly Glu Thr Ala Thr Asn Phe Phe Phe Leu Arg
 20 25 30
 Gln Glu Ser Gly Pro Val Ala Gln Ala Gly Val Gln Trp His Asp Leu
 35 40 45
 Ser Ser Leu Gln Pro Leu Pro His Arg Phe Lys Gln Phe Ser Cys Leu
 50 55 60
 Ser Leu Pro His Ser Trp Asp His Arg Tyr Ala Pro Pro His Leu Ala
 65 70 75 80
 Asn Phe Cys Ser Phe Ser Arg Asp Gly Val Ser Leu Cys Cys Ser Gly
 85 90 95
 Trp Ser Lys Thr Pro Gly Leu Gln Gln Ser Ala Cys Leu Gly Leu Pro
 100 105 110
 Lys Cys Trp Gly Tyr Arg His Lys Pro Pro His Pro Ala Cys His Ile
 115 120 125
 Leu Leu Asn Tyr Gln Val Ser
 130 135

<210> 742

<211> 77

<212> PRT

<213> Homo sapiens

<400> 742

Met His Tyr His Lys Asn Ser Met Gly Lys Ile Pro Pro Ile Ile Gln
 5 10 15
 Ser Pro Pro Thr Arg Ser Pro Pro Thr Arg Gly Ile Gly Trp Gly His
 20 25 30
 Arg Ala Lys Pro Tyr Gln Met Leu Gln Gly Leu Gly Thr Leu Arg Pro
 35 40 45
 Leu Arg Pro Gly Val Ser Val Thr Leu Leu Gly Ser Val Cys Leu Gln
 50 55 60
 Asp Leu Pro Pro Leu Pro Trp Tyr Arg Arg Lys Val Leu
 65 70 75

<210> 743

<211> 60

<212> PRT

<213> Homo sapiens

<400> 743

Met Leu Val His Ile Tyr Ser Cys Cys Gly Met Val Tyr Arg Phe Gly
 5 10 15
 Gln Met Ser Asp Asn Pro Phe Tyr Ile Leu Ala Ser Leu Gly Ser Ser
 20 25 30

Ser Cys Arg Asn Gly Leu Ala Ser Lys Trp Arg Gln Ala Asp Pro Ser
 35 40 45

Asp Gly Tyr Met Glu Pro Cys Phe Gln Leu Leu Phe
 50 55 60

<210> 744

<211> 76

<212> PRT

<213> Homo sapiens

<400> 744

Met Cys Leu Cys Ile Pro Leu Gly Gly Tyr Gln Glu Leu Cys His Cys
 5 10 15

Met Ser Thr Ser Asp Gly Phe Ala Pro Pro Pro Gln Leu Gly Ser Arg
 20 25 30

Cys Ser His Ile Arg Gly Pro Ile Lys Ile Ala Arg Asn Lys Phe Pro
 35 40 45

Arg Thr Leu Thr Ser Gln Glu Leu Arg Arg Phe Ala Glu Tyr Ser Gly
 50 55 60

Met Met Phe Gly Asp Gln Thr Thr Ala Gly Gln Lys
 65 70 75

<210> 745

<211> 76

<212> PRT

<213> Homo sapiens

<400> 745

Met Val Lys Ser Arg Phe Thr Lys Asn Thr Lys Ile Thr Gln Ala Trp
 5 10 15

Trp Arg Ala Pro Val Ile Pro Gly Thr Arg Glu Ala Glu Gly Gly Glu
 20 25 30

Ser Leu Glu Pro Gly Arg Leu Arg Glu Glu Asn Arg Leu Asn Pro Gly
 35 40 45

Gly Arg Gly Cys Ser Glu Pro Arg Ser Cys Cys Cys Thr Pro Ala Trp
 50 55 60

Ser Thr Glu Gln Asp Ser Ala Ser Lys Thr Asn Lys
 65 70 75

<210> 746

<211> 80

<212> PRT

<213> Homo sapiens

<400> 746

Met Leu Leu His Ser Ser Leu Val Asn Arg Ala Arg Leu Cys Leu Lys


```
<210> 747
<211> 72
<212> PRT
<213> Homo sapiens
```

```
<210> 748
<211> 77
<212> PRT
<213> Homo sapiens
```

```

<400> 748
Met His Tyr His Lys Asn Ser Met Gly Lys Ile Pro Pro Ile Ile Gln
          5                      10                      15

Ser Pro Pro Thr Arg Ser Pro Pro Thr Arg Gly Ile Gly Trp Gly His
          20                      25                      30

Arg Ala Lys Pro Tyr Gln Met Leu Gln Gly Leu Gly Thr Leu Arg Pro
          35                      40                      45

Leu Arg Pro Gly Val Ser Val Thr Leu Leu Gly Ser Val Cys Leu Gln
          50                      55                      60

Asp Leu Pro Pro Leu Pro Trp Tyr Arg Arg Lys Val Leu
          65                      70                      75

```

<210> 749
 <211> 60
 <212> PRT
 <213> Homo sapiens

<400> 749
 Met Leu Val His Ile Tyr Ser Cys Cys Gly Met Val Tyr Arg Phe Gly
 5 10 15
 Gln Met Ser Asp Asn Pro Phe Tyr Ile Leu Ala Ser Leu Gly Ser Ser
 20 25 30
 Ser Cys Arg Asn Gly Leu Ala Ser Lys Trp Arg Gln Ala Asp Pro Ser
 35 40 45
 Asp Gly Tyr Met Glu Pro Cys Phe Gln Leu Leu Phe
 50 55 60

<210> 750
 <211> 76
 <212> PRT
 <213> Homo sapiens

<400> 750
 Met Cys Leu Cys Ile Pro Leu Gly Gly Tyr Gln Glu Leu Cys His Cys
 5 10 15
 Met Ser Thr Ser Asp Gly Phe Ala Pro Pro Pro Gln Leu Gly Ser Arg
 20 25 30
 Cys Ser His Ile Arg Gly Pro Ile Lys Ile Ala Arg Asn Lys Phe Pro
 35 40 45
 Arg Thr Leu Thr Ser Gln Glu Leu Arg Arg Phe Ala Glu Tyr Ser Gly
 50 55 60
 Met Met Phe Gly Asp Gln Thr Thr Ala Gly Gln Lys
 65 70 75

<210> 751
 <211> 2479
 <212> DNA
 <213> Homo sapiens

<400> 751
 gtcattattga acattccaga tacctatcat tactcgatgc tgttgataac agcaagatgg 60
 ctttgaactc agggtcacca ccagctattg gaccttacta tgaaaaccat ggataccaac 120
 cggaaaaccc ctatcccgca cagcccaactg tggccccac tgtctacgag gtgcatccgg 180
 ctctagtacta cccgtcccc gtgccccagt acgccccgag ggtcctgacg caggcttcca 240
 accccgtcgt ctgcacgcag ccctctactc catccgggac agtgtgcacc tcaaagacta 300
 agaaagcact gtgcatcacc ttgaccctgg ggaccttct cgtgggagct gcgctggccg 360
 ctggcctact ctggaagttc atgggcagca agtgctccaa ctctgggata gaggcgact 420
 cctcaggtac ctgcatcaac ccctctaact ggtgtgatgg cgtgtcacac tgccccggcg 480
 gggaggacga gaatcggtgt gttcgctct acggaccaaa ctctatcctt cagatgtact 540
 catctcagag gaagtctctg caccctgtgt gccaaagcga ctggaacgag aactacgggc 600

```

gggcgccctg cagggacatg ggctataaga ataattttta ctctagccaa ggaatagtgg 660
atgacagcgg atccaccagc tttatgaaac tgaacacaag tgccggcaat gtcgatatct 720
ataaaaaact gtaccacagt gatgcctggt cttcaaaagc agtgggttct ttacgctggt 780
tagcctgcgg ggtcaacttg aactcaagcc gccagagcag gatcgtgggc ggtgagagcg 840
cgctcccggg ggcttgcccc tggcaggtca gcctgcacgt ccagaacgtc cacgtgtgcg 900
gaggctccat catcaccccc gagtggatcg tgacagccgc cctactgcgtg gaaaaacctc 960
ttaacaatcc atggcatttg acggcatttg cggggatttt gagacaatct ttcatgttct 1020
atggagccgg ataccaagta caaaaagtga tttctcatcc aaattatgac tccaagacca 1080
agaacaatga cattgcgctg atgaagctgc agaagcctct gactttcaac gacctagtga 1140
aaccagtgtg tctgcccac ccaggcatga tgctgcagcc agaacagctc tgctggattt 1200
ccgggtgggg ggccaccgag gagaagggga agacctcaga agtgctgaac gctgccaagg 1260
tgcttctcat tgagacacag agatgcaaca gcagatatgt ctatgacaac ctgatcacac 1320
cagccatgat ctgtgccggc ttcctgcagg ggaacgtcga ttcttgccag ggtgacagtg 1380
gagggccctc ggtccattcg aacaacaata tctggtggct gataggggat acaagctggg 1440
gttctggctg tgccaaagct tacagaccag gagtgtagcg gaatgtgatg gtattcacgg 1500
actggattta tcgacaaatg aaggcaaacg gctaattcac atggtcttcg tccttgacct 1560
cgttttacaa gaaaacaatg gggctgggtt tgcttccccg tgcatgattt actcttagag 1620
atgattcaga ggtcacttca tttttattaa acagtgaact tgtctggctt tggcactctc 1680
tgccatactg tgcaggctgc agtggctccc ctgcccagcc tgctctccct aacctcttgt 1740
ccgcaagggg tgatggccgg ctggttggtg gcactggcgg tcaattgtgg aaggaagagg 1800
gttgaggctt gcccattg agatcttctt gctgagtcct ttccaggggc caattttgga 1860
tgagcatgga gctgtcactt ctcagctgct ggatgacttg agatgaaaaa ggagagacat 1920
ggaaagggag acagccaggt ggcacctgca gcggtgccc tctggggcca cttggtagt 1980
tccccagcct acttcacaag gggattttgc tgatgggttc ttagagcctt agcagccctg 2040
gatggtggcc agaaataaag ggaccagccc ttcattgggtg gtgacgtggt agtcacttgt 2100
aaggggaaca gaaacatttt tgttcttatg gggtagaat atagacagtg cccttggtgc 2160
gaggggaagca attgaaaagg aacttgccct gagcactcct ggtgcaggtc tccacctgca 2220
cattgggtgg ggctcctggg agggagactc agccttcttc ctcactctcc ctgacctgc 2280
tcctagcacc ctggagagtg aatgccctt ggtccctggc agggcgccaa gtttggcacc 2340
atgtcggcct cttcaggcct gatagtcatt ggaaattgag gtccatgggg gaaatcaagg 2400
atgctcagtt taaggtacac tgtttccatg ttatgtttct acacattgat ggtggtgacc 2460
ctgagttcaa agccatctt
2479

```

<210> 752

<211> 492

<212> PRT

<213> Homo sapiens

<400> 752

```

Met Ala Leu Asn Ser Gly Ser Pro Pro Ala Ile Gly Pro Tyr Tyr Glu
      5                      10                      15

Asn His Gly Tyr Gln Pro Glu Asn Pro Tyr Pro Ala Gln Pro Thr Val
      20                      25                      30

Val Pro Thr Val Tyr Glu Val His Pro Ala Gln Tyr Tyr Pro Ser Pro
      35                      40                      45

Val Pro Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val
      50                      55                      60

Val Cys Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys
      65                      70                      75                      80

Thr Lys Lys Ala Leu Cys Ile Thr Leu Thr Leu Gly Thr Phe Leu Val
      85                      90                      95

Gly Ala Ala Leu Ala Ala Gly Leu Leu Trp Lys Phe Met Gly Ser Lys

```

100					105					110					
Cys	Ser	Asn	Ser	Gly	Ile	Glu	Cys	Asp	Ser	Ser	Gly	Thr	Cys	Ile	Asn
		115					120					125			
Pro	Ser	Asn	Trp	Cys	Asp	Gly	Val	Ser	His	Cys	Pro	Gly	Gly	Glu	Asp
		130				135					140				
Glu	Asn	Arg	Cys	Val	Arg	Leu	Tyr	Gly	Pro	Asn	Phe	Ile	Leu	Gln	Met
145					150					155					160
Tyr	Ser	Ser	Gln	Arg	Lys	Ser	Trp	His	Pro	Val	Cys	Gln	Asp	Asp	Trp
				165					170					175	
Asn	Glu	Asn	Tyr	Gly	Arg	Ala	Ala	Cys	Arg	Asp	Met	Gly	Tyr	Lys	Asn
			180					185					190		
Asn	Phe	Tyr	Ser	Ser	Gln	Gly	Ile	Val	Asp	Asp	Ser	Gly	Ser	Thr	Ser
		195					200					205			
Phe	Met	Lys	Leu	Asn	Thr	Ser	Ala	Gly	Asn	Val	Asp	Ile	Tyr	Lys	Lys
	210					215					220				
Leu	Tyr	His	Ser	Asp	Ala	Cys	Ser	Ser	Lys	Ala	Val	Val	Ser	Leu	Arg
225					230					235					240
Cys	Leu	Ala	Cys	Gly	Val	Asn	Leu	Asn	Ser	Ser	Arg	Gln	Ser	Arg	Ile
				245					250					255	
Val	Gly	Gly	Glu	Ser	Ala	Leu	Pro	Gly	Ala	Trp	Pro	Trp	Gln	Val	Ser
			260					265					270		
Leu	His	Val	Gln	Asn	Val	His	Val	Cys	Gly	Gly	Ser	Ile	Ile	Thr	Pro
		275					280					285			
Glu	Trp	Ile	Val	Thr	Ala	Ala	His	Cys	Val	Glu	Lys	Pro	Leu	Asn	Asn
	290					295					300				
Pro	Trp	His	Trp	Thr	Ala	Phe	Ala	Gly	Ile	Leu	Arg	Gln	Ser	Phe	Met
305					310					315					320
Phe	Tyr	Gly	Ala	Gly	Tyr	Gln	Val	Gln	Lys	Val	Ile	Ser	His	Pro	Asn
				325					330					335	
Tyr	Asp	Ser	Lys	Thr	Lys	Asn	Asn	Asp	Ile	Ala	Leu	Met	Lys	Leu	Gln
			340					345					350		
Lys	Pro	Leu	Thr	Phe	Asn	Asp	Leu	Val	Lys	Pro	Val	Cys	Leu	Pro	Asn
		355					360					365			
Pro	Gly	Met	Met	Leu	Gln	Pro	Glu	Gln	Leu	Cys	Trp	Ile	Ser	Gly	Trp
	370					375					380				
Gly	Ala	Thr	Glu	Glu	Lys	Gly	Lys	Thr	Ser	Glu	Val	Leu	Asn	Ala	Ala
385					390					395					400
Lys	Val	Leu	Leu	Ile	Glu	Thr	Gln	Arg	Cys	Asn	Ser	Arg	Tyr	Val	Tyr
				405					410					415	

Asp Asn Leu Ile Thr Pro Ala Met Ile Cys Ala Gly Phe Leu Gln Gly
 420 425 430

Asn Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Thr Ser
 435 440 445

Asn Asn Asn Ile Trp Trp Leu Ile Gly Asp Thr Ser Trp Gly Ser Gly
 450 455 460

Cys Ala Lys Ala Tyr Arg Pro Gly Val Tyr Gly Asn Val Met Val Phe
 465 470 475 480

Thr Asp Trp Ile Tyr Arg Gln Met Lys Ala Asn Gly
 485 490

<210> 753

<211> 683

<212> DNA

<213> Homo sapiens

<400> 753

gtcatattga acattccaga tacctatcat tactcgatgc tgttgataac agcaagatgg 60
 ctttgaactc agggtcacca ccagctattg gaccttacta tgaaaacat ggataccaac 120
 cggaaaaccc ctatcccgca cagcccaactg tggccccac tgtctacgag gtgcatccgg 180
 ctgagtacta cccgtccccc gtgcccagc acgcccagag ggtcctgacg caggcttcca 240
 accccgtcgt ctgcacgcag cccaaatccc catccgggac agtgtgcacc tcaaagacta 300
 agaaagcact gtgcatcacc ttgacctgg ggaccttct cgtgggagct gcgctggccg 360
 ctggcctact ctggaagttc atgggcagca agtgcctcaa ctctgggata gagtgcgact 420
 cctcaggtac ctgcatcaac ccctctaact ggtgtgatgg cgtgtcacac tgccccggcg 480
 gggaggacga gaatcggtgt gttegcctct acggacaaa cttcatcctt cagatgtact 540
 catctcagag gaagtcctgg caccctgtgt gccaaagcga ctggaacgag aactacgggc 600
 gggcggcctg caggacatg ggctataaga ataattttta ctctagccaa ggaatagtgg 660
 atgacagcgg atccaccagc ttt 683

<210> 754

<211> 209

<212> PRT

<213> Homo sapiens

<400> 754

Met Ala Leu Asn Ser Gly Ser Pro Pro Ala Ile Gly Pro Tyr Tyr Glu
 1 5 10 15
 Asn His Gly Tyr Gln Pro Glu Asn Pro Tyr Pro Ala Gln Pro Thr Val
 20 25 30
 Val Pro Thr Val Tyr Glu Val His Pro Ala Gln Tyr Tyr Pro Ser Pro
 35 40 45
 Val Pro Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val
 50 55 60
 Val Cys Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys
 65 70 75 80
 Thr Lys Lys Ala Leu Cys Ile Thr Leu Thr Leu Gly Thr Phe Leu Val
 85 90 95

297

Gly Ala Ala Leu Ala Ala Gly Leu Leu Trp Lys Phe Met Gly Ser Lys
 100 105 110
 Cys Ser Asn Ser Gly Ile Glu Cys Asp Ser Ser Gly Thr Cys Ile Asn
 115 120 125
 Pro Ser Asn Trp Cys Asp Gly Val Ser His Cys Pro Gly Gly Glu Asp
 130 135 140
 Glu Asn Arg Cys Val Arg Leu Tyr Gly Pro Asn Phe Ile Leu Gln Met
 145 150 155 160
 Tyr Ser Ser Gln Arg Lys Ser Trp His Pro Val Cys Gln Asp Asp Trp
 165 170 175
 Asn Glu Asn Tyr Gly Arg Ala Ala Cys Arg Asp Met Gly Tyr Lys Asn
 180 185 190
 Asn Phe Tyr Ser Ser Gln Gly Ile Val Asp Asp Ser Gly Ser Thr Ser
 195 200 205
 Phe

<210> 755

<211> 27

<212> PRT

<213> Homo sapiens

<400> 755

Val Gly Glu Gly Leu Tyr Gln Gly Val Pro Arg Ala Glu Pro Gly Thr
 1 5 10 15
 Glu Ala Arg Arg His Tyr Asp Glu Gly Val Arg
 20 25

<210> 756

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 756

ggatccgccg ccaccatgtc actttctagc ctgct

35

<210> 757

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 757

gtcgactcag ctggaccaca gccgcag

27

<210> 758

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 758
ggatccgccg ccaccatggg ctgcaggctg ctct

34

<210> 759
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 759
gtcgactcag aaatcctttc tcttgac

27

<210> 760
<211> 936
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...()
<223> n = A,T,C or G

<400> 760
atgggctgca ggctgntctg ctgtgcggtt ctctgtctcc tgggagcggg ccccatggaa 60
acgggagtta cgagacacc aagacacctg gtcattggaa tgacaaataa gaagtctttg 120
aaatgtgaac aacatctggg tcataacgct atgtattggg acaagcaaag tgctaagaag 180
ccactggagc tcatgtttgt ctacagtctt gaagaacggg ttgaaaacaa cagtgtgcca 240
agtcgcttct cacctgaatg ccccaacagc tctcacttat tccttcacct acacaccctg 300
cagccagaag actcggccct gtatctctgc gccagcagcc aagaccggac aagcagctcc 360
tacgagcagt acttcgggcc gggcaccagg ctcacgggtc cagaggacct gaaaaacgtg 420
ttcccacccg aggtcgctgt gtttgagcca tcagaagcag agatctocca caccctaaaag 480
gccacactgg tgtgcctggc cacaggcttc taccocgacc acgtggagct gagctgggtg 540
gtgaatggga aggaggtgca cagtggggtc agcacagacc cgcagccctt caaggagcag 600
cccgccctca atgactccag atactgcctg agcagccgcc tgagggtctc ggccaccttc 660
tggcagaacc cccgcaacca cttccgctgt caagtccagt tctacgggct ctcgagaaat 720
gacgagtgga cccaggatag ggccaaacct gtcacccaga tcgtcagcgc cgaggccttg 780
ggtagagcag actgtggctt cacctccgag tcttaccagc aaggggtcct gtctgccacc 840
atcctctatg agatcttgct agggaaaggc accttgatat cctgtctggt cagtgccttc 900
gtgctgatgg ccatgggtcaa gagaaaggat ttctga 936

<210> 761
<211> 834
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...()
<223> n = A,T,C or G

<400> 761
atgtcacttt ctacgctgct naagggtggtc acagcttcac tgtggctagg acctggcatt 60
gccagaaga taactcaaac ccaaccagga atgttcgtgc aggaaaagga ggctgtgact 120
ctggactgca catatgacac cagtgatcaa agttatggtc tcttctggtc caagcagccc 180

```

agcagtgggg aaatgatttt tcttatttat caggggtctt atgacgagca aaatgcaaca 240
gaaggtcgct actcattgaa tttccagaag gcaagaaaat ccgccaacct tgtcatctcc 300
gcttcacaac tgggggactc agcaatgtat ttctgtgcaa tgagagaggg cgcgggagga 360
ggaaacaacac tcacctttgg gacaggcact cagctaaaag tggaaactcaa tatccagaac 420
cctgaccctg ccgtgtacca gctgagagac tctaaatcca gtgacaagtc tgtctgccta 480
ttcaccgatt ttgattctca aacaaatgtg tcacaaagta aggattctga tgtgtatata 540
acagacaaaa ctgtgctaga catgaggtct atggacttca agagcaacag tgctgtggcc 600
tggagcaaca aatctgactt tgcattgtgca aacgccttca acaacagcat tattccagaa 660
gacaccttct tccccagccc agaaagtcc tgtgatgtca agctggtcga gaaaagcttt 720
gaaacagata cgaacctaaa ctttcaaac ctgtcagtga ttgggttccg aatcctcctc 780
ctgaaagtgg ccgggtttaa tctgctcatg acgctgcggc tgtggtccag ctga      834

```

<210> 762

<211> 311

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(311)

<223> Xaa = Any amino acid

<400> 762

```

Met Gly Cys Arg Leu Xaa Cys Cys Ala Val Leu Cys Leu Leu Gly Ala
      5                      10                      15

```

```

Val Pro Met Glu Thr Gly Val Thr Gln Thr Pro Arg His Leu Val Met
      20                      25                      30

```

```

Gly Met Thr Asn Lys Lys Ser Leu Lys Cys Glu Gln His Leu Gly His
      35                      40                      45

```

```

Asn Ala Met Tyr Trp Tyr Lys Gln Ser Ala Lys Lys Pro Leu Glu Leu
      50                      55                      60

```

```

Met Phe Val Tyr Ser Leu Glu Glu Arg Val Glu Asn Asn Ser Val Pro
      65                      70                      75                      80

```

```

Ser Arg Phe Ser Pro Glu Cys Pro Asn Ser Ser His Leu Phe Leu His
      85                      90                      95

```

```

Leu His Thr Leu Gln Pro Glu Asp Ser Ala Leu Tyr Leu Cys Ala Ser
     100                      105                      110

```

```

Ser Gln Asp Arg Thr Ser Ser Ser Tyr Glu Gln Tyr Phe Gly Pro Gly
     115                      120                      125

```

```

Thr Arg Leu Thr Val Thr Glu Asp Leu Lys Asn Val Phe Pro Pro Glu
     130                      135                      140

```

```

Val Ala Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys
     145                      150                      155                      160

```

```

Ala Thr Leu Val Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu
     165                      170                      175

```

```

Leu Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr
     180                      185                      190

```


300

Asp Pro Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr
 195 200 205
 Cys Leu Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro
 210 215 220
 Arg Asn His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn
 225 230 235 240
 Asp Glu Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser
 245 250 255
 Ala Glu Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Glu Ser Tyr
 260 265 270
 Gln Gln Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly
 275 280 285
 Lys Ala Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala
 290 295 300
 Met Val Lys Arg Lys Asp Phe
 305 310

<210> 763
 <211> 277
 <212> PRT
 <213> Homo sapiens

<400> 763
 Met Ser Leu Ser Ser Leu Leu Lys Val Val Thr Ala Ser Leu Trp Leu
 5 10 15
 Gly Pro Gly Ile Ala Gln Lys Ile Thr Gln Thr Gln Pro Gly Met Phe
 20 25 30
 Val Gln Glu Lys Glu Ala Val Thr Leu Asp Cys Thr Tyr Asp Thr Ser
 35 40 45
 Asp Gln Ser Tyr Gly Leu Phe Trp Tyr Lys Gln Pro Ser Ser Gly Glu
 50 55 60
 Met Ile Phe Leu Ile Tyr Gln Gly Ser Tyr Asp Glu Gln Asn Ala Thr
 65 70 75 80
 Glu Gly Arg Tyr Ser Leu Asn Phe Gln Lys Ala Arg Lys Ser Ala Asn
 85 90 95
 Leu Val Ile Ser Ala Ser Gln Leu Gly Asp Ser Ala Met Tyr Phe Cys
 100 105 110
 Ala Met Arg Glu Gly Ala Gly Gly Gly Asn Lys Leu Thr Phe Gly Thr
 115 120 125
 Gly Thr Gln Leu Lys Val Glu Leu Asn Ile Gln Asn Pro Asp Pro Ala
 130 135 140

Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu
145 150 155 160

Phe Thr Asp Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser
165 170 175

Asp Val Tyr Ile Thr Asp Lys Thr Val Leu Asp Met Arg Ser Met Asp
180 185 190

Phe Lys Ser Asn Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala
195 200 205

Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe
210 215 220

Pro Ser Pro Glu Ser Ser Cys Asp Val Lys Leu Val Glu Lys Ser Phe
225 230 235 240

Glu Thr Asp Thr Asn Leu Asn Phe Gln Asn Leu Ser Val Ile Gly Phe
245 250 255

Arg Ile Leu Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu
260 265 270

Arg Leu Trp Ser Ser
275

<210> 764

<211> 1536

<212> DNA

<213> Homo sapiens

<400> 764

atgtacaacc tgttgctgtc ctacgacaga catggggacc acctgcagcc cctggacctc 60
gtgcccatac accagggtct caccctttc aagctggctg gaggaggagg taacactgtg 120
atgtttcagc acctgatgca gaagcggaag cacacccagt ggacgtatgg accactgacc 180
tcgactctct atgacctcac agagatcgac tcctcagggg atgagcagtc cctgtgggaa 240
cttatcatca ccaccaagaa gcgggaggct cgccagatcc tggaccagac gccggtgaag 300
gagctgggtga gcctcaagtg gaagcggtag gggcgccgt acttctgcat gctgggtgcc 360
atatatctgc tgtatcatcat ctgcttcacc atgtgctgca tctaccgccc cctcaagccc 420
aggaccaata accgcacgag ccccgggac aacaccctct tacagcagaa gctacttcag 480
gaagcctaca tgacccctaa ggacgatata cggctggctg gggagctggt gactgtcatt 540
ggggctatca tcctcctgct ggtagaggtt ccagacatct tcagaatggg ggtcactcgc 600
ttctttggac agaccatcct tggggggcca ttccatgtcc tcatcatcac ctatgccttc 660
atggtgctgg tgaccatggt gatgcggctc atcagtgcc a gcggggagg ggtacccatg 720
tcctttgcac tcgtgctggg ctggtgcaac gtcatgtact tcgcccagg attccagatg 780
ctaggccctt tcaccatcat gattcagaag atgattttt ggcacctgat gcgattctgc 840
tggctgatgg ctgtggtcat cctgggcttt gcttcagcct tctatatcat cttccagaca 900
gaggaccccg aggagctagg ccacttctac gactaccca tggccctgtt cagcaccttc 960
gagctgttcc ttaccatcat cgatggccca gccaaactaca acgtggacct gcccttcatt 1020
tacagcatca cctatgctgc ctttgccatc atcgccacac tgctcatgct caacctctc 1080
attgccatga tgggcgacac tcaactggcg gtggcccatg agcgggatga gctgtggagg 1140
gccagattg tggccaccac ggtgatgctg gagcggaagc tgccctcgtg cctgtggcct 1200
cgctccggga tctgcggacg ggagtatggc ctgggagacc gctggttcct gcgggtggaa 1260
gacaggcaag atctcaaccg gcagcggatc caacgtacg cacaggcctt ccacaccgg 1320
ggctctgagg atttgacaa agactcagtg gaaaaactag agctgggctg tcccttcagc 1380

```
<210> 765
<211> 1533
<212> DNA
<213> Homo sapiens
```

<400> 765						
atgtacaacc	tgttgctgtc	ctacgacaga	catggggacc	acctgcagcc	cctggacctc	60
gtgcccaatc	accagggtct	cacccctttc	aagctggctg	gagtggaggg	taacactgtg	120
atgtttcagc	acctgatgca	gaagcggaag	cacaccaggt	ggacgtatgg	accactgacc	180
tgcactctct	atgacctcac	agagatcgac	tcctcagggg	atgagcagtc	cctgctggaa	240
cttatcatca	ccaccaagaa	gcggggaggct	cgccagatcc	tggaccagac	gccggtgaag	300
gagctggtga	gcctcaagtg	gaagcgggtac	ggcgggccgt	acctctgcac	gctgggtgcc	360
atatattctg	tgtacatcat	ctgcttcacc	atgtgtctga	tctaccgccc	cctcaagccc	420
aggaccaata	accgcacgag	cccccgggac	aacacctctt	tacagcagaa	gctacttcag	480
gaagcctaca	tgacccctaa	ggacgatatc	cggctggctg	gggagctggg	gactgtcatt	540
ggggctatca	tcatcctgct	ggtagagggt	ccagacatct	tcagaatggg	gggtactcgc	600
ttctttggac	agaccatcct	tggggggcca	ttccatgtcc	tcacatcac	ctatgccttc	660
atggtgctgg	tgaccatggg	gatgcggctc	atcagtcca	gcggggaggt	ggtagccatg	720
tcctttgcac	tcgtgctggg	ctggtgcaac	gtcatgtact	tcgcccaggg	attccagatg	780
ctaggcccct	tcaccatcat	gattcagaag	atgatttttg	gcgacctgat	gcgattctgc	840
tggctgatgg	ctgtggtcat	cctgggcttc	gcttcagcct	tctatatcat	cttcacagaa	900
gaggaccctg	aggagctagg	ccacttctac	gactaaccca	tgcgctgtt	cgcaccttc	960
gagctgttcc	ttaccatcat	cgatggccca	gccaactaca	acgtggacct	gccttcatg	1020
tacagcatca	cctatgctgc	ctttgccatc	atcgccacac	tgtcatgct	caacctcctc	1080
attgccatga	tgggcgacac	tactggcgga	gtggcccatg	agcgggatga	gctgtggagg	1140
gccagattg	tggccaccac	ggtgatgctg	gagcggaagc	tgcctcgctg	cctgtggcct	1200
cgctccggga	tctgcggacg	ggagtatggc	ctgggagacc	gctggttcct	gcgggtgaa	1260
gacaggcaag	atctcaaccg	gcagcggatc	caacgctacg	cacaggcctt	ccacaccggg	1320
ggctctgagg	atttggaaca	agactcagtg	gaaaaactag	agctgggctg	tccttccagc	1380
ccccacctgt	cccttctcat	gccctcagtg	tctcgaagta	cctccgcag	cagtccaat	1440
tgggaagagc	ttcggcaagg	gcacctgagg	atagaccctg	gtgggataat	caacaggggg	1500
ctggaaggac	qqaagaagctg	qqaatatcaq	atc			1533

```
<210> 766
<211> 511
<212> PRT
<213> Homo sapiens
```

<400> 766
Met Tyr Asn Leu·Leu Leu Ser Tyr Asp Arg His Gly Asp His Leu Gln
 5 10 15

Pro Leu Asp Leu Val Pro Asn His Gln Gly Leu Thr Pro Phe Lys Leu
20 25 30

Ala Gly Val Glu Gly Asn Thr Val Met Phe Gln His Leu Met Gln Lys
35 40 45

Arg Lys His Thr Gln Trp Thr Tyr Gly Pro Leu Thr Ser Thr Leu Tyr
50 55 60

Asp Leu Thr Glu Ile Asp Ser Ser Gly Asp Glu Gln Ser Leu Leu Glu
65 70 75 80

Leu	Ile	Ile	Thr	Thr	Lys	Lys	Arg	Glu	Ala	Arg	Gln	Ile	Leu	Asp	Gln
				85						90				95	
Thr	Pro	Val	Lys	Glu	Leu	Val	Ser	Leu	Lys	Trp	Lys	Arg	Tyr	Gly	Arg
			100					105					110		
Pro	Tyr	Phe	Cys	Met	Leu	Gly	Ala	Ile	Tyr	Leu	Leu	Tyr	Ile	Ile	Cys
		115					120					125			
Phe	Thr	Met	Cys	Cys	Ile	Tyr	Arg	Pro	Leu	Lys	Pro	Arg	Thr	Asn	Asn
		130				135					140				
Arg	Thr	Ser	Pro	Arg	Asp	Asn	Thr	Leu	Leu	Gln	Gln	Lys	Leu	Leu	Gln
145					150					155					160
Glu	Ala	Tyr	Met	Thr	Pro	Lys	Asp	Asp	Ile	Arg	Leu	Val	Gly	Glu	Leu
				165					170					175	
Val	Thr	Val	Ile	Gly	Ala	Ile	Ile	Ile	Leu	Leu	Val	Glu	Val	Pro	Asp
			180					185					190		
Ile	Phe	Arg	Met	Gly	Val	Thr	Arg	Phe	Phe	Gly	Gln	Thr	Ile	Leu	Gly
		195					200					205			
Gly	Pro	Phe	His	Val	Leu	Ile	Ile	Thr	Tyr	Ala	Phe	Met	Val	Leu	Val
		210				215					220				
Thr	Met	Val	Met	Arg	Leu	Ile	Ser	Ala	Ser	Gly	Glu	Val	Val	Pro	Met
225					230					235					240
Ser	Phe	Ala	Leu	Val	Leu	Gly	Trp	Cys	Asn	Val	Met	Tyr	Phe	Ala	Arg
				245					250					255	
Gly	Phe	Gln	Met	Leu	Gly	Pro	Phe	Thr	Ile	Met	Ile	Gln	Lys	Met	Ile
			260					265					270		
Phe	Gly	Asp	Leu	Met	Arg	Phe	Cys	Trp	Leu	Met	Ala	Val	Val	Ile	Leu
		275					280					285			
Gly	Phe	Ala	Ser	Ala	Phe	Tyr	Ile	Ile	Phe	Gln	Thr	Glu	Asp	Pro	Glu
		290				295					300				
Glu	Leu	Gly	His	Phe	Tyr	Asp	Tyr	Pro	Met	Ala	Leu	Phe	Ser	Thr	Phe
305					310					315					320
Glu	Leu	Phe	Leu	Thr	Ile	Ile	Asp	Gly	Pro	Ala	Asn	Tyr	Asn	Val	Asp
				325					330					335	
Leu	Pro	Phe	Met	Tyr	Ser	Ile	Thr	Tyr	Ala	Ala	Phe	Ala	Ile	Ile	Ala
			340					345					350		
Thr	Leu	Leu	Met	Leu	Asn	Leu	Leu	Ile	Ala	Met	Met	Gly	Asp	Thr	His
			355				360					365			
Trp	Arg	Val	Ala	His	Glu	Arg	Asp	Glu	Leu	Trp	Arg	Ala	Gln	Ile	Val
						375					380				
Ala	Thr	Thr	Val	Met	Leu	Glu	Arg	Lys	Leu	Pro	Arg	Cys	Leu	Trp	Pro

385 390 395 400
 Arg Ser Gly Ile Cys Gly Arg Glu Tyr Gly Leu Gly Asp Arg Trp Phe
 405 410 415
 Leu Arg Val Glu Asp Arg Gln Asp Leu Asn Arg Gln Arg Ile Gln Arg
 420 425 430
 Tyr Ala Gln Ala Phe His Thr Arg Gly Ser Glu Asp Leu Asp Lys Asp
 435 440 445
 Ser Val Glu Lys Leu Glu Leu Gly Cys Pro Phe Ser Pro His Leu Ser
 450 455 460
 Leu Pro Met Pro Ser Val Ser Arg Ser Thr Ser Arg Ser Ser Ala Asn
 465 470 475 480
 Trp Glu Arg Leu Arg Gln Gly Thr Leu Arg Arg Asp Leu Arg Gly Ile
 485 490 495
 Ile Asn Arg Gly Leu Glu Asp Gly Glu Ser Trp Glu Tyr Gln Ile
 500 505 510

<210> 767

<211> 134

<212> PRT

<213> Homo sapiens

<400> 767

Met Tyr Asn Leu Leu Leu Ser Tyr Asp Arg His Gly Asp His Leu Gln
 5 10 15

Pro Leu Asp Leu Val Pro Asn His Gln Gly Leu Thr Pro Phe Lys Leu
 20 25 30

Ala Gly Val Glu Gly Asn Thr Val Met Phe Gln His Leu Met Gln Lys
 35 40 45

Arg Lys His Thr Gln Trp Thr Tyr Gly Pro Leu Thr Ser Thr Leu Tyr
 50 55 60

Asp Leu Thr Glu Ile Asp Ser Ser Gly Asp Glu Gln Ser Leu Leu Glu
 65 70 75 80

Leu Ile Ile Thr Thr Lys Lys Arg Glu Ala Arg Gln Ile Leu Asp Gln
 85 90 95

Thr Pro Val Lys Glu Leu Val Ser Leu Lys Trp Lys Arg Tyr Gly Arg
 100 105 110

Pro Tyr Phe Cys Met Leu Gly Ala Ile Tyr Leu Leu Tyr Ile Ile Cys
 115 120 125

Phe Thr Met Cys Cys Ile
 130

<210> 768
<211> 55
<212> PRT
<213> Homo sapiens

<400> 768
Ala Tyr Arg Pro Leu Lys Pro Arg Thr Asn Asn Arg Thr Ser Pro Arg
 5 10 15

Asp Asn Thr Leu Leu Gln Gln Lys Leu Leu Gln Glu Ala Tyr Met Thr
 20 25 30

Pro Lys Asp Asp Ile Arg Leu Val Gly Glu Leu Val Thr Val Ile Gly
 35 40 45

Ala Ile Ile Ile Leu Leu Val
 50 55

<210> 769
<211> 39
<212> PRT
<213> Homo sapiens

<400> 769
Glu Val Pro Asp Ile Phe Arg Met Gly Val Thr Arg Phe Phe Gly Gln
 5 10 15

Thr Ile Leu Gly Gly Pro Phe His Val Leu Ile Ile Thr Tyr Ala Phe
 20 25 30

Met Val Leu Val Thr Met Val
 35

<210> 770
<211> 19
<212> PRT
<213> Homo sapiens

<400> 770
Met Arg Leu Ile Ser Ala Ser Gly Glu Val Val Pro Met Ser Phe Ala
 5 10 15

Leu Val Leu

<210> 771
<211> 52
<212> PRT
<213> Homo sapiens

<400> 771
Gly Trp Cys Asn Val Met Tyr Phe Ala Arg Gly Phe Gln Met Leu Gly
 5 10 15

Pro Phe Thr Ile Met Ile Gln Lys Met Ile Phe Gly Asp Leu Met Arg

306

20 25 30
 Phe Cys Trp Leu Met Ala Val Val Ile Leu Gly Phe Ala Ser Ala Phe
 35 40 45
 Tyr Ile Ile Phe
 50
 <210> 772
 <211> 213
 <212> PRT
 <213> Homo sapiens
 <400> 772
 Gln Thr Glu Asp Pro Glu Glu Leu Gly His Phe Tyr Asp Tyr Pro Met
 5 10 15
 Ala Leu Phe Ser Thr Phe Glu Leu Phe Leu Thr Ile Ile Asp Gly Pro
 20 25 30
 Ala Asn Tyr Asn Val Asp Leu Pro Phe Met Tyr Ser Ile Thr Tyr Ala
 35 40 45
 Ala Phe Ala Ile Ile Ala Thr Leu Leu Met Leu Asn Leu Leu Ile Ala
 50 55 60
 Met Met Gly Asp Thr His Trp Arg Val Ala His Glu Arg Asp Glu Leu
 65 70 75 80
 Trp Arg Ala Gln Ile Val Ala Thr Thr Val Met Leu Glu Arg Lys Leu
 85 90 95
 Pro Arg Cys Leu Trp Pro Arg Ser Gly Ile Cys Gly Arg Glu Tyr Gly
 100 105 110
 Leu Gly Asp Arg Trp Phe Leu Arg Val Glu Asp Arg Gln Asp Leu Asn
 115 120 125
 Arg Gln Arg Ile Gln Arg Tyr Ala Gln Ala Phe His Thr Arg Gly Ser
 130 135 140
 Glu Asp Leu Asp Lys Asp Ser Val Glu Lys Leu Glu Leu Gly Cys Pro
 145 150 155 160
 Phe Ser Pro His Leu Ser Leu Pro Met Pro Ser Val Ser Arg Ser Thr
 165 170 175
 Ser Arg Ser Ser Ala Asn Trp Glu Arg Leu Arg Gln Gly Thr Leu Arg
 180 185 190
 Arg Asp Leu Arg Gly Ile Ile Asn Arg Gly Leu Glu Asp Gly Glu Ser
 195 200 205
 Trp Glu Tyr Gln Ile
 210

<210> 773
 <211> 1302
 <212> DNA
 <213> Homo sapiens

<400> 773
 tggacaaaagg ggggtcacaca ttccttccat acgggtgagc ctctacctgc ctggtgctgg 60
 tcacagttca gcttcttcat gatggtggat cccaatggca atgaatccag tgctacatac 120
 ttcattcctaa taggcctccc tggtttagaa gaggtcagc tctggttggc ctccccattg 180
 tgctccctct acctattgc tgtgctaggt aacttgacaa tcatctacat tgtgcggact 240
 gagcacagcc tgcattgagcc catgtatata tttctttgca tgccttcagg cattgacatc 300
 ctcatctcca cctcatccat gcccaaaatg ctggccatct tctggttcaa ttccactacc 360
 atccagtttg atgcttgtct gctacagatg tttgccatcc actccttacc tggcatggaa 420
 tccacagtgc tgcctggccat ggcttttgac cgctatgtgg ccatctgtca cccactgcgc 480
 catgccacag tacttacgtt gcctcgtgtc accaaaattg gtgtggctgc tgtggtgcgg 540
 ggggctgcac tgatggcacc ccttctgtgc ttcattcaagc agctgccctt ctgccgctcc 600
 aatatacctt cccattccta ctgcctacac caagatgtca tgaagctggc ctgtgatgat 660
 atocgggtca atgtcgtcta tggccttacc gtcatcatct ccgccattgg cctggactca 720
 cttctcatct ctttctcata tctgcttatt cttaagactg tgttgggctt gacacgtgaa 780
 gccaggcca aggcatttgg cacttgcgtc tctcatgtgt gtgctgtgtt catattctat 840
 gtacctttca ttggattgtc catggtgcat cgcttagca agcggcgtga ctctccgctg 900
 ccgctcatct tggccaatat ctatctgtgt gttcctcctg tgcacaacc aattgtctat 960
 ggagtgaaga caaaggagat tcgacagcgc atccttcgac ttttccatgt ggccacacac 1020
 gcttcagagc cctaggtgtc agtgatcaaa cttcttttcc attcagagtc ctctgattca 1080
 gatttttaag ttaacatttt ggaagacagt attcagaaaa aaaatttccct taataaaaaat 1140
 acaactcaga tcottcaaat atgaaactgg ttggggaatc tccatttttt caatattatt 1200
 ttcttctttg ttttcttgc tcatataatt attaatatccc tgactaggtt gtggtttgag 1260
 gggtattact tttcatttta ccattgcagtc caaatctaaa ct 1302

<210> 774
 <211> 2061
 <212> DNA
 <213> Homo sapiens

<400> 774
 acgattcgac agcgcattct tcgacttttc catgtggcca cacacgcttc agagccctag 60
 gtgtcagtgat tcaaaacttct tttccattca gattcctctg attcagattt taatgttaac 120
 attttggaag acagtattca gaaaaaaat ttccttaata aaaatacaac tcagatcctt 180
 caaatatgaa actggttggg gaattctccat tttttcaata ttattttctt ctttgttttc 240
 ttgtacata taattattaa taccctgact aggttgtggt tggaggggta ttacttttca 300
 ttttaccatg cagtccaaat cttaaactgct tctactgatg gtttacagca ttctgagata 360
 agaatggtac atctagagaa catttgccaa aggcctaagc acggcaaagg aaaataaaca 420
 cagaatataa taaaatgaga taatctagct taaaactata acttcctctt cagaactccc 480
 aaccacattg gatctcagaa aaatgctgtc ttcaaaatga cttctacaga gaagaaataa 540
 tttttcctct ggacactagc acttaagggg aagattggaa gtaaaagcctt gaaaagagta 600
 catttaccta cgttaatgaa agttgacaca ctgttctgag agttttcaca gcatatggac 660
 cctgtttttc ctatttaatt ttcttatcaa ccctttaatt aggcacagat attattagta 720
 ccctcattgt agccatggga aaattgatgt tcagtgggga tcagtgaatt aaatggggtc 780
 atacaagtat aaaaaataaa aaaaaaggac ttcatgcccc atctcatatg atgtggaaga 840
 actgttagag agaccaacag ggtagtgggt tagagatttc cagagtctta cattttctag 900
 aggaggtatt taattttctt tcaactcatcc agtgtgtgat ttaggaattt cctggcaaca 960
 gaactcatgg ctttaattccc actagctatt gcttattgtc ctggtccaat tgccaattac 1020
 ctgtgtcttg gaagaagtga tttctaggtt caccattatg gaagattctt attcagaaag 1080
 tctgcatagg gcttatagca agttatttat ttttaaaagt tccatagggtg attctgatag 1140
 gcagtgaggt tagggagcca ccagttatga tgggaagtat ggaatggcag gtcttgaaga 1200
 taacattggc cttttgagtg tgactcgtag ctggaaagtg agggaaatct caggaccatg 1260
 ctttatttgg ggctttgtgc agtatggaac agggactttg agaccaggaa agcaatctga 1320


```

cttaggcatg ggaatcaggc atttttgctt ctgaggggct attaccaagg gttaataggt 1380
ttcatcttca acaggatatg acaacagtgt taaccaagaa actcaaatta caaatactaa 1440
aacatgtgat catatatgtg gtaagtttca ttttctttt caatcctcag gttccctgat 1500
atggattcct ataacatgct ttcatccctt tttgtaatgg atatcatatt tggaaatgcc 1560
tatttaatac ttgtatttgc tgctggactg taagcccatg agggcactgt ttattattga 1620
atgtcatctc tgttcatcat tgactgctct ttgctcatca ttgaatcccc cagcaaaagt 1680
cctagaacat aatagtgtt atgcttgaca ccggttattt ttcatcaaac ctgattcctt 1740
ctgtcctgaa cacatagcca ggcaattttc cagccttctt tgagttgggt attattaaat 1800
tctggccatt acttccaatg tgagtggaag tgacatgtgc aatttctata cctggctcat 1860
aaaaccctcc catgtgcagc ctttcatgtt gacattaaat gtgacttggg aagctatgtg 1920
ttacacagag taaatcacca gaagcctgga tttctgaaaa aactgtgcag agccaaacct 1980
ctgtcatttg caactccac ttgtatttgt acgaggcagt tggataagtg aaaaataaag 2040
tactattgtg tcaagtctct g

```

<210> 775

<211> 957

<212> DNA

<213> Homo sapiens

<400> 775

```

atgatggtgg atcccaatgg caatgaatcc agtgctacat acttcatcct aataggcctc 60
cctgggtttag aagaggctca gttctggttg gccttcccat tgtgctccct ctaccttatt 120
gctgtgctag gtaacttgac aatcatctac attgtgcgga ctgagcacag cctgcatgag 180
cccattgata tatttctttg catgctttca ggcattgaca tctcatctc cacctcatcc 240
atgccccaaa tgctggccat cttctggttc aattccacta ccatccagtt tgatgcttgt 300
ctgctacaga tgtttgccat ccactcctta tctggcatgg aatccacagt gctgctggcc 360
atggcttttg accgctatgt ggccatctgt caccactgc gccatgccac agtacttacg 420
ttgctcgtg tcacaaaaat tgggtgtggt gctgtggtgc ggggggctgc actgatggca 480
ccccttctg tcttcatcaa gcagctgccc ttctgccgct ccaatatcct ttccattcc 540
tactgcctac accaagatgt catgaagctg gcctgtgatg atatccgggt caatgtcgtc 600
tatggcctta tcgtcatcat ctccgccatt ggccctggact cacttctcat ctcttctca 660
tatctgctta ttcttaagac tgtgttgggc ttgacacgtg aagcccaggc caaggcattt 720
ggcacttgcg tctctcatgt gtgtgctgtg ttcatattct atgtacctt cattggattg 780
tccatggtgc atcgcttttag caagcggcgt gactctccgc tgcccgtcat cttggccaat 840
atctatctgc tggttcctcc tgtgtctaac ccaattgtct atggagtga gacaaaggag 900
atcgcacagc gcctccttcg acttttccat gtggccacac acgcttcaga gccctag 957

```

<210> 776

<211> 954

<212> DNA

<213> Homo sapiens

<400> 776

```

atgatggtgg atcccaatgg caatgaatcc agtgctacat acttcatcct aataggcctc 60
cctgggtttag aagaggctca gttctggttg gccttcccat tgtgctccct ctaccttatt 120
gctgtgctag gtaacttgac aatcatctac attgtgcgga ctgagcacag cctgcatgag 180
cccattgata tatttctttg catgctttca ggcattgaca tctcatctc cacctcatcc 240
atgccccaaa tgctggccat cttctggttc aattccacta ccatccagtt tgatgcttgt 300
ctgctacaga tgtttgccat ccactcctta tctggcatgg aatccacagt gctgctggcc 360
atggcttttg accgctatgt ggccatctgt caccactgc gccatgccac agtacttacg 420
ttgctcgtg tcacaaaaat tgggtgtggt gctgtggtgc ggggggctgc actgatggca 480
ccccttctg tcttcatcaa gcagctgccc ttctgccgct ccaatatcct ttccattcc 540
tactgcctac accaagatgt catgaagctg gcctgtgatg atatccgggt caatgtcgtc 600
tatggcctta tcgtcatcat ctccgccatt ggccctggact cacttctcat ctcttctca 660
tatctgctta ttcttaagac tgtgttgggc ttgacacgtg aagcccaggc caaggcattt 720
ggcacttgcg tctctcatgt gtgtgctgtg ttcatattct atgtacctt cattggattg 780
tccatggtgc atcgcttttag caagcggcgt gactctccgc tgcccgtcat cttggccaat 840

```

atctatctgc tggttcctcc tgtgctcaac ccaattgtct atggagtga gacaaaggag 900
 attcgacagc gcatacttcg acttttccat gtggccacac acgcttcaga gccc 954

<210> 777

<211> 318

<212> PRT

<213> Homo sapiens

<400> 777

Met	Met	Val	Asp	Pro	Asn	Gly	Asn	Glu	Ser	Ser	Ala	Thr	Tyr	Phe	Ile	5	10	15
Leu	Ile	Gly	Leu	Pro	Gly	Leu	Glu	Glu	Ala	Gln	Phe	Trp	Leu	Ala	Phe	20	25	30
Pro	Leu	Cys	Ser	Leu	Tyr	Leu	Ile	Ala	Val	Leu	Gly	Asn	Leu	Thr	Ile	35	40	45
Ile	Tyr	Ile	Val	Arg	Thr	Glu	His	Ser	Leu	His	Glu	Pro	Met	Tyr	Ile	50	55	60
Phe	Leu	Cys	Met	Leu	Ser	Gly	Ile	Asp	Ile	Leu	Ile	Ser	Thr	Ser	Ser	65	70	75
Met	Pro	Lys	Met	Leu	Ala	Ile	Phe	Trp	Phe	Asn	Ser	Thr	Thr	Ile	Gln	85	90	95
Phe	Asp	Ala	Cys	Leu	Leu	Gln	Met	Phe	Ala	Ile	His	Ser	Leu	Ser	Gly	100	105	110
Met	Glu	Ser	Thr	Val	Leu	Leu	Ala	Met	Ala	Phe	Asp	Arg	Tyr	Val	Ala	115	120	125
Ile	Cys	His	Pro	Leu	Arg	His	Ala	Thr	Val	Leu	Thr	Leu	Pro	Arg	Val	130	135	140
Thr	Lys	Ile	Gly	Val	Ala	Ala	Val	Val	Arg	Gly	Ala	Ala	Leu	Met	Ala	145	150	155
Pro	Leu	Pro	Val	Phe	Ile	Lys	Gln	Leu	Pro	Phe	Cys	Arg	Ser	Asn	Ile	165	170	175
Leu	Ser	His	Ser	Tyr	Cys	Leu	His	Gln	Asp	Val	Met	Lys	Leu	Ala	Cys	180	185	190
Asp	Asp	Ile	Arg	Val	Asn	Val	Val	Tyr	Gly	Leu	Ile	Val	Ile	Ile	Ser	195	200	205
Ala	Ile	Gly	Leu	Asp	Ser	Leu	Leu	Ile	Ser	Phe	Ser	Tyr	Leu	Leu	Ile	210	215	220
Leu	Lys	Thr	Val	Leu	Gly	Leu	Thr	Arg	Glu	Ala	Gln	Ala	Lys	Ala	Phe	225	230	235
Gly	Thr	Cys	Val	Ser	His	Val	Cys	Ala	Val	Phe	Ile	Phe	Tyr	Val	Pro	245	250	255

310

Phe Ile Gly Leu Ser Met Val His Arg Phe Ser Lys Arg Arg Asp Ser
 260 265 270

Pro Leu Pro Val Ile Leu Ala Asn Ile Tyr Leu Leu Val Pro Pro Val
 275 280 285

Leu Asn Pro Ile Val Tyr Gly Val Lys Thr Lys Glu Ile Arg Gln Arg
 290 295 300

Ile Leu Arg Leu Phe His Val Ala Thr His Ala Ser Glu Pro
 305 310 315

<210> 778

<211> 28

<212> PRT

<213> Homo sapiens

<400> 778

Met Met Val Asp Pro Asn Gly Asn Glu Ser Ser Ala Thr Tyr Phe Ile
 5 10 15

Leu Ile Gly Leu Pro Gly Leu Glu Glu Ala Gln Phe
 20 25

<210> 779

<211> 9

<212> PRT

<213> Homo sapiens

<400> 779

Arg Thr Glu His Ser Leu His Glu Pro
 5

<210> 780

<211> 21

<212> PRT

<213> Homo sapiens

<400> 780

Lys Met Leu Ala Ile Phe Trp Phe Asn Ser Thr Thr Ile Gln Phe Asp
 5 10 15

Ala Cys Leu Leu Gln
 20

<210> 781

<211> 20

<212> PRT

<213> Homo sapiens

<400> 781

Asp Arg Tyr Val Ala Ile Cys His Pro Leu Arg His Ala Thr Val Leu
 5 10 15

311

Thr Leu Pro Arg
20

<210> 782
<211> 37
<212> PRT
<213> Homo sapiens

<400> 782
Phe Ile Lys Gln Leu Pro Phe Cys Arg Ser Asn Ile Leu Ser His Ser
5 10 15

Tyr Cys Leu His Gln Asp Val Met Lys Leu Ala Cys Asp Asp Ile Arg
20 25 30

Val Asn Val Val Tyr
35

<210> 783
<211> 13
<212> PRT
<213> Homo sapiens

<400> 783
Lys Thr Val Leu Gly Leu Thr Arg Glu Ala Gln Ala Lys
5 10

<210> 784
<211> 10
<212> PRT
<213> Homo sapiens

<400> 784
Val His Arg Phe Ser Lys Arg Arg Asp Ser
5 10

<210> 785
<211> 22
<212> PRT
<213> Homo sapiens

<400> 785
Lys Thr Lys Glu Ile Arg Gln Arg Ile Leu Arg Leu Phe His Val Ala
5 10 15

Thr His Ala Ser Glu Pro
20

<210> 786
<211> 3245
<212> DNA
<213> Homo sapiens

<400> 786

gtcgaccac	gcgtccgcgc	gagctaagca	ggaggcggag	gcggaggcgg	agggcgaggg	60
gcggggagcg	ccgcctggag	cgcggcagg	catattgaac	attccagata	cctatcatta	120
ctcgatgctg	ttgataacag	caagatggct	ttgaactcag	ggtcaccacc	agctattgga	180
ccttactatg	aaaaccatgg	ataccaaccg	gaaaaccocct	atcccgcaca	gcccactgtg	240
gtccccactg	tctacgaggt	gcatccggct	cagtactacc	cgtccccgt	gccccagtag	300
gccccgaggg	tcctgacgca	ggcttccaac	cccgtcgtct	gcacgcagcc	caaataccca	360
tccgggacag	tgtgcacctc	aaagactaag	aaagcactgt	gcatcacctt	gaccttggg	420
accttcctcg	tgggagctgc	gctggccgct	ggcctactct	ggaagtccat	gggcagcaag	480
tgetccaact	ctgggataga	gtgcgactcc	tcaggtagct	gcatcaaccc	ctctaactgg	540
tgtgatggcg	tgtcacactg	ccccggcggg	gaggacgaga	atcgggtgtg	tcgcctctac	600
ggatcaaact	tcatecttca	ggtgtactca	tctcagagga	agtcctggca	ccctgtgtgc	660
caagacgact	ggaacgagaa	ctacggcg	gcggcctgca	gggacatggg	ctataagaat	720
aatttttact	ctagccaagg	aatagtggat	gacagcggat	ccaccagctt	tatgaaactg	780
aacacaagtg	ccggcaatgt	cgatatctat	aaaaaactgt	accacagtga	tgctgtttct	840
tcaaaagcag	tggtttcttt	acgctgtata	gcctgcgggg	tcaacttgaa	ctcaagccgc	900
cagagcagga	ttgtggcg	cgagagcgcg	ctcccggggg	cctggccctg	gcaggtcagc	960
ctgcacgtcc	agaacgtcca	cgtgtgcgga	ggctccatca	tcacccccga	gtggatcgtg	1020
acagccgccc	actgctgga	aaaacctctt	aacaatccat	ggcattggac	ggcatttgcc	1080
gggattttga	gacaatcttt	catgttctat	ggagccggat	accaagtaga	aaaagtgtat	1140
tctcatccaa	attatgactc	caagaccaag	aacaatgaca	ttgcgctgat	gaagctgcag	1200
aagcctctga	ctttcaacga	cctagtga	ccagtgtgtc	tgcccaacc	aggcatgatg	1260
ctgcagccag	aacagctctg	ctggatttcc	gggtggggg	ccaccgagga	gaaagggag	1320
acctcagaag	tgctgaacgc	tgccaaggtg	cttctcattg	agacacagag	atgcaacagc	1380
agatatgtct	atgacaacct	gatcacacca	gccatgatct	gtgccggctt	cctgcagggg	1440
aacgtcgatt	cttgccaggg	tgacagtgga	gggcctctgg	tcacttcgaa	gaacaatatc	1500
tgggtggctga	taggggatac	aagctgggg	tctggctgtg	ccaaagctta	cagaccagga	1560
gtgtacggag	attgatgg	attcacggac	tggatttata	gacaaatgag	ggcagacggc	1620
taatccacat	gggtctctgc	cttgacgtcg	ttttacaaga	aaacaatggg	gctgggtttg	1680
cttccccgtg	catgatttac	tcttagagat	gattcagagg	tcacttcatt	tttattaaac	1740
agtgaacttg	tctggctttg	gcactctctg	ccattctgtg	caggctgcag	tggtctccct	1800
gcccagcctg	ctctccctaa	ccccttgtcc	gcaaggggtg	atggccggct	ggttgtgggc	1860
actggcggtc	aagtgtggag	gagaggggtg	gaggctgccc	cattgagatc	ttcctgctga	1920
gtcctttcca	ggggccaatt	ttggatgagc	atggagctgt	cacctctcag	ctgctggagt	1980
aatttgagag	aaaaaggaga	gacatggaaa	gggagacagc	caggtggcac	ctgcagcggc	2040
tgccctctgg	ggccacttgg	tagtgtcccc	agcctacctc	tccacaaggg	gattttgctg	2100
atgggttctt	agagccttag	cagccctgga	tggtggccag	aaataaagg	accagccctt	2160
catgggtgg	gacgtggtag	tcacttgtaa	ggggaacaga	aacatTTTTg	ttcttatggg	2220
gtgagaatat	agacagtgcc	cttgggtcga	gggaagcaat	tgaaaaggaa	cttgccctga	2280
gcactcctgg	tgcaggtctc	cacctgcaca	ttgggtgggg	ctcctgggag	ggagactcag	2340
ccttctctct	catctctcct	gacctgctc	ctagcaccct	ggagagtgc	catgcccctt	2400
ggtcctggca	ggcgccaag	tctggcacca	tggtggcctc	ttcaggcctg	ctagtcaactg	2460
gaaattgagg	tccatggggg	aaatcaagga	tgctcagttt	aaggtacact	gtttccatgt	2520
tatgtttcta	cacattgcta	cctcagtgtc	cctggaaact	tagcttttga	tgtctccaag	2580
tagtccacct	tcatttaact	ctttgaaact	gtatcatctt	tgccaagtaa	gagtgggtggc	2640
ctatttcagc	tgttttgaca	aaatgactgg	ctcctgactt	aacgttctat	aaatgaatgt	2700
gctgaagcaa	agtgcccatg	gtggcggcga	agaagagaaa	gatgtgtttt	gttttgact	2760
ctctgtggtc	ccttccaatg	ctgtgggttt	ccaaccaggg	gaagggtccc	ttttgcattg	2820
ccaagtggca	taaccatgag	cactactcta	ccatggttct	gcctcctggc	caagcaggct	2880
ggtttgcaag	aatgaaatga	atgattctac	agctaggact	taaccttgaa	atggaaagtc	2940
ttgcaatccc	atttgacgga	tccgtctgtg	cacatgcctc	tgtagagagc	agcattccca	3000
gggaccttgg	aaacagttgg	cactgtaagg	tgcttgcctc	ccaagacaca	tcctaaaagg	3060
tgttgtaatg	gtgaaaacgt	cttctctctt	tattgcccct	tcttatttat	gtgaacaact	3120
gtttgtcttt	ttttgtatct	tttttaact	gtaaaagttca	attgtgaaaa	tgaatatcat	3180
gcaaataaat	tatgcgattt	ttttttcaaa	gtaaaaaaa	aaaaaaaaa	aaaaagggcg	3240
gccgc						3245

<210> 787
 <211> 1479
 <212> DNA
 <213> Homo sapiens

<400> 787
 atggctttga actcagggtc accaccagct attggacctt actatgaaaa ccatggatac 60
 caaccggaaa acccctatcc cgcacagccc actgtggtcc ccactgtcta cgagggtgcat 120
 ccggtcagc actaccgctc ccccggtgcc cagtacgccc cgagggtcct gacgcaggct 180
 tccaaccccg tcgtctgcac gcagcccaaa tccccatccg ggacagtgtg cacctcaaaag 240
 actaagaaag cactgtgcat caccttgacc ctggggacct tcctcgtggg agctgcgctg 300
 gccgtggcc tactctggaa gttcatgggc agcaagtgtc ccaactctgg gatagagtgc 360
 gactcctcag gtacctgcat caaccctct aactggtgtg atggcgtgtc aactgcccc 420
 ggcggggagg acgagaatcg gtgtgttcgc ctctacggat caaacttcat ccttcagggtg 480
 tactcatctc agaggaaagc ctggcaccct gtgtgccaag acgactggaa cgagaactac 540
 gggcgggcgg cctgcaggga catgggctat aagaataatt ttactctag ccaaggaata 600
 gtggatgaca gcggatccac cagctttatg aaactgaaca caagtgcgg caatgtcgat 660
 atctataaaa aactgtacca cagtgtgcc tgttcttcaa aagcagtggg ttctttacgc 720
 tgtatagcct gcggggtcaa cttgaactca agccgccaga gcaggattgt gggcggcgag 780
 agcgcgctcc cgggggcctg gccctggcag gtcagcctgc acgtccagaa cgtccacgtg 840
 tgcgagggtc ccatcatcac ccccgagtgg atcgtgacag ccgcccactg cgtggaaaaa 900
 cctcttaaca atccatggca ttggacggca tttgcgggga ttttgagaca atctttcatg 960
 ttctatggag ccggatacca agtagaaaaa gtgatttctc atccaaatta tgactccaag 1020
 accaagaaca atgacattgc gctgatgaag ctgcagaagc ctctgacttt caacgacctg 1080
 gtgaaaccag tgtgtctgcc caaccagggc atgatgctgc agccagaaca gctctgctgg 1140
 atttcggggt ggggggcccac cgaggagaaa ggggaagacct cagaagtgtc gaacgctgcc 1200
 aaggtgcttc tcattgagac acagagatgc aacagcagat atgtctatga caacctgatc 1260
 acaccagcca tgatctgtgc cggcttcctg caggggaaacg tcgattcttg ccagggtgac 1320
 agtggagggc ctctggtcac ttcaagaac aatatctggt ggctgatagg ggatacaagc 1380
 tggggttctg gctgtgccaa agcttacaga ccaggagtgt acgggaatgt gatggtattc 1440
 acggactgga tttatcgaca aatgagggca gacggctaa 1479

<210> 788
 <211> 1476
 <212> DNA
 <213> Homo sapiens

<400> 788
 atggctttga actcagggtc accaccagct attggacctt actatgaaaa ccatggatac 60
 caaccggaaa acccctatcc cgcacagccc actgtggtcc ccactgtcta cgagggtgcat 120
 ccggtcagc actaccgctc ccccggtgcc cagtacgccc cgagggtcct gacgcaggct 180
 tccaaccccg tcgtctgcac gcagcccaaa tccccatccg ggacagtgtg cacctcaaaag 240
 actaagaaag cactgtgcat caccttgacc ctggggacct tcctcgtggg agctgcgctg 300
 gccgtggcc tactctggaa gttcatgggc agcaagtgtc ccaactctgg gatagagtgc 360
 gactcctcag gtacctgcat caaccctct aactggtgtg atggcgtgtc aactgcccc 420
 ggcggggagg acgagaatcg gtgtgttcgc ctctacggat caaacttcat ccttcagggtg 480
 tactcatctc agaggaaagc ctggcaccct gtgtgccaag acgactggaa cgagaactac 540
 gggcgggcgg cctgcaggga catgggctat aagaataatt ttactctag ccaaggaata 600
 gtggatgaca gcggatccac cagctttatg aaactgaaca caagtgcgg caatgtcgat 660
 atctataaaa aactgtacca cagtgtgcc tgttcttcaa aagcagtggg ttctttacgc 720
 tgtatagcct gcggggtcaa cttgaactca agccgccaga gcaggattgt gggcggcgag 780
 agcgcgctcc cgggggcctg gccctggcag gtcagcctgc acgtccagaa cgtccacgtg 840
 tgcgagggtc ccatcatcac ccccgagtgg atcgtgacag ccgcccactg cgtggaaaaa 900
 cctcttaaca atccatggca ttggacggca tttgcgggga ttttgagaca atctttcatg 960
 ttctatggag ccggatacca agtagaaaaa gtgatttctc atccaaatta tgactccaag 1020
 accaagaaca atgacattgc gctgatgaag ctgcagaagc ctctgacttt caacgacctg 1080
 gtgaaaccag tgtgtctgcc caaccagggc atgatgctgc agccagaaca gctctgctgg 1140

atttccgggt gggggggccac cgaggagaaa gggaagacct cagaagtgtt gaacgtgtcc 1200
 aaggtgcttc tcattgagac acagagatgc aacagcagat atgtctatga caacctgac 1260
 acaccagcca tgatctgtgc cggcttcctg caggggaacg tcgattcttg ccagggtgac 1320
 agtggagggc ctctggtcac ttcgaagaac aatatctggt ggctgatagg ggatacaagc 1380
 tggggttctg gctgtgcca agcttacaga ccaggagtgt acgggaatgt gatggtattc 1440
 acggactgga tttatcgaca aatgagggca gacggc 1476

<210> 789

<211> 492

<212> PRT

<213> Homo sapiens

<400> 789

Met	Ala	Leu	Asn	Ser	Gly	Ser	Pro	Pro	Ala	Ile	Gly	Pro	Tyr	Tyr	Glu	5	10	15
Asn	His	Gly	Tyr	Gln	Pro	Glu	Asn	Pro	Tyr	Pro	Ala	Gln	Pro	Thr	Val	20	25	30
Val	Pro	Thr	Val	Tyr	Glu	Val	His	Pro	Ala	Gln	Tyr	Tyr	Pro	Ser	Pro	35	40	45
Val	Pro	Gln	Tyr	Ala	Pro	Arg	Val	Leu	Thr	Gln	Ala	Ser	Asn	Pro	Val	50	55	60
Val	Cys	Thr	Gln	Pro	Lys	Ser	Pro	Ser	Gly	Thr	Val	Cys	Thr	Ser	Lys	65	70	75
Thr	Lys	Lys	Ala	Leu	Cys	Ile	Thr	Leu	Thr	Leu	Gly	Thr	Phe	Leu	Val	85	90	95
Gly	Ala	Ala	Leu	Ala	Ala	Gly	Leu	Leu	Trp	Lys	Phe	Met	Gly	Ser	Lys	100	105	110
Cys	Ser	Asn	Ser	Gly	Ile	Glu	Cys	Asp	Ser	Ser	Gly	Thr	Cys	Ile	Asn	115	120	125
Pro	Ser	Asp	Trp	Cys	Asp	Gly	Val	Ser	His	Cys	Pro	Gly	Gly	Glu	Asp	130	135	140
Glu	Asn	Arg	Cys	Val	Arg	Leu	Tyr	Gly	Ser	Asn	Phe	Ile	Leu	Gln	Val	145	150	155
Tyr	Ser	Ser	Gln	Arg	Lys	Ser	Trp	His	Pro	Val	Cys	Gln	Asp	Asp	Trp	165	170	175
Asn	Glu	Asn	Tyr	Gly	Arg	Ala	Ala	Cys	Arg	Asp	Met	Gly	Tyr	Lys	Asn	180	185	190
Asn	Phe	Tyr	Ser	Ser	Gln	Gly	Ile	Val	Asp	Asp	Ser	Gly	Ser	Thr	Ser	195	200	205
Phe	Met	Lys	Leu	Asn	Thr	Ser	Ala	Gly	Asn	Val	Asp	Ile	Tyr	Lys	Lys	210	215	220
Leu	Tyr	His	Ser	Asp	Ala	Cys	Ser	Ser	Lys	Ala	Val	Val	Ser	Leu	Arg	225	230	235
Cys	Ile	Ala	Cys	Gly	Val	Asn	Leu	Asn	Ser	Ser	Arg	Gln	Ser	Arg	Ile	245	250	255
Val	Gly	Gly	Glu	Ser	Ala	Leu	Pro	Gly	Ala	Trp	Pro	Trp	Gln	Val	Ser	260	265	270
Leu	His	Val	Gln	Asn	Val	His	Val	Cys	Gly	Gly	Ser	Ile	Ile	Thr	Pro	275	280	285
Glu	Trp	Ile	Val	Thr	Ala	Ala	His	Cys	Val	Glu	Lys	Pro	Leu	Asn	Asn	290	295	300
Pro	Trp	His	Trp	Thr	Ala	Phe	Ala	Gly	Ile	Leu	Arg	Gln	Ser	Phe	Met	305	310	315
Phe	Tyr	Gly	Ala	Gly	Tyr	Gln	Val	Glu	Lys	Val	Ile	Ser	His	Pro	Asn	325	330	335
Tyr	Asp	Ser	Lys	Thr	Lys	Asn	Asn	Asp	Ile	Ala	Leu	Met	Lys	Leu	Gln	340	345	350

```
<210> 790
<211> 100
<212> PRT
<213> Homo sapiens
```

<400> 790

[illegible]

```
<210> 791
<211> 393
<212> PRT
<213> Homo sapiens
```

<400> 791

Leu	Ala	Ala	Gly	Leu	Leu	Trp	Lys	Phe	Met	Gly	Ser	Lys	Cys	Ser	Asn
				5					10					15	
Ser	Gly	Ile	Glu	Cys	Asp	Ser	Ser	Gly	Thr	Cys	Ile	Asn	Pro	Ser	Asn
			20					25					30		
Trp	Cys	Asp	Gly	Val	Ser	His	Cys	Pro	Gly	Gly	Glu	Asp	Glu	Asn	Arg
		35				40						45			
Cys	Val	Arg	Leu	Tyr	Gly	Ser	Asn	Phe	Ile	Leu	Gln	Val	Tyr	Ser	Ser
	50					55					60				
Gln	Arg	Lys	Ser	Trp	His	Pro	Val	Cys	Gln	Asp	Trp	Asn	Glu	Asn	
65					70					75				80	


```
<210> 792
<211> 595
<212> PRT
<213> Homo sapiens
```

```

<400> 792
Met Ser Phe Leu Asn Phe Thr Ala Val Leu Phe Ala Ala Ser Ser Ala
 1          5          10          15
Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln Ile
          20          25          30
Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe Asp
          35          40          45
Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu Phe
          50          55          60
Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val Ser
65          70          75          80

```

Leu Glu Lys Arg Glu Ala Glu Ala Met Val Leu Gly Ile Gly Pro Val
 85 90 95
 Leu Gly Leu Val Cys Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp
 100 105 110
 Arg Gly Arg Tyr Gly Arg Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu
 115 120 125
 Gly Ile Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala
 130 135 140
 Gly Leu Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu Ala Leu Leu Ile
 145 150 155 160
 Leu Gly Val Gly Leu Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro
 165 170 175
 Leu Glu Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg
 180 185 190
 Gln Ala Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu
 195 200 205
 Gly Tyr Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro
 210 215 220
 Tyr Leu Gly Thr Gln Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile
 225 230 235 240
 Phe Leu Thr Cys Val Ala Ala Thr Leu Leu Val Ala Glu Glu Ala Ala
 245 250 255
 Leu Gly Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala Pro Ser Leu Ser
 260 265 270
 Pro His Cys Cys Pro Cys Arg Ala Arg Leu Ala Phe Arg Asn Leu Gly
 275 280 285
 Ala Leu Leu Pro Arg Leu His Gln Leu Cys Cys Arg Met Pro Arg Thr
 290 295 300
 Leu Arg Arg Leu Phe Val Ala Glu Leu Cys Ser Trp Met Ala Leu Met
 305 310 315 320
 Thr Phe Thr Leu Phe Tyr Thr Asp Phe Val Gly Glu Gly Leu Tyr Gln
 325 330 335
 Gly Val Pro Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp
 340 345 350
 Glu Gly Val Arg Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile
 355 360 365
 Ser Leu Val Phe Ser Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly
 370 375 380
 Thr Arg Ala Val Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala
 385 390 395 400
 Gly Ala Thr Cys Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala
 405 410 415
 Ala Leu Thr Gly Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr
 420 425 430
 Leu Ala Ser Leu Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr
 435 440 445
 Arg Gly Asp Thr Gly Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser
 450 455 460
 Phe Leu Pro Gly Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val
 465 470 475 480
 Gly Ala Gly Gly Ser Gly Leu Leu Pro Pro Pro Pro Ala Leu Cys Gly
 485 490 495
 Ala Ser Ala Cys Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr
 500 505 510
 Glu Ala Arg Val Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile
 515 520 525
 Leu Asp Ser Ala Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met
 530 535 540

[illegible]